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(54) **DESIGNER CALVIN-CYCLE-CHANNELED AND HYDROGENOTROPHIC PRODUCTION OF BUTANOL AND RELATED HIGHER ALCOHOLS**

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§ 371 (c)(1),
(2), (4) Date: **Jun. 22, 2013**

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(52) **U.S. Cl.**
CPC ***C12P 7/16*** (2013.01)
USPC **435/160**; 435/157

(57) **ABSTRACT**

Designer Calvin-cycle-channeled and hydrogenotrophic biofuel-production pathways, the associated designer genes and designer transgenic organisms for autotrophic production of butanol and related higher alcohols from carbon dioxide, hydrogen, and/or water are provided. The butanol and related higher alcohols include 1-butanol, 2-methyl-1-butanol, isobutanol, 3-methyl-1-butanol, 1-hexanol, 1-octanol, 1-pentanol, 1-heptanol, 3-methyl-1-pentanol, 4-methyl-1-hexanol, 5-methyl-1-heptanol, 4-methyl-1-pentanol, 5-methyl-1-hexanol, and 6-methyl-1-heptanol. The designer autotrophic organisms such as designer transgenic oxyphotobacteria and algae comprise designer Calvin-cycle-channeled and hydrogenotrophic pathway gene(s) and biosafety-guarding technology for enhanced autotrophic production of butanol and related higher alcohols from carbon dioxide and water.

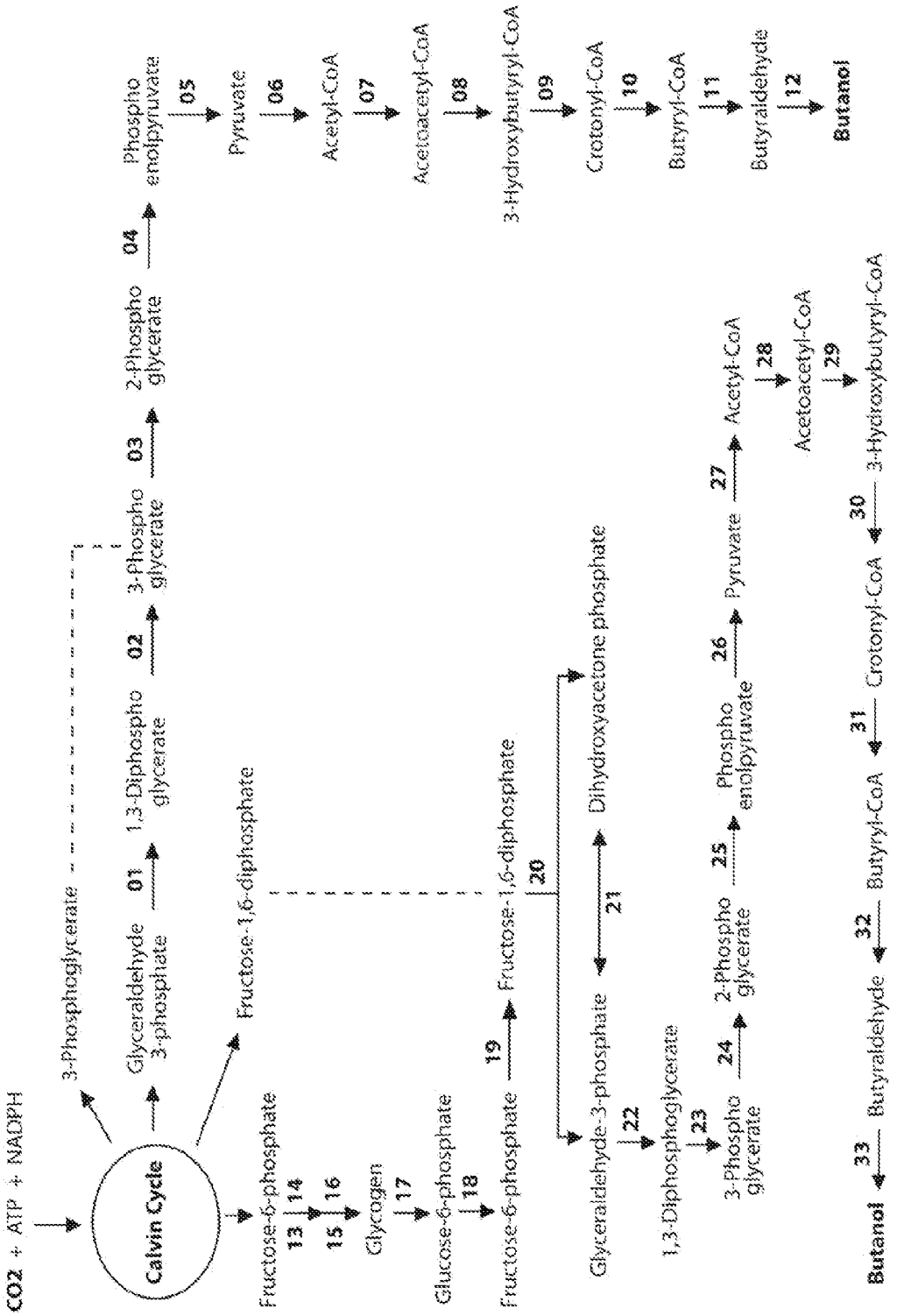
CO2 + ATP + NADPH
Calvin Cycle
3-Phosphoglycerate
Glyceraldehyde 3-phosphate
01
1,3-Diphospho glycerate
02
3-Phospho glycerate
03
2-Phospho glycerate
04
Phospho enolpyruvate
05
Pyruvate
06
Acetyl-CoA
07
Acetoacetyl-CoA
08
3-Hydroxybutyryl-CoA
09
Crotonyl-CoA
10
Butyryl-CoA
11
Butyraldehyde
12
Butanol
Fructose-1,6-diphosphate
Fructose-6-phosphate
13
14
15
16
Glycogen
17
Glucose-6-phosphate
18
Fructose-6-phosphate
19
Fructose-1,6-diphosphate
20
Dihydroxyacetone phosphate
21
Glyceraldehyde-3-phosphate
22
1,3-Diphosphoglycerate
23
3-Phospho glycerate
24
2-Phospho glycerate
25
Phospho enolpyruvate
26
Pyruvate
27
Acetyl-CoA
28
Acetoacetyl-CoA
29
3-Hydroxybutyryl-CoA
30
Crotonyl-CoA
31
Butyryl-CoA
32
Butyraldehyde
33
Butanol

FIG. 1

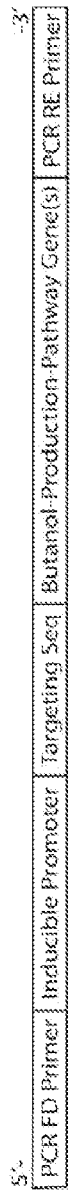

FIG. 2A

FIG. 2B

FIG. 2C

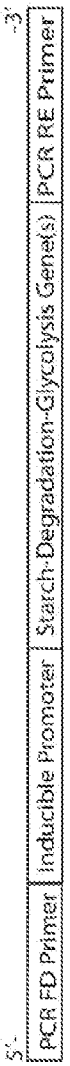

FIG. 2D

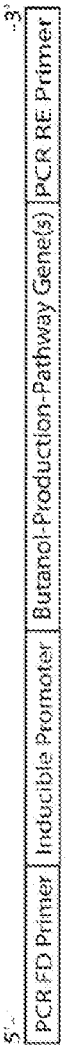

FIG. 2E

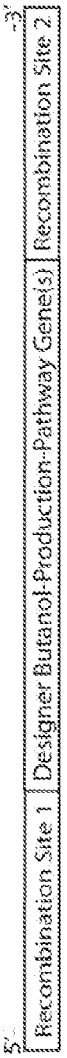

FIG. 2F

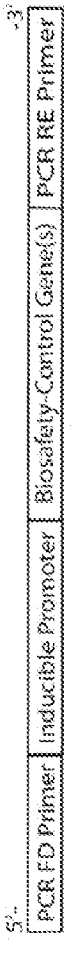

FIG. 2G

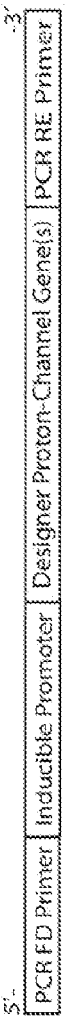

FIG. 2H

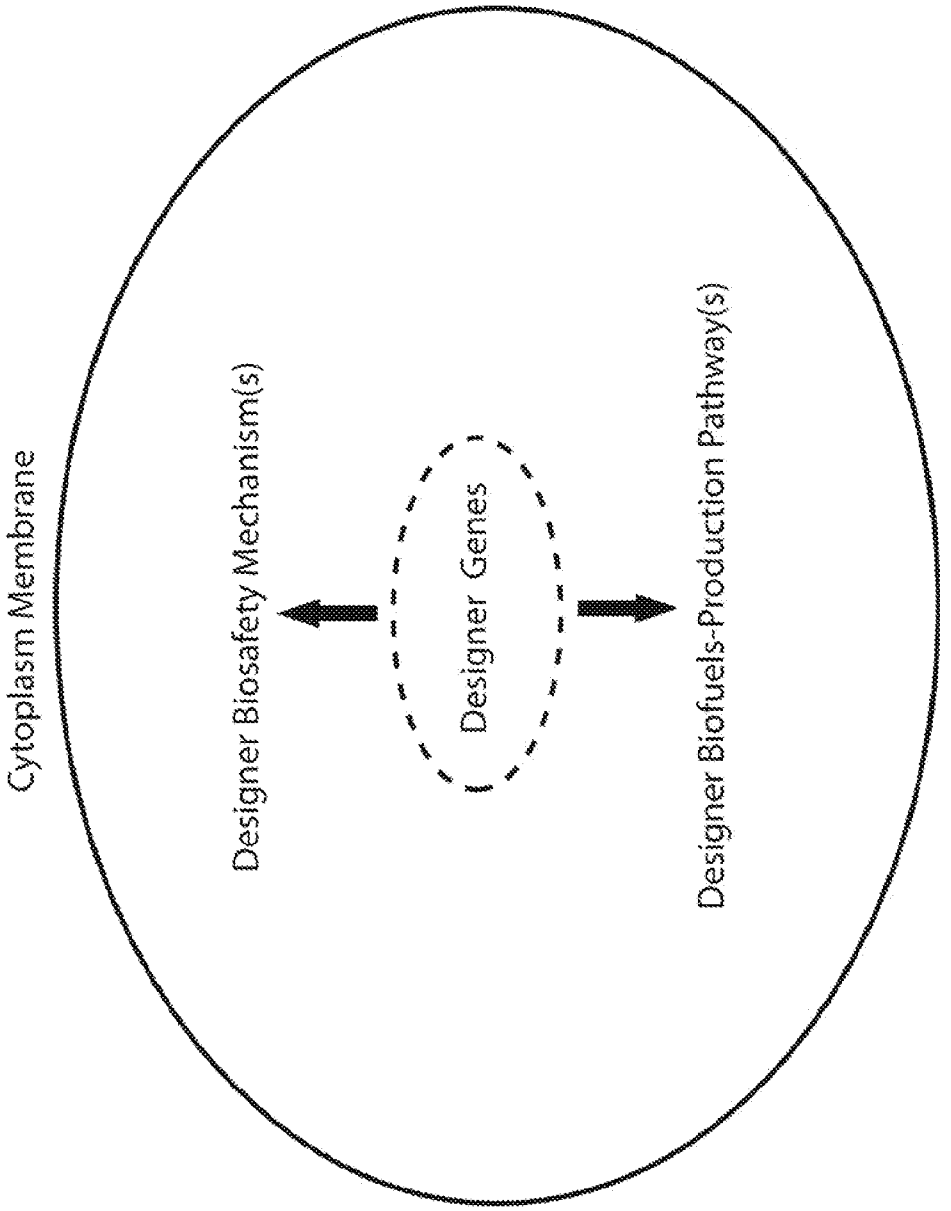
Cytoplasm Membrane
Designer Biosafety Mechanism(s)
Designer Genes
Designer Biofuels-Production Pathway(s)

FIG. 3A

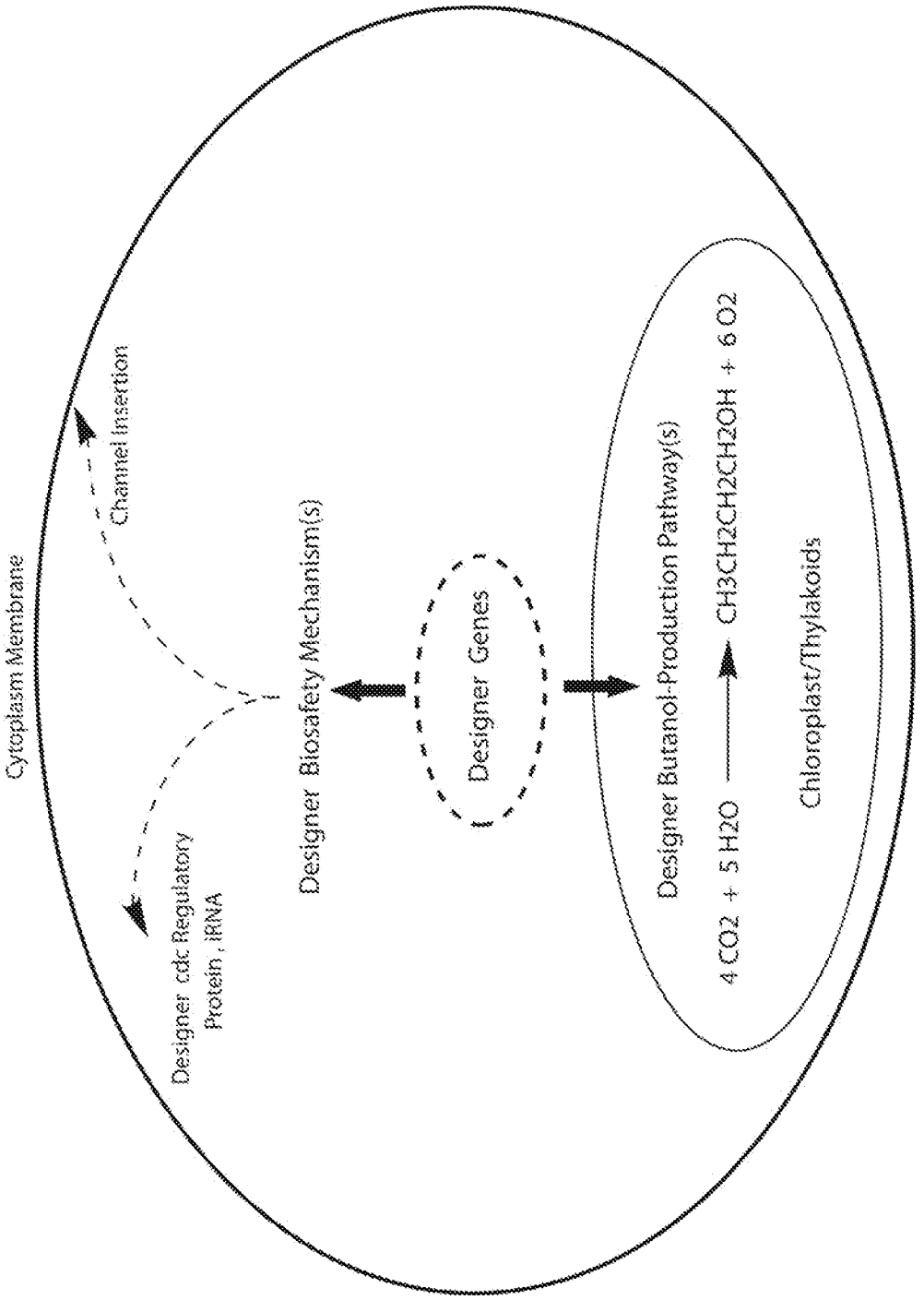
Cytoplasm Membrane
Channel insertion
Designer cdc Regulatory Protein , iRNA
Designer Biosafety Mechanism(s)
Designer Genes
Designer Butanol-Production Pathway(s)
4 CO2 + 5 H2O
CH3CH2CH2CH2OH + 6 O2
Chloroplast/Thylakoids

FIG. 3B

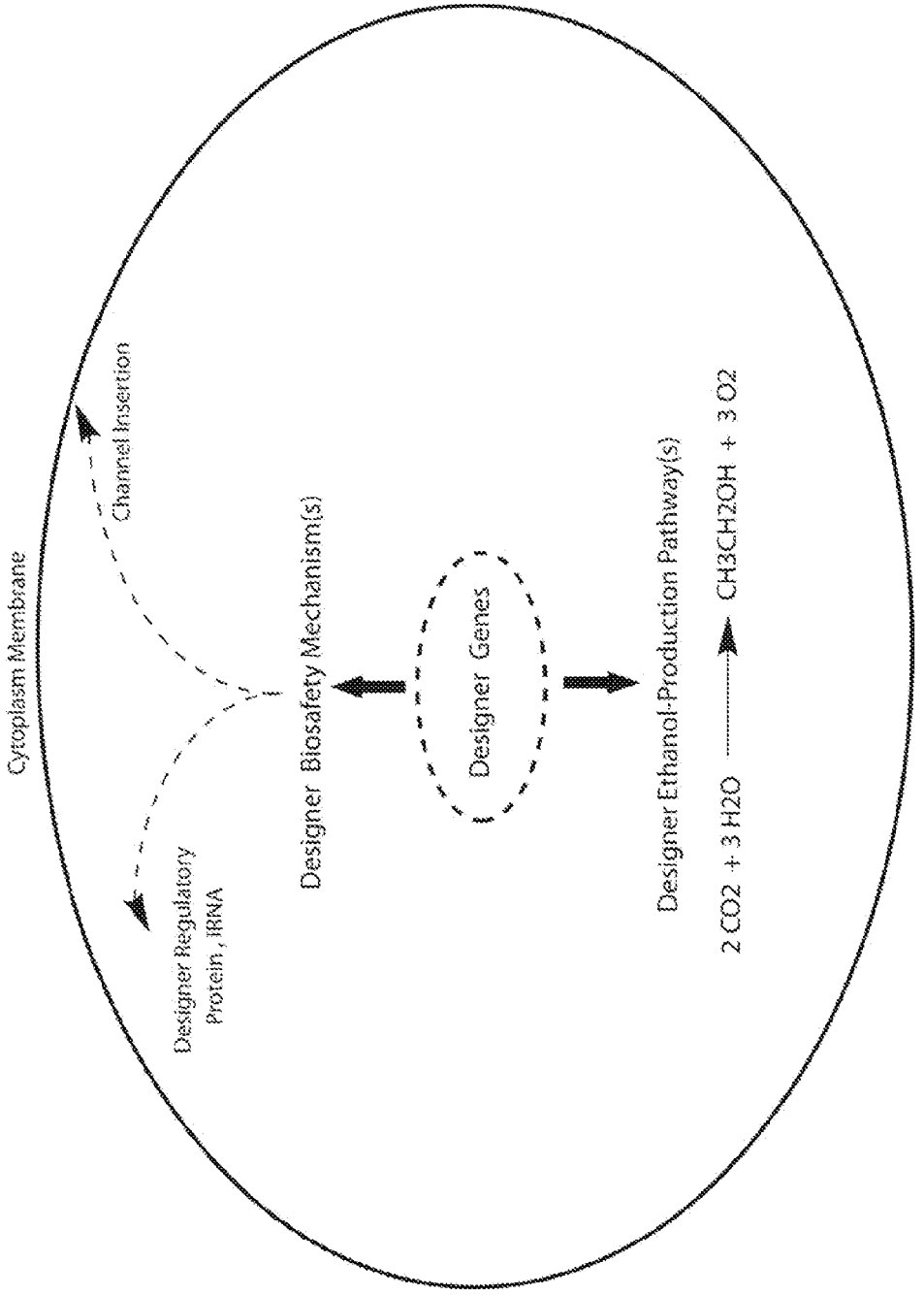
Cytoplasm Membrane
Channel Insertion
Designer Regulatory Protein, IRNA
Designer Biosafety Mechanism(s)
Designer Genes
Designer Ethanol-Production Pathway(s)
2 CO2 + 3 H2O
CH3CH2OH + 3 O2

FIG. 3C

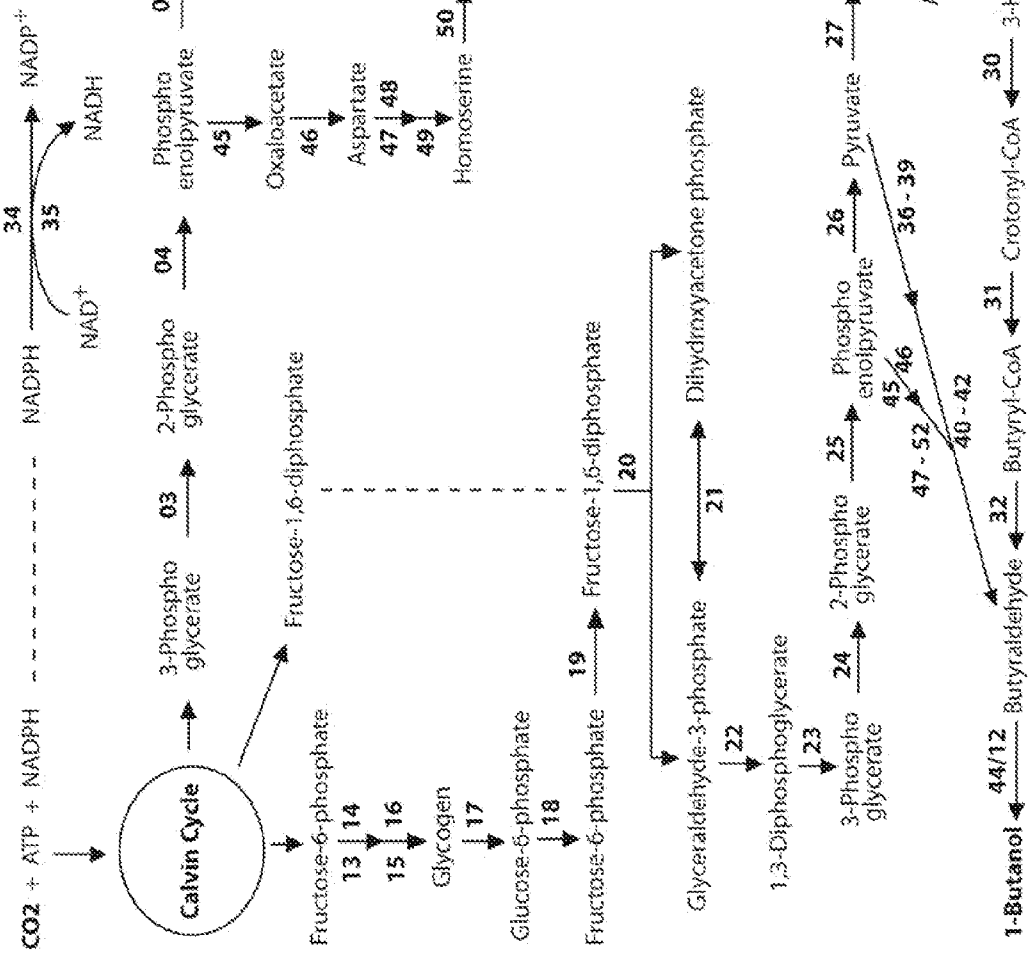
CO2 + ATP + NADPH
Calvin Cycle
NADPH
NADP+
NAD+
NADH
34
35
3-Phospho glycerate
03
2-Phospho glycerate
04
Phospho enolpyruvate
05
Pyruvate
36
Citramalate
37
Citraconate
38
Methyl-D-malate
39
2-Ketobutyrate
41
2-Ketovalerate
42
Butyraldehyde
(44/12)
1-Butanol
Fructose-1,6-diphosphate
Fructose-6-phosphate
13
14
15
16
Glycogen
17
Glucose-6-phosphate
18
Fructose-6-phosphate
19
Fructose-1,6-diphosphate
20
Glyceraldehyde-3-phosphate
21
Dihydroxyacetone phosphate
22
1,3-Diphosphoglycerate
23
3-Phospho glycerate
24
2-Phospho glycerate
25
Phospho enolpyruvate
26
Pyruvate
27
Acetyl-CoA
28
Acetoacetyl-CoA
29
3-Hydroxybutyryl-CoA
30
Crotonyl-CoA
31
Butyryl-CoA
32
Butyraldehyde
44/12
1-Butanol
Oxaloacetate
46
Aspartate
47
48
49
Homoserine
50
51
Threonine
52
45
47 - 52
46
45
40 - 42
36 - 39
40
39

FIG. 4

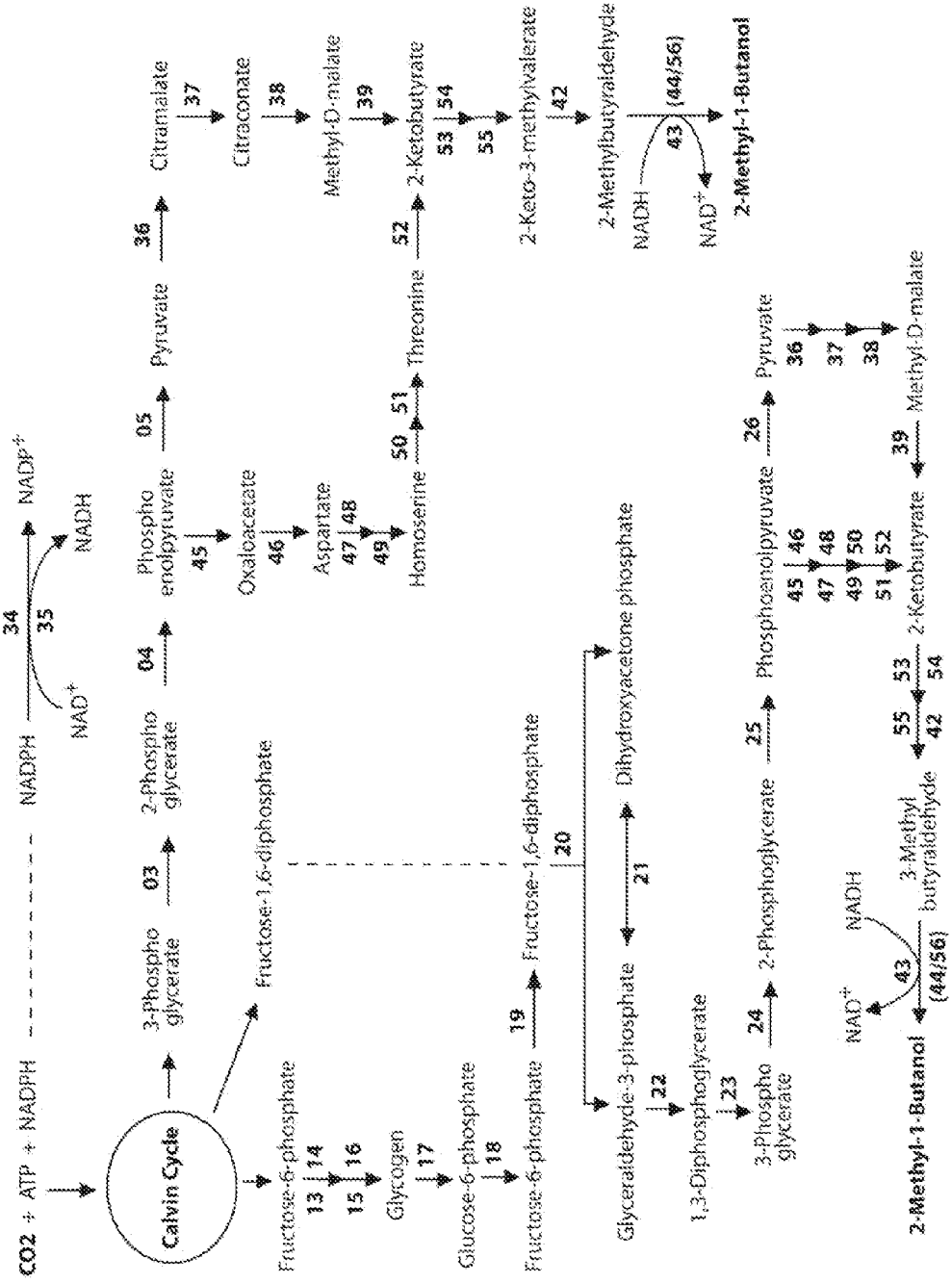
CO2 + ATP + NADPH
Calvin Cycle
NADPH
NADP+
NADH
NAD+
34
35
3-Phospho glycerate
03
2-Phospho glycerate
04
Phospho enolpyruvate
45
05
Pyruvate
36
Citramalate
37
Citraconate
38
Methyl-D-malate
39
Oxaloacetate
46
Aspartate
47 48
49
Homoserine
50 51
Threonine
52
2-Ketobutyrate
53 54
55
2-Keto-3-methylvalerate
42
2-Methylbutyraldehyde
43 (44/56)
2-Methyl-1-Butanol
Fructose-1,6-diphosphate
Fructose-6-phosphate
13 14
15 16
Glycogen
17
Glucose-6-phosphate
18
Fructose-6-phosphate
19
Fructose-1,6-diphosphate
20
Dihydroxyacetone phosphate
21
Glyceraldehyde-3-phosphate
22
1,3-Diphosphoglycerate
23
3-Phospho glycerate
24
2-Phosphoglycerate
25
Phosphoenolpyruvate
26
Pyruvate
36
37
38
Methyl-D-malate
39
2-Ketobutyrate
53
54
42
55
3-Methyl butyraldehyde
(44/56)
43
NADH
NAD+
2-Methyl-1-Butanol

FIG. 5

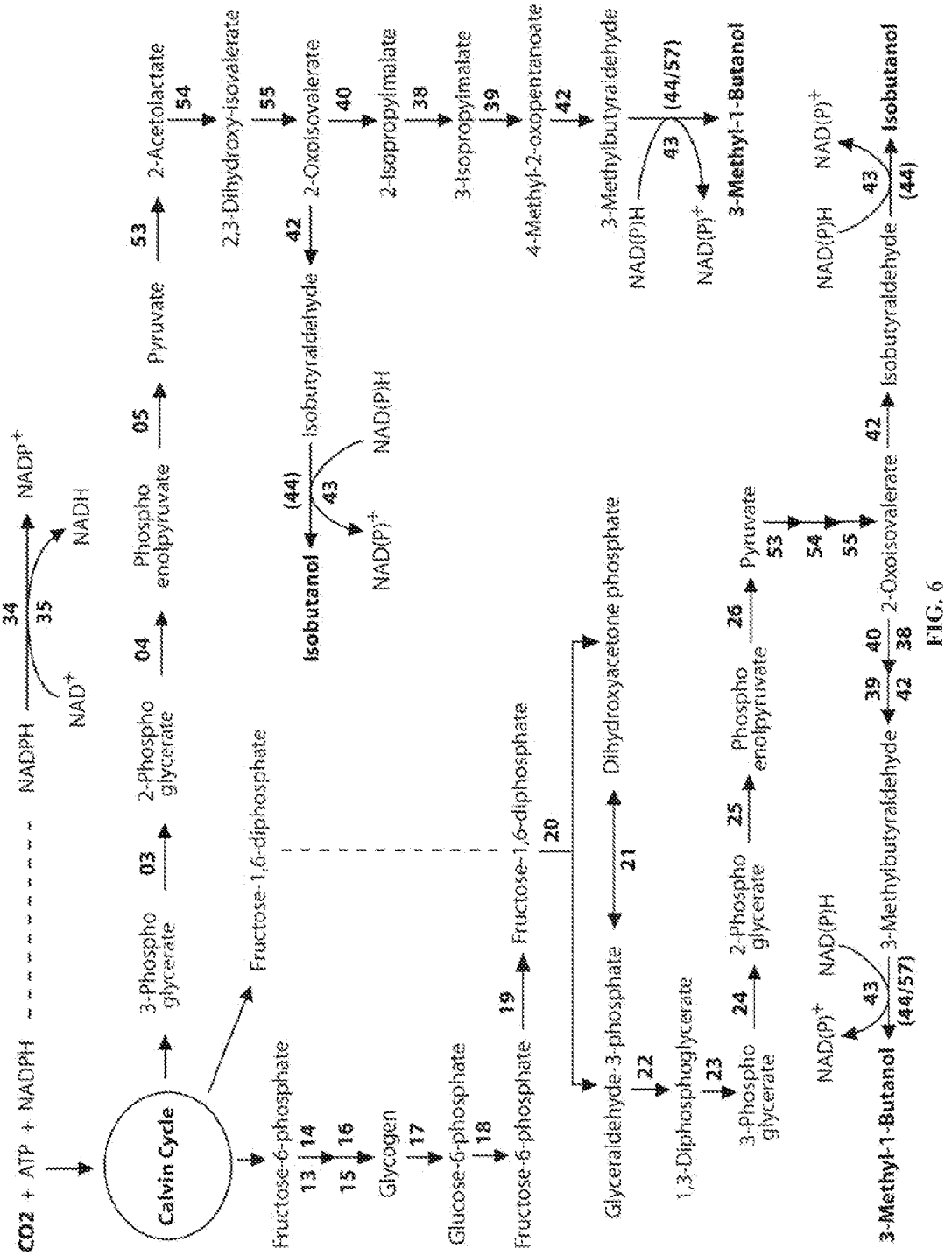
CO2 + ATP + NADPH
Calvin Cycle
NADPH
NADP+
NADH
NAD+
34
35
3-Phospho glycerate
03
2-Phospho glycerate
04
Phospho enolpyruvate
05
Pyruvate
53
2-Acetolactate
54
2,3-Dihydroxy-isovalerate
55
Fructose-1,6-diphosphate
Fructose-6-phosphate
13
14
15
16
Glycogen
17
Glucose-6-phosphate
18
Fructose-6-phosphate
19
Fructose-1,6-diphosphate
20
Isobutanol
(44)
Isobutyraldehyde
42
2-Oxoisovalerate
40
43
NAD(P)+
NAD(P)H
2-Isopropylmalate
38
3-Isopropylmalate
39
4-Methyl-2-oxopentanoate
42
Glyceraldehyde-3-phosphate
21
Dihydroxyacetone phosphate
22
3-Methylbutyraldehyde
NAD(P)H
43
(44/57)
NAD(P)+
3-Methyl-1-Butanol
1,3-Diphosphoglycerate
23
3-Phospho glycerate
24
2-Phospho glycerate
25
Phospho enolpyruvate
26
Pyruvate
53
54
55
NAD(P)+
NAD(P)H
43
(44/57)
3-Methyl-1-Butanol
NAD(P)H
NAD(P)+
39
42
3-Methylbutyraldehyde
40
38
2-Oxoisovalerate
42
Isobutyraldehyde
43
(44)
Isobutanol

FIG. 6

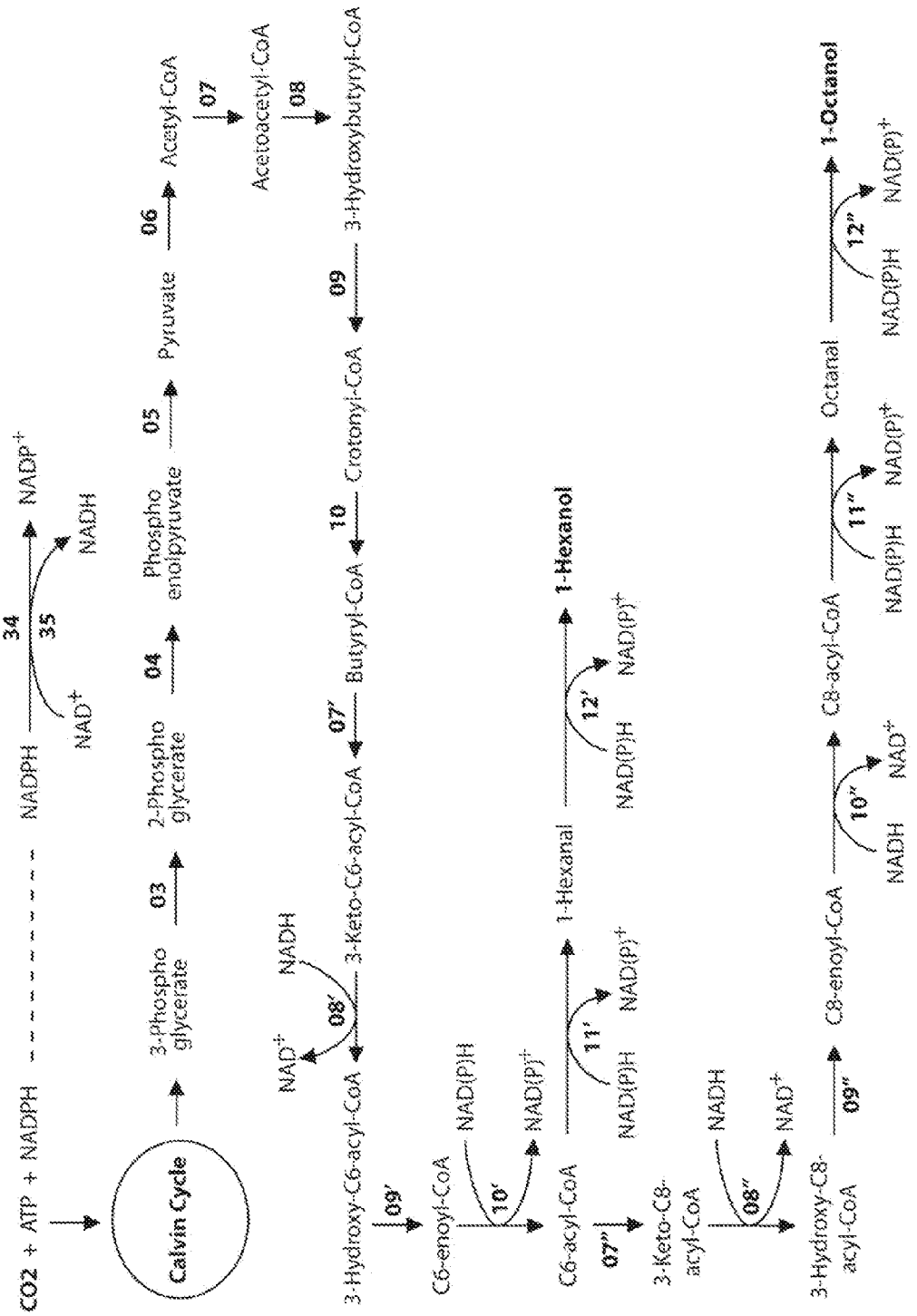
CO2 + ATP + NADPH
Calvin Cycle
3-Phospho glycerate
03
2-Phospho glycerate
04
Phospho enolpyruvate
05
Pyruvate
06
Acetyl-CoA
07
Acetoacetyl-CoA
08
3-Hydroxybutyryl-CoA
09
Crotonyl-CoA
10
Butyryl-CoA
07'
3-Keto-C6-acyl-CoA
08'
3-Hydroxy-C6-acyl-CoA
09'
C6-enoyl-CoA
10'
C6-acyl-CoA
11'
1-Hexanal
12'
1-Hexanol
07"
3-Keto-C8-acyl-CoA
08"
3-Hydroxy-C8-acyl-CoA
09"
C8-enoyl-CoA
10"
C8-acyl-CoA
11"
Octanal
12"
1-Octanol
NADPH
NADP+
NADH
NAD+
34
35
NAD(P)H
NAD(P)+

FIG. 7

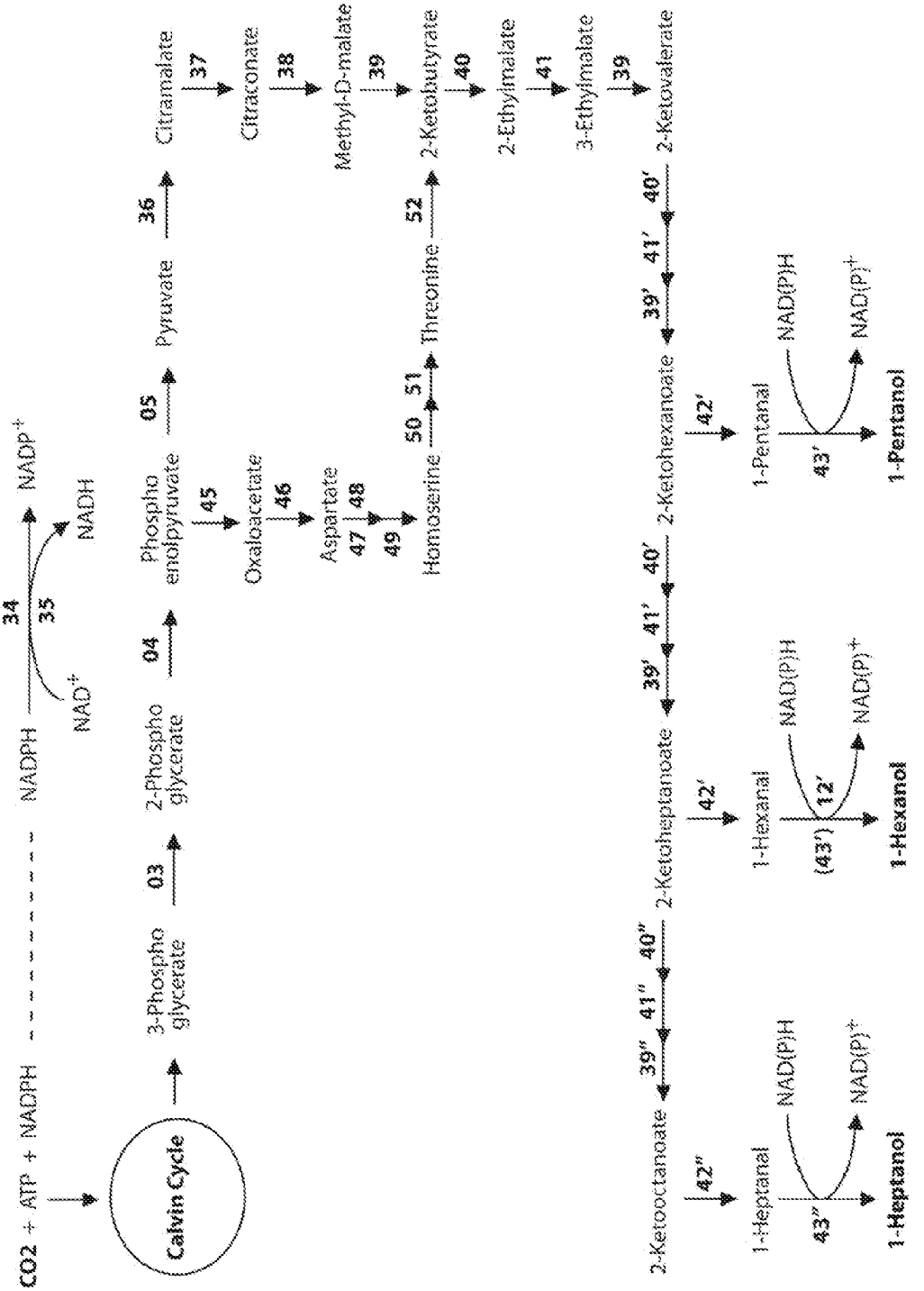
CO2 + ATP + NADPH
Calvin Cycle
NADPH
NADP+
NAD+
NADH
34
35
3-Phospho glycerate
03
2-Phospho glycerate
04
Phospho enolpyruvate
45
05
Pyruvate
36
Citramalate
37
Oxaloacetate
46
Citraconate
38
Aspartate
47
48
49
Methyl-D-malate
39
Homoserine
50
51
Threonine
52
2-Ketobutyrate
40
2-Ethylmalate
41
3-Ethylmalate
39
2-Ketooctanoate
39″
41″
40″
2-Ketoheptanoate
39′
41′
40′
2-Ketohexanoate
39′
41′
40′
2-Ketovalerate
42″
42′
42′
1-Heptanal
NAD(P)H
43″
NAD(P)+
1-Heptanol
1-Hexanal
NAD(P)H
(43′)
12′
NAD(P)+
1-Hexanol
1-Pentanal
NAD(P)H
43′
NAD(P)+
1-Pentanol

FIG. 8

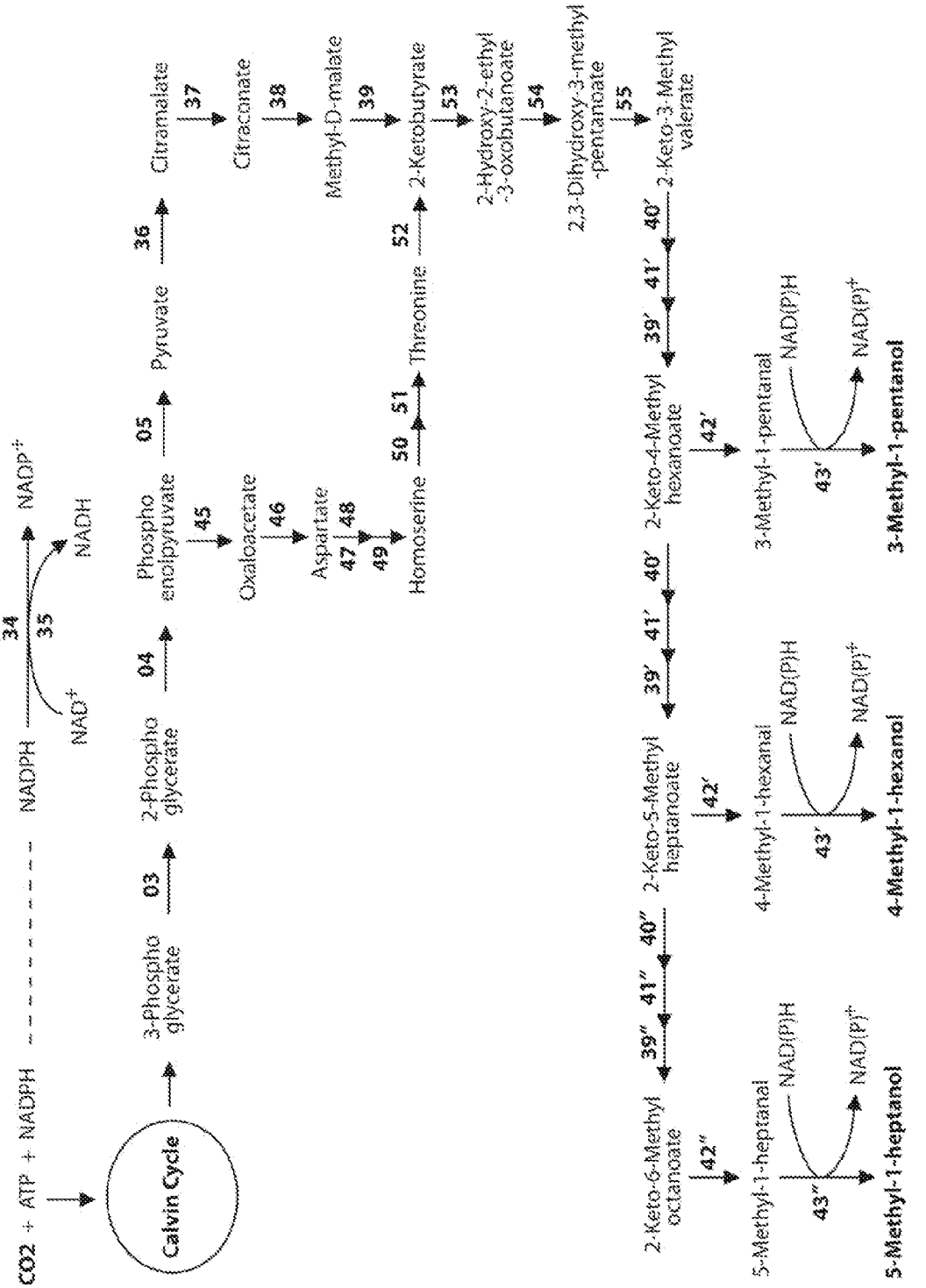
CO2 + ATP + NADPH
Calvin Cycle
NADPH
NADP+
NADH
NAD+
34
35
3-Phospho glycerate
03
2-Phospho glycerate
04
Phospho enolpyruvate
05
Pyruvate
36
Citramalate
37
45
Oxaloacetate
46
Citraconate
38
Aspartate
47
48
49
Methyl-D-malate
39
50
51
Homoserine
Threonine
52
2-Ketobutyrate
53
2-Hydroxy-2-ethyl -3-oxobutanoate
54
2,3-Dihydroxy-3-methyl -pentanoate
55
2-Keto-6-Methyl octanoate
42″
39″
41″
40″
2-Keto-5-Methyl heptanoate
42′
39′
41′
40′
2-Keto-4-Methyl hexanoate
42′
39′
41′
40′
2-Keto-3-Methyl valerate
5-Methyl-1-heptanal
NAD(P)H
43″
NAD(P)+
4-Methyl-1-hexanal
NAD(P)H
43′
NAD(P)+
3-Methyl-1-pentanal
NAD(P)H
43′
NAD(P)+
5-Methyl-1-heptanol
4-Methyl-1-hexanol
3-Methyl-1-pentanol

FIG. 9

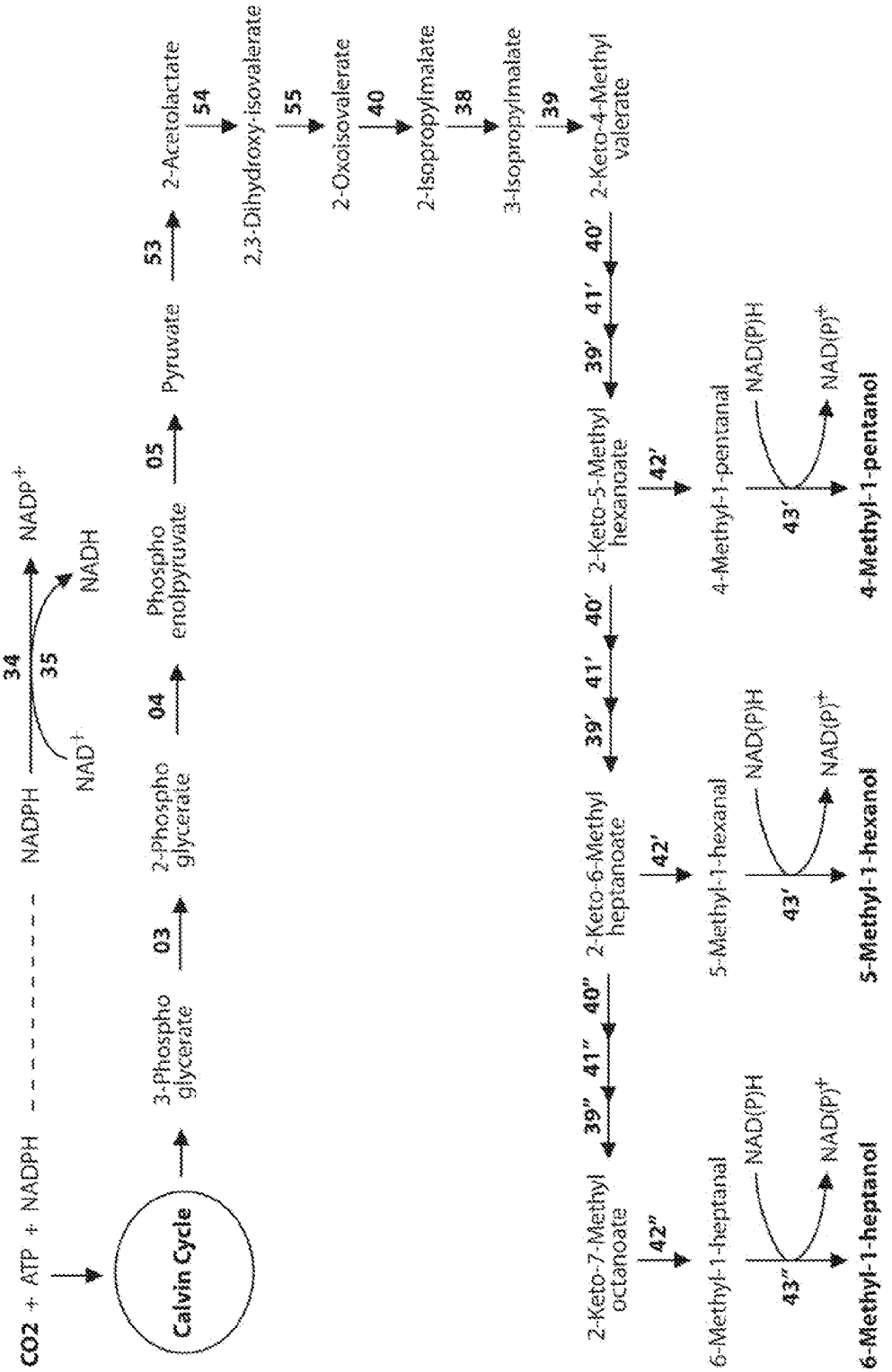
CO2 + ATP + NADPH
Calvin Cycle
NADPH
NADP+
NAD+
NADH
34
35
3-Phospho glycerate
03
2-Phospho glycerate
04
Phospho enolpyruvate
05
Pyruvate
53
2-Acetolactate
54
2,3-Dihydroxy-isovalerate
55
2-Oxoisovalerate
40
2-Isopropylmalate
38
3-Isopropylmalate
39
2-Keto-4-Methyl valerate
39' 41' 40'
2-Keto-5-Methyl hexanoate
42'
4-Methyl-1-pentanal
NAD(P)H
43'
NAD(P)+
4-Methyl-1-pentanol
2-Keto-6-Methyl heptanoate
39' 41' 40'
42'
5-Methyl-1-hexanal
NAD(P)H
43'
NAD(P)+
5-Methyl-1-hexanol
2-Keto-7-Methyl octanoate
39" 41" 40"
42"
6-Methyl-1-heptanal
NAD(P)H
43"
NAD(P)+
6-Methyl-1-heptanol

FIG. 10

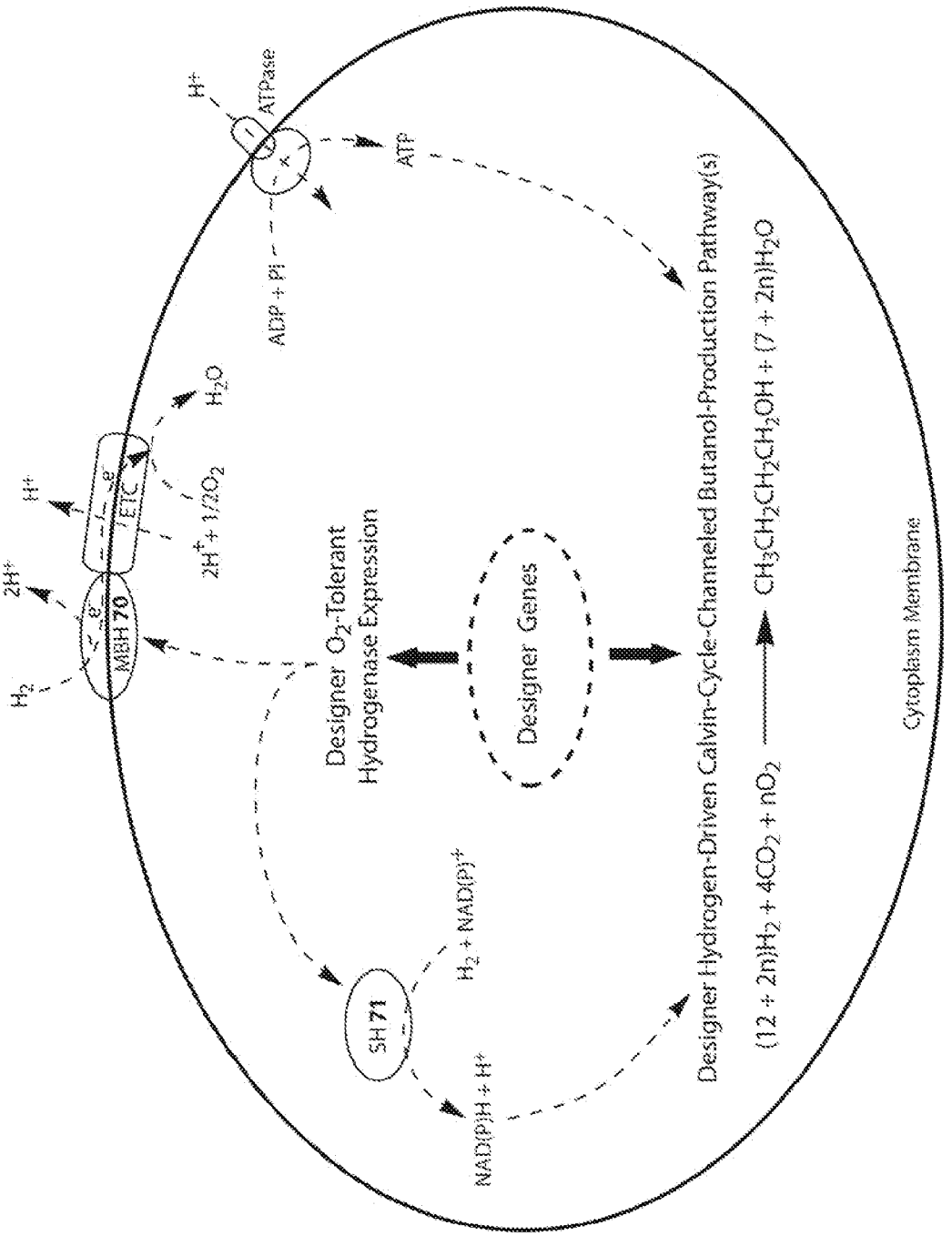
H2
2H+
MBH 70
e-
ETC
H+
2H+ + 1/2O2
H2O
H+
ATPase
ADP + Pi
ATP
Designer O2-Tolerant Hydrogenase Expression
Designer Genes
Designer Hydrogen-Driven Calvin-Cycle-Channeled Butanol-Production Pathway(s)
(12 + 2n)H2 + 4CO2 + nO2
CH3CH2CH2CH2OH + (7 + 2n)H2O
SH 71
H2 + NAD(P)+
NAD(P)H + H+
Cytoplasm Membrane

FIG. 11

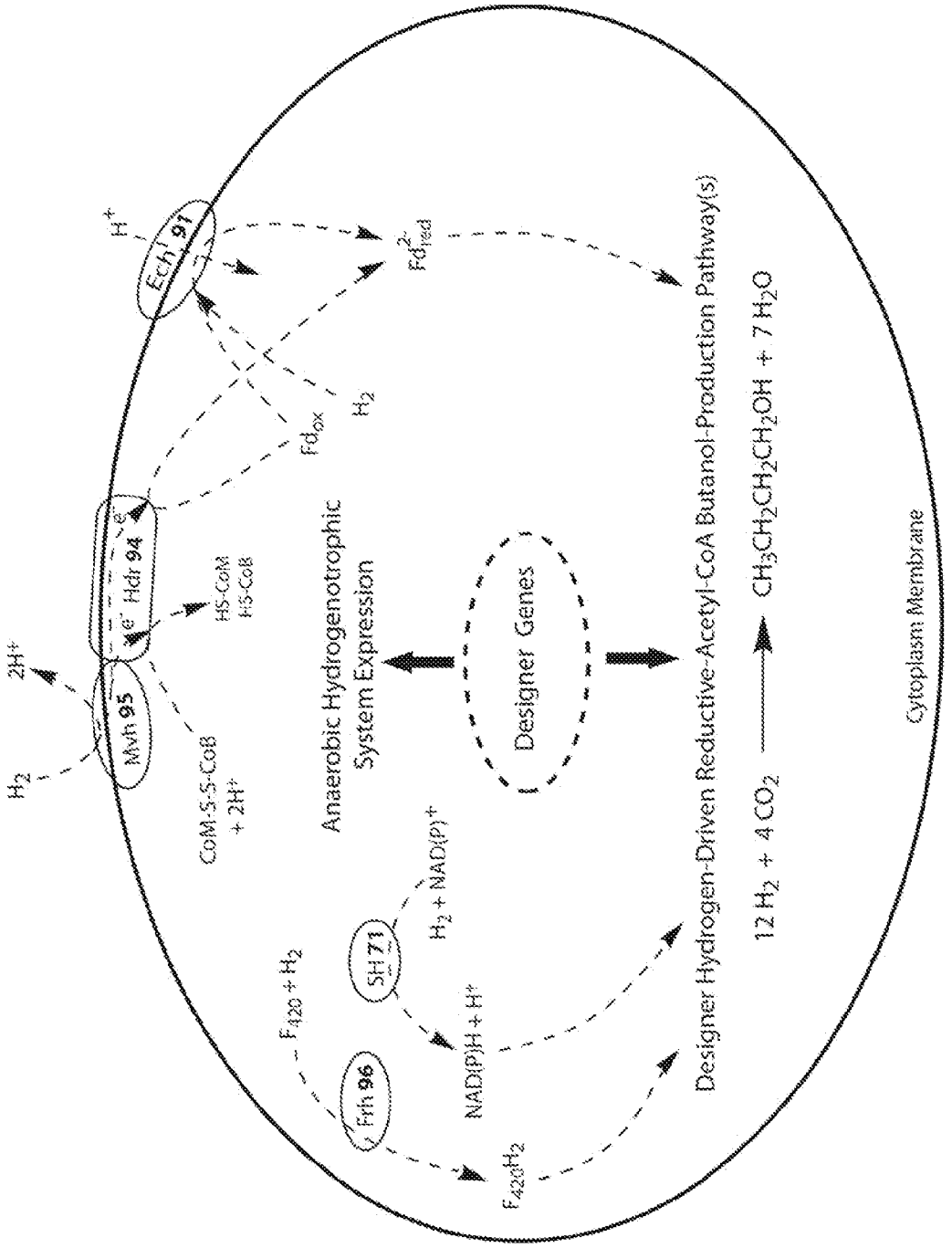
H2
2H+
Mvh 95
e-
e-
Hdr 94
e-
HS-CoM
HS-CoB
CoM-S-S-CoB
+ 2H+
Fdox
H2
H+
Ech 91
Fd2red
Anaerobic Hydrogenotrophic
System Expression
Designer Genes
H2 + NAD(P)+
SH 71
F420 + H2
Frh 96
NAD(P)H + H+
F420H2
Designer Hydrogen-Driven Reductive-Acetyl-CoA Butanol-Production Pathway(s)
12 H2 + 4 CO2
CH3CH2CH2CH2OH + 7 H2O
Cytoplasm Membrane

FIG. 12

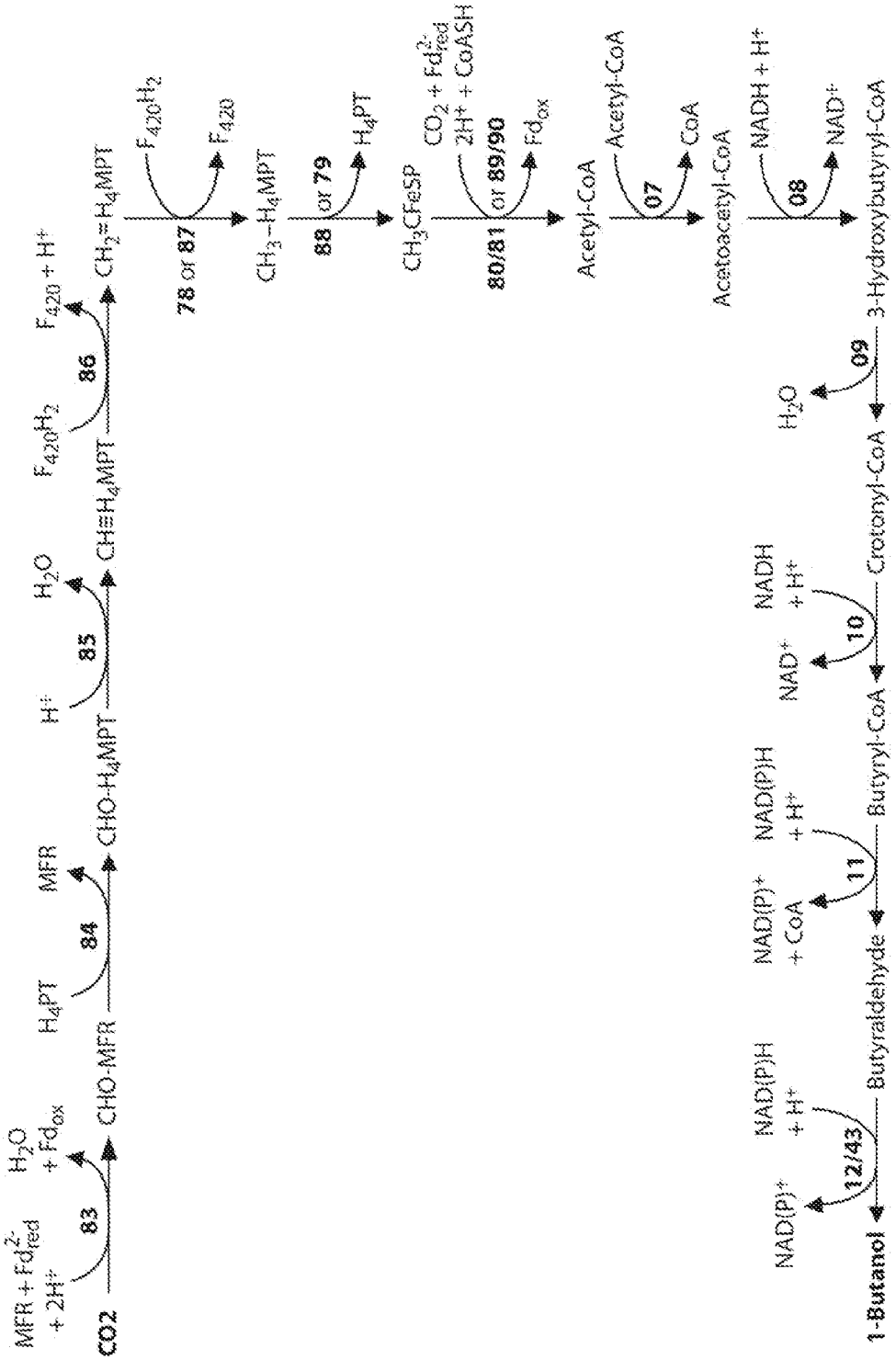
CO2
MFR + Fd²⁻red + 2H⁺
83
H2O + Fdox
CHO-MFR
H4PT
84
MFR
CHO-H4MPT
H⁺
85
H2O
CH≡H4MPT
F420H2
86
F420 + H⁺
CH2=H4MPT
78 or 87
F420H2
F420
CH3-H4MPT
88 or 79
H4PT
CH3CFeSP
CO2 + Fd²⁻red + 2H⁺ + CoASH
80/81 or 89/90
Fdox
Acetyl-CoA
Acetyl-CoA
07
CoA
Acetoacetyl-CoA
NADH + H⁺
08
NAD⁺
H2O
09
3-Hydroxybutyryl-CoA
NAD+
NAD(P)H + H⁺
10
Crotonyl-CoA
NAD(P)+ + CoA
NAD(P)H + H⁺
11
Butyryl-CoA
NAD(P)+
NAD(P)H + H⁺
12/43
Butyraldehyde
1-Butanol

FIG. 13

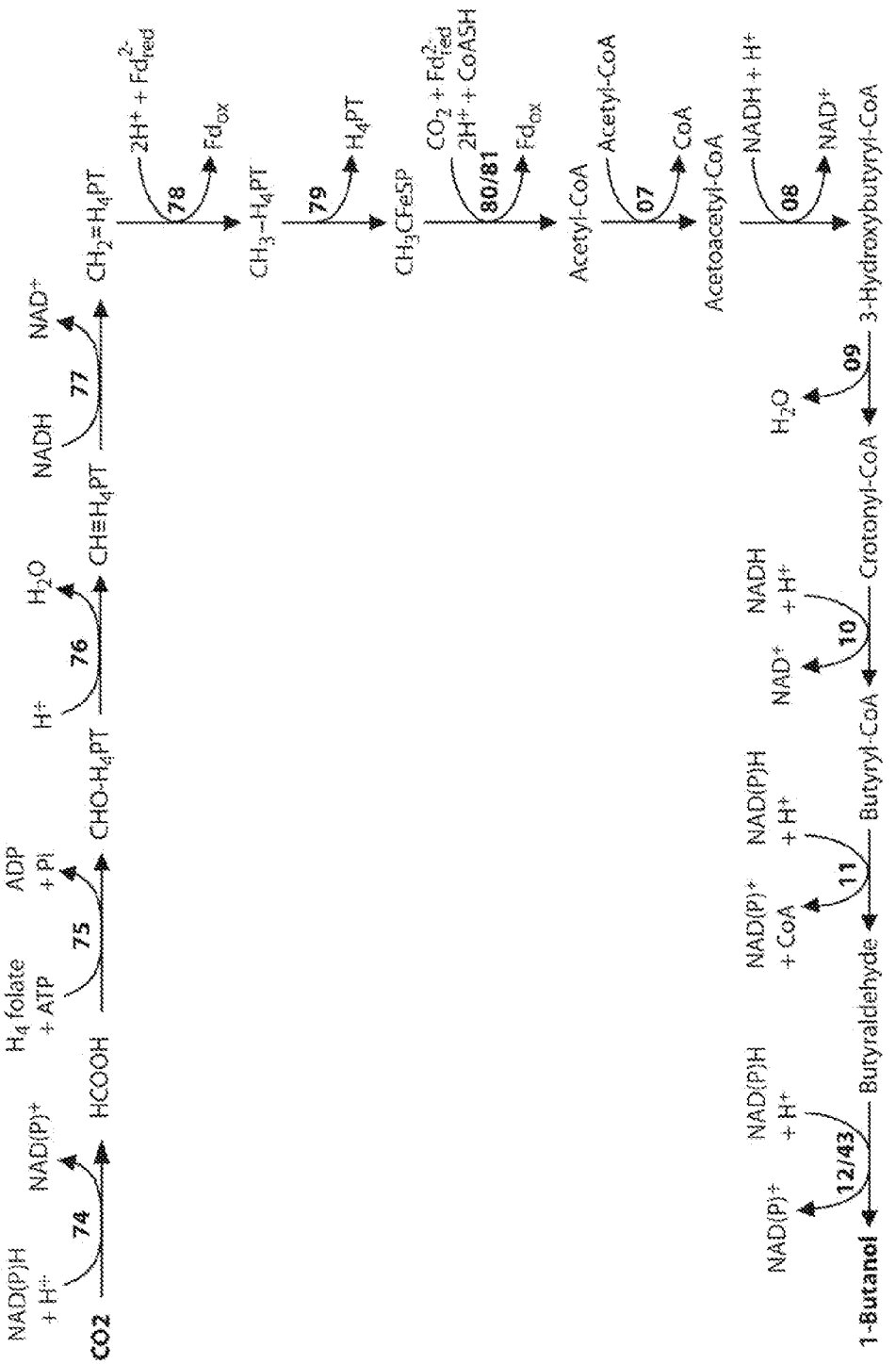
NAD(P)H + H+
CO2
74
NAD(P)+
HCOOH
H4 folate + ATP
75
ADP + Pi
CHO-H4PT
H+
76
H2O
CH≡H4PT
NADH
77
NAD+
CH2=H4PT
2H+ + Fdred2-
78
Fdox
CH3–H4PT
79
H4PT
CH3CFeSP
CO2 + Fdred2-
2H+ + CoASH
80/81
Fdox
Acetyl-CoA
Acetyl-CoA
07
CoA
Acetoacetyl-CoA
NADH + H+
08
NAD+
H2O
09
3-Hydroxybutyryl-CoA
NADH + H+
NAD+
10
Crotonyl-CoA
NAD(P)H + H+
NAD(P)+ + CoA
11
Butyryl-CoA
NAD(P)H + H+
NAD(P)+
12/43
Butyraldehyde
1-Butanol

FIG. 14

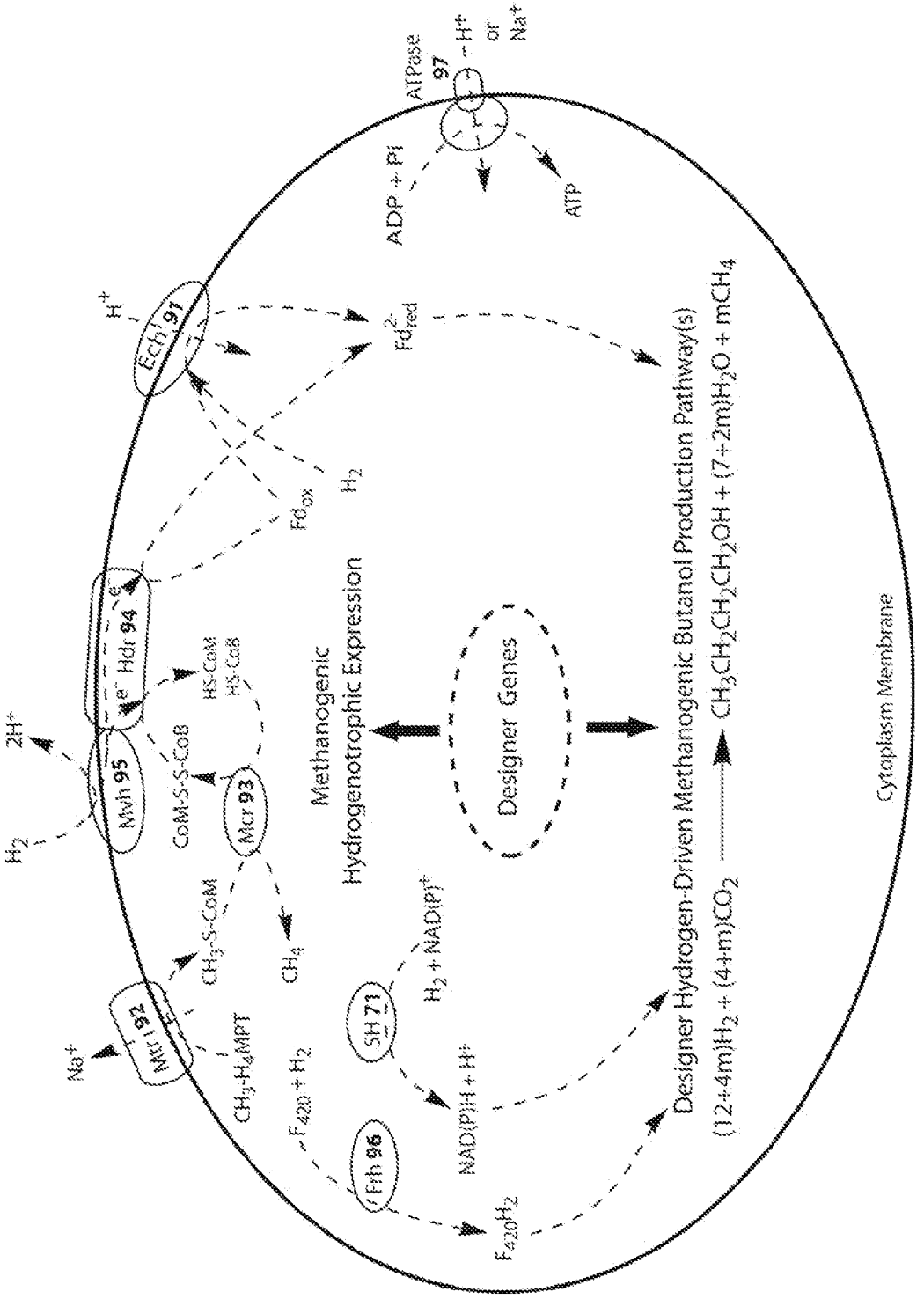
Na+
Mrr 92
CH3-H4MPT
F420 + H2
Frh 96
F420H2
CH3-S-CoM
CH4
CoM-S-S-CoB
Mcr 93
HS-CoM
HS-CoB
H2
2H+
Mvh 95
e-
Hdr 94
e-
Fdox
H+
Ech 91
Fd2-red
H2
SH 71
H2 + NAD(P)+
NAD(P)H + H+
Methanogenic
Hydrogenotrophic Expression
Designer Genes
Designer Hydrogen-Driven Methanogenic Butanol Production Pathway(s)
(12+4m)H2 + (4+m)CO2
CH3CH2CH2CH2OH + (7+2m)H2O + mCH4
ADP + Pi
ATPase 97
ATP
H+ or Na+
Cytoplasm Membrane

FIG. 15

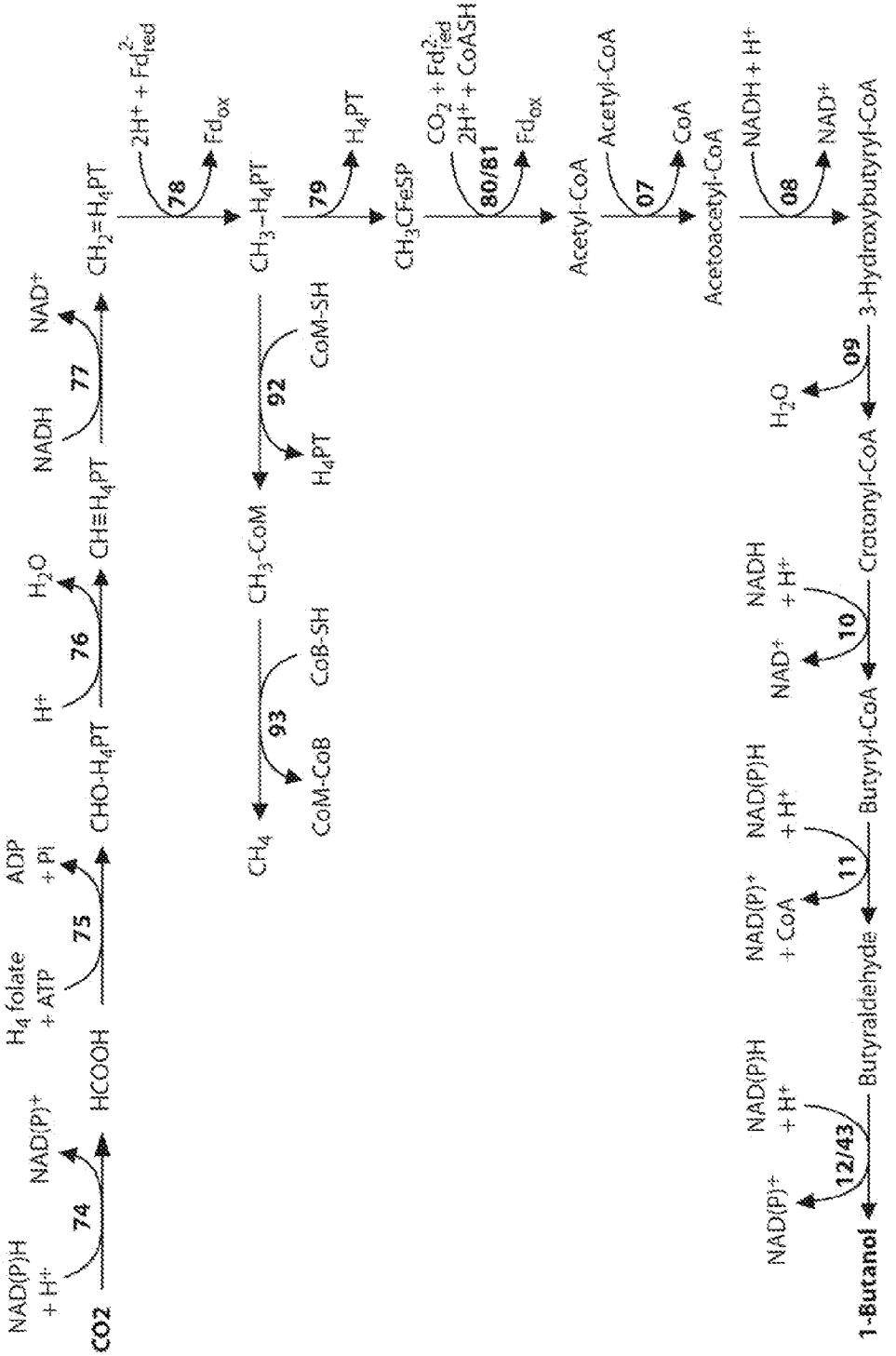
CO2
NAD(P)H + H+
74
HCOOH
NAD(P)+
H4 folate + ATP
75
CHO-H4PT
ADP + Pi
H+
76
CH≡H4PT
H2O
NADH
77
CH2=H4PT
NAD+
2H+ + Fdred2-
78
Fdox
CH3–H4PT
79
H4PT
CH3FeSP
CO2 + Fdred2-
2H+ + CoASH
80/81
Fdox
Acetyl-CoA
Acetyl-CoA
07
CoA
Acetoacetyl-CoA
NADH + H+
08
NAD+
3-Hydroxybutyryl-CoA
H2O
09
Crotonyl-CoA
NADH + H+
10
NAD+
Butyryl-CoA
NAD(P)H + H+
11
NAD(P)+ + CoA
Butyraldehyde
NAD(P)H + H+
12/43
NAD(P)+
1-Butanol
CH3-CoM
92
H4PT
CoM-SH
CH4
93
CoM-CoB
CoB-SH

FIG. 16

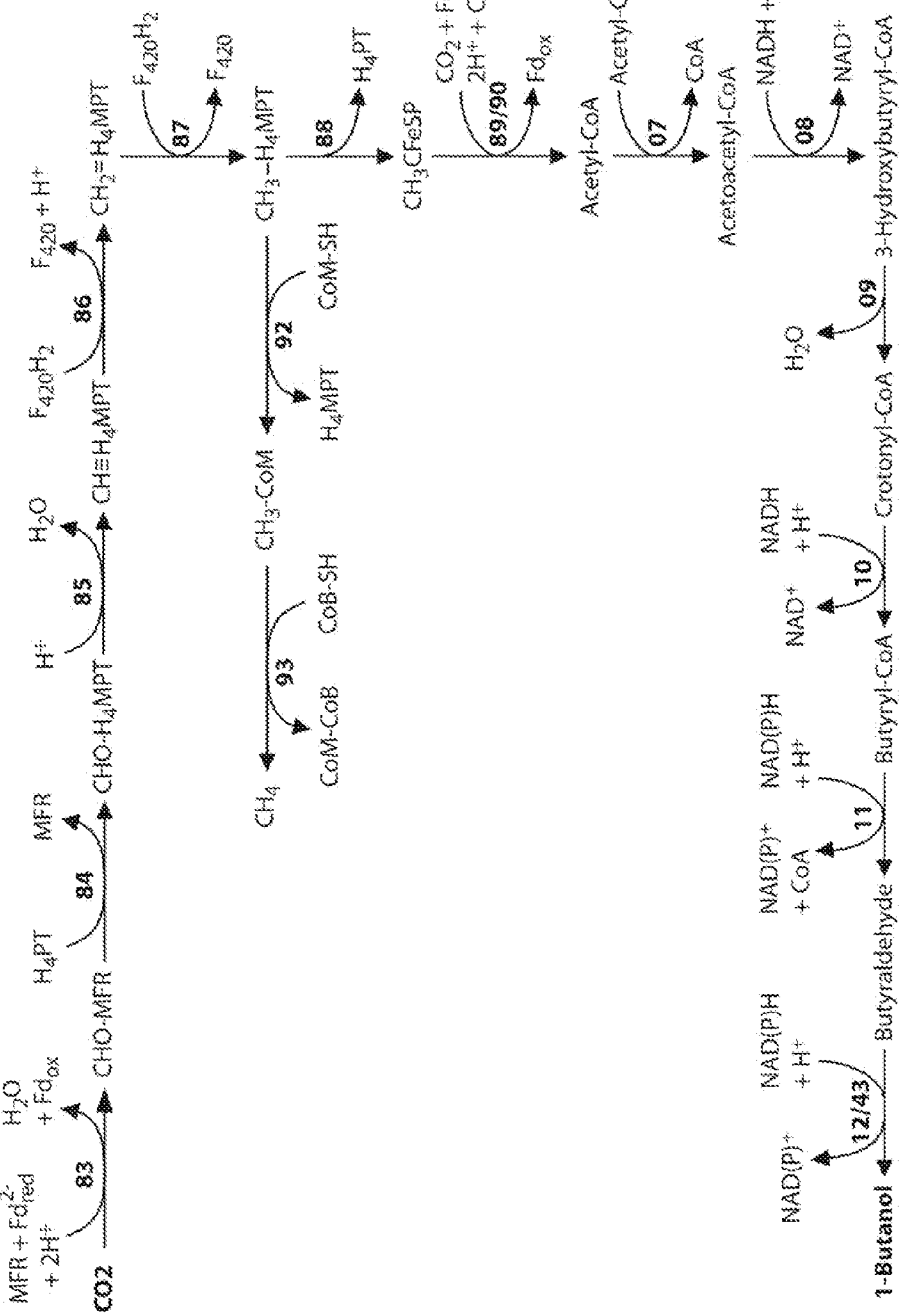
MFR + Fd^{2-}_{red} + $2H^+$
H_2O + Fd_{ox}
CO2
83
CHO-MFR
H_4PT
84
MFR
CHO-H_4MPT
H^+
85
H_2O
CH≡H_4MPT
$F_{420}H_2$
86
F_{420} + H^+
CH_2=H_4MPT
$F_{420}H_2$
87
F_{420}
CH_3–H_4MPT
88
H_4PT
CH_3FeSP
CO_2 + Fd^{2-}_{red}
$2H^+$ + CoASH
89/90
Fd_{ox}
Acetyl-CoA
Acetyl-CoA
07
CoA
Acetoacetyl-CoA
NADH + H^+
08
NAD^+
3-Hydroxybutyryl-CoA
09
H_2O
Crotonyl-CoA
NADH + H^+
10
NAD^+
Butyryl-CoA
NAD(P)H + H^+
11
NAD(P)+ + CoA
Butyraldehyde
NAD(P)H + H^+
12/43
NAD(P)+
1-Butanol
CH_3-CoM
92
H_4MPT
CoM-SH
CH_4
93
CoM-CoB
CoB-SH

FIG. 17

DESIGNER CALVIN-CYCLE-CHANNELED AND HYDROGENOTROPHIC PRODUCTION OF BUTANOL AND RELATED HIGHER ALCOHOLS

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit of U.S. patent application Ser. No. 13/075,153 filed on Mar. 29, 2011, which is a continuation-in-part of co-pending U.S. patent application Ser. No. 12/918,784 filed on Aug. 20, 2010, which is the National Stage of International Application No. PCT/US2009/034801 filed on Feb. 21, 2009, which claims the benefit of U.S. Provisional Application No. 61/066,845 filed on Feb. 23, 2008, and U.S. Provisional Application No. 61/066,835 filed on Feb. 23, 2008. This application also claims the benefit of U.S. Provisional Application No. 61/426,147 filed on Dec. 22, 2010. The entire disclosures of all of these applications are incorporated herein by reference.

FIELD OF THE INVENTION

[0002] The present invention generally relates to biosafety-guarded biofuel energy production technology. More specifically, the present invention provides an autotrophic advanced-biofuels production methodology based on designer transgenic plants, such as transgenic algae, blue-green algae (cyanobacteria and oxychlorobacteria), plant cells or bacterial cells that are created to use the reducing power (NADPH) or Hydrogen (H_2), and energy (ATP) acquired from the photosynthetic and/or hydrogenotrophic process for autotrophic synthesis of butanol and/or related higher alcohols from carbon dioxide (CO_2) and water (H_2O).

REFERENCE TO SEQUENCE LISTING

[0003] The present invention contains references to amino acid sequences and/or nucleic acid sequences which have been submitted concurrently herewith as the sequence listing text file "JWL_004_PCT_SeqListingFull_ST25.txt" updated on Dec. 18, 2911 from the efile of "JWL_004_US1_SeqListingFull_ST25.txt", file size 429 KB, created on Mar. 29, 2011, in electronic format using the Electronic Filing System of the U.S. Patent and Trademark Office. The aforementioned sequence listing was prepared with PatentIn 3.5, which complies with all format requirements specified in World Intellectual Property Organization Standard (WIPO) ST.25 and the related United States (US) final rule, and is incorporated herein by reference in its entirety including pursuant to 37 C.F.R. §1.52(e)(5) where applicable.

BACKGROUND OF THE INVENTION

[0004] Butanol and/or related higher alcohols can be used as a liquid fuel to run engines such as cars. Butanol can replace gasoline and the energy contents of the two fuels are nearly the same (110,000 Btu per gallon for butanol; 115,000 Btu per gallon for gasoline). Butanol has many superior properties as an alternative fuel when compared to ethanol as well. These include: 1) Butanol has higher energy content (110,000 Btu per gallon butanol) than ethanol (84,000 Btu per gallon ethanol); 2) Butanol is six times less "evaporative" than ethanol and 13.5 times less evaporative than gasoline, making it safer to use as an oxygenate and thereby eliminating the need for very special blends during the summer and winter seasons; 3) Butanol can be transported through the existing fuel infrastructure including the gasoline pipelines whereas ethanol must be shipped via rail, barge or truck; and 4) Butanol can be used as replacement for gasoline gallon for gallon e.g. 100% or any other percentage, whereas ethanol can only be used as an additive to gasoline up to about 85% (E-85) and then only after significant modification to the engine (while butanol can work as a 100% replacement fuel without having to modify the current car engine).

[0005] A significant potential market for butanol and/or related higher alcohols as a liquid fuel already exists in the current transportation and energy systems. Butanol is also used as an industrial solvent. In the United States, currently, butanol is manufactured primarily from petroleum. Historically (1900s-1950s), biobutanol was manufactured from corn and molasses in a fermentation process that also produced acetone and ethanol and was known as an ABE (acetone, butanol, ethanol) fermentation typically with certain butanol-producing bacteria such as *Clostridium acetobutylicum* and *Clostridium beijerinckii*. When the USA lost its low-cost sugar supply from Cuba around 1954, however, butanol production by fermentation declined mainly because the price of petroleum dropped below that of sugar. Recently, there is renewed R&D interest in producing butanol and/or ethanol from biomass such as corn starch using Clostridia- and/or yeast-fermentation process. However, similarly to the situation of "cornstarch ethanol production," the "cornstarch butanol production" process also requires a number of energy-consuming steps including agricultural corn-crop cultivation, corn-grain harvesting, corn-grain starch processing, and starch-to-sugar-to-butanol fermentation. The "cornstarch butanol production" process could also probably cost nearly as much energy as the energy value of its product butanol. This is not surprising, understandably because the cornstarch that the current technology can use represents only a small fraction of the corn crop biomass that includes the corn stalks, leaves and roots. The cornstovers are commonly discarded in the agricultural fields where they slowly decompose back to CO_2, because they represent largely lignocellulosic biomass materials that the current biorefinery industry cannot efficiently use for ethanol or butanol production. There are research efforts in trying to make ethanol or butanol from lignocellulosic plant biomass materials—a concept called "cellulosic ethanol" or "cellulosic butanol". However, plant biomass has evolved effective mechanisms for resisting assault on its cell-wall structural sugars from the microbial and animal kingdoms. This property underlies a natural recalcitrance, creating roadblocks to the cost-effective transformation of lignocellulosic biomass to fermentable sugars. Therefore, one of its problems known as the "lignocellulosic recalcitrance" represents a formidable technical barrier to the cost-effective conversion of plant biomass to fermentable sugars. That is, because of the recalcitrance problem, lignocellulosic biomasses (such as cornstover, switchgrass, and woody plant materials) could not be readily converted to fermentable sugars to make ethanol or butanol without certain pretreatment, which is often associated with high processing cost. Despite more than 50 years of R&D efforts in lignocellulosic biomass pretreatment and fermentative butanol-production processing, the problem of recalcitrant lignocellulosics still remains as a formidable technical barrier that has not yet been eliminated so far. Furthermore, the steps of lignocellulosic biomass cultivation, harvesting, pretreatment processing, and cellulose-to-sugar-to-butanol fermentation

all cost energy. Therefore, any new technology that could bypass these bottleneck problems of the biomass technology would be useful.

[0006] Oxyphotobacteria (also known as blue-green algae including cyanobacteria and oxychlorobacteria) and algae (such as *Chlamydomonas reinhardtii, Platymonas subcordiformis, Chlorella fusca, Dunaliella salina, Ankistrodesmus braunii*, and *Scenedesmus obliquus*), which can perform photosynthetic assimilation of CO_2 with O_2 evolution from water in a liquid culture medium with a maximal theoretical solar-to-biomass energy conversion of about 10%, have tremendous potential to be a clean and renewable energy resource. However, the wild-type oxygenic photosynthetic green plants, such as blue-green algae and eukaryotic algae, do not possess the ability to produce butanol directly from CO_2 and H_2O. The wild-type photosynthesis uses the reducing power (NADPH) and energy (ATP) from the photosynthetic water splitting and proton gradient-coupled electron transport process through the algal thylakoid membrane system to reduce CO_2 into carbohydrates $(CH_2O)_n$ such as starch with a series of enzymes collectively called the "Calvin cycle" at the stroma region in an algal or green-plant chloroplast. The net result of the wild-type photosynthetic process is the conversion of CO_2 and H_2O into carbohydrates $(CH_2O)_n$ and O_2 using sunlight energy according to the following process reaction:

$$nCO_2+nH_2O\rightarrow(CH_2O)n+nO_2 \quad [1]$$

The carbohydrates $(CH_2O)n$ are then further converted to all kinds of complicated cellular (biomass) materials including proteins, lipids, and cellulose and other cell-wall materials during cell metabolism and growth.

[0007] In certain alga such as *Chlamydomonas reinhardtii*, some of the organic reserves such as starch could be slowly metabolized to ethanol (but not to butanol) through a secondary fermentative metabolic pathway. The algal fermentative metabolic pathway is similar to the yeast-fermentation process, by which starch is breakdown to smaller sugars such as glucose that is, in turn, transformed into pyruvate by a glycolysis process. Pyruvate may then be converted to formate, acetate, and ethanol by a number of additional metabolic steps (Gfeller and Gibbs (1984) "Fermentative metabolism of *Chlamydomonas reinhardtii*," *Plant Physiol.* 75:212-218). The efficiency of this secondary metabolic process is quite limited, probably because it could use only a small fraction of the limited organic reserve such as starch in an algal cell. Furthermore, the native algal secondary metabolic process could not produce any butanol. As mentioned above, butanol (and/or related higher alcohols) has many superior physical properties to serve as a replacement for gasoline as a fuel. Therefore, a new photobiological and/or hydrogenotrophic butanol (and/or related higher alcohols)-producing mechanism with a high energy conversion efficiency is needed.

[0008] International Application No. PCT/US2009/034801 discloses a set of methods on designer photosynthetic organisms (such as designer transgenic plant, plant cells, algae and oxyphotobacteria) for photobiological production of butanol from carbon dioxide (CO_2) and water (H_2O).

SUMMARY OF THE INVENTION

[0009] The present invention discloses designer Calvin-cycle-channeled and/or hydrogenotrophic pathways, the associated designer genes and designer transgenic photosynthetic organisms for autotrophic production of butanol and/or related higher alcohols that are selected from the group that consists of: 1-butanol, 2-methyl-1-butanol, isobutanol, 3-methyl-1-butanol, 1-hexanol, 1-octanol, 1-pentanol, 1-heptanol, 3-methyl-1-pentanol, 4-methyl-1-hexanol, 5-methyl-1-heptanol, 4-methyl-1-pentanol, 5-methyl-1-hexanol, 6-methyl-1-heptanol, and combinations thereof.

[0010] The designer autotrophic organisms such as designer transgenic oxyphotobacteria and algae comprise designer Calvin-cycle-channeled and photosynthetic NADPH-enhanced pathway gene(s) and biosafety-guarding technology for enhanced photobiological production of butanol and related higher alcohols from carbon dioxide and water.

[0011] According to another embodiment, the transgenic autotrophic organism comprises a transgenic designer plant or plant cells selected from the group consisting of aquatic plants, plant cells, green algae, red algae, brown algae, blue-green algae (oxyphotobacteria including cyanobacteria and oxychlorobacteria), diatoms, marine algae, freshwater algae, salt-tolerant algal strains, cold-tolerant algal strains, heat-tolerant algal strains, antenna-pigment-deficient mutants, butanol-tolerant algal strains, higher-alcohols-tolerant algal strains, butanol-tolerant oxyphotobacteria, higher-alcohols-tolerant oxyphotobacteria, and combinations thereof.

[0012] According to one of the various embodiments, a designer Calvin-cycle-channeled photosynthetic NADPH-enhanced pathway that takes the Calvin-cycle intermediate product, 3-phosphoglycerate, and converts it into 1-butanol comprises a set of enzymes selected from the group consisting of: NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase, NAD-dependent glyceraldehyde-3-phosphate dehydrogenase, phosphoglycerate mutase, enolase, pyruvate kinase, citramalate synthase, 2-methylmalate dehydratase, 3-isopropylmalate dehydratase, 3-isopropylmalate dehydrogenase, 2-isopropylmalate synthase, isopropylmalate isomerase, 2-keto acid decarboxylase, alcohol dehydrogenase, NADPH-dependent alcohol dehydrogenase, and butanol dehydrogenase.

[0013] According to one of the various embodiments, another designer Calvin-cycle-channeled photosynthetic NADPH-enhanced 1-butanol-production pathway comprises a set of enzymes selected from the group consisting of: NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase, NAD-dependent glyceraldehyde-3-phosphate dehydrogenase, phosphoglycerate mutase, enolase, phosphoenolpyruvate carboxylase, aspartate aminotransferase, aspartokinase, aspartate-semialdehyde dehydrogenase, homoserine dehydrogenase, homoserine kinase, threonine synthase, threonine ammonia-lyase, 2-isopropylmalate synthase, isopropylmalate isomerase, 3-isopropylmalate dehydrogenase, 2-keto acid decarboxylase, and NAD-dependent alcohol dehydrogenase, NADPH-dependent alcohol dehydrogenase, and butanol dehydrogenase.

[0014] According to another embodiment, a designer Calvin-cycle-channeled photosynthetic NADPH-enhanced pathway that takes the Calvin-cycle intermediate product, 3-phosphoglycerate, and converts it into 2-methyl-1-butanol, comprises a set of enzymes selected from the group consisting of: NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase, NAD-dependent glyceraldehyde-3-phosphate dehydrogenase, phosphoglycerate mutase, enolase, pyruvate kinase, citramalate synthase, 2-methylmalate dehydratase, 3-isopropylmalate dehydratase, 3-isopropylmalate dehydrogenase, acetolactate synthase, ketol-acid reductoi-

somerase, dihydroxy-acid dehydratase, 2-keto acid decarboxylase, NAD-dependent alcohol dehydrogenase, NADPH-dependent alcohol dehydrogenase, and 2-methylbutyraldehyde reductase.

[0015] According to another embodiment, a designer Calvin-cycle-channeled photosynthetic NADPH-enhanced pathway for photobiological production of 2-methyl-1-butanol production comprises a set of enzymes selected from the group consisting of: NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase, NAD-dependent glyceraldehyde-3-phosphate dehydrogenase, phosphoglycerate mutase, enolase, phosphoenolpyruvate carboxylase, aspartate aminotransferase, aspartokinase, aspartate-semialdehyde dehydrogenase, homoserine dehydrogenase, homoserine kinase, threonine synthase, threonine ammonia-lyase, acetolactate synthase, ketol-acid reductoisomerase, dihydroxy-acid dehydratase, 2-keto acid decarboxylase, and NAD dependent alcohol dehydrogenase, NADPH dependent alcohol dehydrogenase, and 2-methylbutyraldehyde reductase.

[0016] According to another embodiment, a designer Calvin-cycle-channeled photosynthetic NADPH-enhanced pathway for photobiological production of isobutanol comprises a set of enzymes selected from the group consisting of: NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase, NAD-dependent glyceraldehyde-3-phosphate dehydrogenase, phosphoglycerate mutase, enolase, pyruvate kinase, acetolactate synthase, ketol-acid reductoisomerase, dihydroxy-acid dehydratase, 2-keto acid decarboxylase, and NAD-dependent alcohol dehydrogenase, and NADPH-dependent alcohol dehydrogenase.

[0017] Likewise, a number of other designer Calvin-cycle-channeled photosynthetic NADPH-enhanced pathways are also disclosed according to one of the various embodiments for photobiological production of butanol and/or related higher alcohols such as 3-methyl-1-butanol, 1-hexanol, 1-octanol, 1-pentanol, 1-heptanol, 3-methyl-1-pentanol, 4-methyl-1-hexanol, 5-methyl-1-heptanol, 4-methyl-1-pentanol, 5-methyl-1-hexanol, and/or 6-methyl-1-heptanol.

[0018] According to one of various embodiments, a method for photobiological production and harvesting of butanol and related higher alcohols comprises: a) introducing a transgenic photosynthetic organism into a photobiological reactor system, the transgenic photosynthetic organism comprising transgenes coding for a set of enzymes configured to act on an intermediate product of a Calvin cycle and to convert the intermediate product into butanol and/or related higher alcohols; b) using reducing power NADPH and energy ATP associated with the transgenic photosynthetic organism acquired from photosynthetic water splitting and proton gradient coupled electron transport process in the photobioreactor to synthesize butanol and/or related higher alcohols from carbon dioxide and water; and c) using a product separation process to harvest the synthesized butanol and/or related higher alcohols from the photobioreactor.

[0019] According to another embodiment, designer hydrogen-driven Calvin-cycle-channeled biofuel-production organisms for chemolithoautotrophic production of butanol and related higher alcohols comprises a set of oxygen-tolerant soluble hydrogenase and membrane-bound hydrogenases in combination with the designer Calvin-cycle-channeled biofuel-production pathways.

[0020] According to another embodiment, a designer organism comprises a designer anaerobic hydrogenotrophic system and a reductive-acetyl-CoA biofuel-production pathway(s) for hydrogen-driven chemolithoautotrophic production of 1-butanol($CH_3CH_2CH_2CH_2OH$) from hydrogen (H_2) and carbon dioxide (CO_2) with its maximal H_2-to-butanol energy conversion efficiency as high as 91%. This designer autotrophic organism comprises a set of designer genes (e.g., designer DNA constructs) that express the designer anaerobic hydrogenotrophic butanol-production-pathway system comprising: energy converting hydrogenase (Ech), [NiFe]-hydrogenase (Mvh), Coenzyme F_{420}-reducing hydrogenase (Frh), native (or heterologous) soluble hydrogenase (SH), heterodissulfide reductase (Hdr), formylmethanofuran dehydroganse, formyl transferase, 10-methenyl-tetrahydromethanopterin cyclohydrolase, 10-methylene-H_4 methanopterin dehydrogenase, 10-methylene-H_4-methanopterin reductase, methyl-H_4-methanopterin: corrinoid iron-sulfur protein methyltransferase, corrinoid iron-sulfur protein, CO dehydrogenase/acetyl-CoA synthase, thiolase, 3-hydroxybutyryl-CoA dehydrogenase, crotonase, butyryl-CoA dehydrogenase, butyaldehyde dehydrogenase, butanol dehydrogenase and/or alcohol dehydrogenase.

[0021] According to one of the various embodiments, a designer autotrophic organism comprises a designer methanogenic hydrogenotrophic system and a reductive-acetyl-CoA biofuel-production pathway(s) for anaerobic chemolithoautotrophic production of both 1-butanol ($CH_3CH_2CH_2CH_2OH$) and methane (CH_4) from hydrogen (H_2) and carbon dioxide (CO_2). This designer autotrophic organism comprises a set of designer genes that express a designer methanogenic hydrogenotrophic butanol-production-pathway system comprising: methyl-H4MPT: coenzyme-M methyltransferase Mtr, native (or heterologous) A_1A_o-ATP synthase, methyl-coenzyme M reductase Mcr, energy converting hydrogenase (Ech), [NiFe]-hydrogenase (Mvh), Coenzyme F_{420}-reducing hydrogenase (Frh), soluble hydrogenase (SH), heterodissulfide reductase (Hdr), formate dehydroganse, 10-formyl-H_4 folate synthetase, methenyltetrahydrofolate cyclohydrolase, 10-methylene-H_4 folate dehydrogenase, 10-methylene-H_4 folate reductase, methyl-H_4 folate: corrinoid iron-sulfur protein methyltransferase, corrinoid iron-sulfur protein, CO dehydrogenase/acetyl-CoA synthase, thiolase, 3-hydroxybutyryl-CoA dehydrogenase, crotonase, butyryl-CoA dehydrogenase, butyaldehyde dehydrogenase, and butanol dehydrogenase and/or alcohol dehydrogenase.

BRIEF DESCRIPTION OF THE DRAWINGS

[0022] FIG. **1** presents designer butanol-production pathways branched from the Calvin cycle using the reducing power (NADPH) and energy (ATP) from the photosynthetic water splitting and proton gradient-coupled electron transport process to reduce carbon dioxide (CO_2) into butanol $CH_3CH_2CH_2CH_2OH$ with a series of enzymatic reactions.

[0023] FIG. **2**A presents a DNA construct for designer butanol-production-pathway gene(s).

[0024] FIG. **2**B presents a DNA construct for NADPH/NADH-conversion designer gene for NADPH/NADH interconversion.

[0025] FIG. **2**C presents a DNA construct for a designer iRNA starch/glycogen-synthesis inhibitor(s) gene.

[0026] FIG. **2**D presents a DNA construct for a designer starch-degradation-glycolysis gene(s).

[0027] FIG. **2**E presents a DNA construct of a designer butanol-production-pathway gene(s) for cytosolic expression.

[0028] FIG. **2**F presents a DNA construct of a designer butanol-production-pathway gene(s) with two recombination sites for integrative genetic transformation in oxyphotobacteria.

[0029] FIG. **2**G presents a DNA construct of a designer biosafety-control gene(s).

[0030] FIG. **2**H presents a DNA construct of a designer proton-channel gene(s).

[0031] FIG. **3**A illustrates a cell-division-controllable designer organism that contains two key functions: designer biosafety mechanism(s) and designer biofuel-production pathway(s).

[0032] FIG. **3**B illustrates a cell-division-controllable designer organism for photobiological production of butanol ($CH_3CH_2CH_2CH_2OH$) from carbon dioxide (CO_2) and water (H_2O) with designer biosafety mechanism(s).

[0033] FIG. **3**C illustrates a cell-division-controllable designer organism for biosafety-guarded photobiological production of other biofuels such as ethanol (CH_3CH_2OH) from carbon dioxide (CO_2) and water (H_2O).

[0034] FIG. **4** presents designer Calvin-cycle-channeled and photosynthetic NADPH-enhanced pathways using the reducing power (NADPH) and energy (ATP) from the photosynthetic water splitting and proton gradient-coupled electron transport process to reduce carbon dioxide (CO_2) into 1-butanol($CH_3CH_2CH_2CH_2OH$) with a series of enzymatic reactions.

[0035] FIG. **5** presents designer Calvin-cycle-channeled and photosynthetic NADPH-enhanced pathways using NADPH and ATP from the photosynthetic water splitting and proton gradient-coupled electron transport process to reduce carbon dioxide (CO_2) into 2-methyl-1-butanol ($CH_3CH_2CH(CH_3)CH_2OH$) with a series of enzymatic reactions.

[0036] FIG. **6** presents designer Calvin-cycle-channeled and photosynthetic NADPH-enhanced pathways using NADPH and ATP from the photosynthetic water splitting and proton gradient-coupled electron transport process to reduce carbon dioxide (CO_2) into isobutanol ($(CH_3)_2CHCH_2OH$) and 3-methyl-1-butanol($CH_3CH(CH_3)CH_2CH_2OH$) with a series of enzymatic reactions.

[0037] FIG. **7** presents designer Calvin-cycle-channeled and photosynthetic NADPH-enhanced pathways using NADPH and ATP from the photosynthetic water splitting and proton gradient-coupled electron transport process to reduce carbon dioxide (CO_2) into 1-hexanol ($CH_3CH_2CH_2CH_2CH_2CH_2OH$) and 1-octanol ($CH_3CH_2CH_2CH_2CH_2CH_2CH_2CH_2OH$) with a series of enzymatic reactions.

[0038] FIG. **8** presents designer Calvin-cycle-channeled and photosynthetic NADPH-enhanced pathways using NADPH and ATP from the photosynthetic water splitting and proton gradient-coupled electron transport process to reduce carbon dioxide (CO_2) into 1-pentanol ($CH_3CH_2CH_2CH_2CH_2OH$), 1-hexanol ($CH_3CH_2CH_2CH_2CH_2CH_2OH$), and 1-heptanol ($CH_3CH_2CH_2CH_2CH_2CH_2CH_2OH$) with a series of enzymatic reactions.

[0039] FIG. **9** presents designer Calvin-cycle-channeled and photosynthetic NADPH-enhanced pathways using NADPH and ATP from the photosynthetic water splitting and proton gradient-coupled electron transport process to reduce carbon dioxide (CO_2) into 3-methyl-1-pentanol ($CH_3CH_2CH(CH_3)CH_2CH_2OH$), 4-methyl-1-hexanol ($CH_3CH_2CH(CH_3)CH_2CH_2CH_2OH$), and 5-methyl-1-heptanol ($CH_3CH_2CH(CH_3)CH_2CH_2CH_2CH_2OH$) with a series of enzymatic reactions.

[0040] FIG. **10** presents designer Calvin-cycle-channeled and photosynthetic NADPH-enhanced pathways using NADPH and ATP from the photosynthetic water splitting and proton gradient-coupled electron transport process to reduce carbon dioxide (CO_2) into 4-methyl-1-pentanol ($CH_3CH(CH_3)CH_2CH_2CH_2OH$), 5-methyl-1-hexanol ($CH_3CH(CH_3)CH_2CH_2CH_2CH_2OH$), and 6-methyl-1-heptanol ($CH_3CH(CH_3)CH_2CH_2CH_2CH_2CH_2OH$) with a series of enzymatic reactions.

[0041] FIG. **11** illustrates a designer organism with designer oxygen-tolerant hydrogenases and Calvin-cycle-channeled biofuel-production pathway(s) for aerobic chemolithoautotrophic production of biofuels such as butanol ($CH_3CH_2CH_2CH_2OH$) from hydrogen (H_2), carbon dioxide (CO_2), and oxygen (O_2).

[0042] FIG. **12** illustrates a designer organism that comprises a designer anaerobic hydrogenotrophic system with reductive-acetyl-CoA biofuel-production pathway(s) for anaerobic chemolithotrophic production of 1-butanol ($CH_3CH_2CH_2CH_2OH$) from hydrogen (H_2) and carbon dioxide (CO_2).

[0043] FIG. **13** presents a designer reductive-acetyl-CoA biofuel-production pathway for anaerobic hydrogenotrophic production of 1-butanol(CH_3CH_2 CH_2CH_2OH) from carbon dioxide (CO_2) with a series of enzymatic reactions.

[0044] FIG. **14** presents a designer ATP-required reductive-acetyl-CoA biofuel-production pathway for anaerobic hydrogenotrophic production of 1-butanol(CH_3 CH_2 CH_2CH_2OH) from carbon dioxide (CO_2) with a series of enzymatic reactions.

[0045] FIG. **15** illustrates a designer organism that comprises a designer methanogenic hydrogenotrophic system with reductive-acetyl-CoA biofuel-production pathway(s) for anaerobic chemolithotrophic production of both 1-butanol($CH_3CH_2CH_2CH_2OH$) and methane (CH_4) from hydrogen (H_2) and carbon dioxide (CO_2).

[0046] FIG. **16** presents designer reductive-acetyl-CoA biofuel-production pathways for anaerobic hydrogenotrophic production of both 1-butanol ($CH_3CH_2CH_2CH_2OH$) and methane (CH_4) from carbon dioxide (CO_2) with a series of enzymatic reactions.

[0047] FIG. **17** presents designer ATP-required reductive-acetyl-CoA biofuel-production pathways for anaerobic hydrogenotrophic production of both 1-butanol ($CH_3CH_2CH_2CH_2OH$) and methane (CH_4) from carbon dioxide (CO_2) and with a series of enzymatic reactions.

DETAILED DESCRIPTION OF THE INVENTION

[0048] The present invention is directed to an autotrophic butanol and related high alcohols production technology based on designer autotrophic organisms such as designer transgenic plants (e.g., algae and oxyphotobacteria), plant cells, or bacteria. In this context throughout this specification, a "higher alcohol" or "related higher alcohol" refers to an alcohol that comprises at least four carbon atoms, which includes both straight and branched alcohols such as 1-butanol and 2-methyl-1-butanol. The Calvin-cycle-channeled and photosynthetic-NADPH-enhanced pathways are constructed with designer enzymes expressed through use of designer genes in host photosynthetic organisms such as algae and oxyphotobacteria (including cyanobacteria and

oxychlorobacteria) organisms for photobiological production of butanol and related higher alcohols. The said butanol and related higher alcohols are selected from the group consisting of: 1-butanol, 2-methyl-1-butanol, isobutanol, 3-methyl-1-butanol, 1-hexanol, 1-octanol, 1-pentanol, 1-heptanol, 3-methyl-1-pentanol, 4-methyl-1-hexanol, 5-methyl-1-heptanol, 4-methyl-1-pentanol, 5-methyl-1-hexanol, and 6-methyl-1-heptanol. The designer plants and plant cells are created using genetic engineering techniques such that the endogenous photosynthesis regulation mechanism is tamed, and the reducing power (NADPH) and energy (ATP) acquired from the photosynthetic water splitting and proton gradient-coupled electron transport process can be used for immediate synthesis of higher alcohols, such as 1-butanol ($CH_3CH_2CH_2CH_2OH$) and 2-methyl-1-butanol($CH_3CH_2CH(CH_3)CH_2OH$), from carbon dioxide (CO_2) and water (H_2O) according to the following generalized process reaction (where m, n, x and y are its molar coefficients) in accordance of the present invention:

$$m(CO_2)+n(H_2O)\rightarrow x(\text{higher alcohols})+y(O_2) \quad [2]$$

The photobiological higher-alcohols-production methods of the present invention completely eliminate the problem of recalcitrant lignocellulosics by bypassing the bottleneck problem of the biomass technology. As shown in FIG. **1**, for example, the photosynthetic process in a designer organism effectively uses the reducing power (NADPH) and energy (ATP) from the photosynthetic water splitting and proton gradient-coupled electron transport process for immediate synthesis of butanol ($CH_3CH_2CH_2CH_2OH$) directly from carbon dioxide (CO_2) and water (H_2O) without being drained into the other pathway for synthesis of the undesirable lignocellulosic materials that are very hard and often inefficient for the biorefinery industry to use. This approach is also different from the existing "cornstarch butanol production" process. In accordance with this invention, butanol can be produced directly from carbon dioxide (CO_2) and water (H_2O) without having to go through many of the energy consuming steps that the cornstarch butanol-production process has to go through, including corn crop cultivation, corn-grain harvesting, corn-grain cornstarch processing, and starch-to-sugar-to-butanol fermentation. As a result, the photosynthetic butanol-production technology of the present invention is expected to have a much (more than 10-times) higher solar-to-butanol energy-conversion efficiency than the current technology. Assuming a 10% solar energy conversion efficiency for the proposed photosynthetic butanol production process, the maximal theoretical productivity (yield) could be about 72,700 kg of butanol per acre per year, which could support about 70 cars (per year per acre). Therefore, this invention could bring a significant capability to the society in helping to ensure energy security. The present invention could also help protect the Earth's environment from the dangerous accumulation of CO_2 in the atmosphere, because the present methods convert CO_2 directly into clean butanol energy.

[0049] A fundamental feature of the present methodology is utilizing a plant (e.g., an alga or oxyphotobacterium) or plant cells, introducing into the plant or plant cells nucleic acid molecules encoding for a set of enzymes that can act on an intermediate product of the Calvin cycle and convert the intermediate product into butanol as illustrated in FIG. **1**, instead of making starch and other complicated cellular (biomass) materials as the end products by the wild-type photosynthetic pathway. Accordingly, the present invention provides, inter alia, methods for producing butanol and/or related higher alcohols based on a designer plant (such as a designer alga and a designer oxyphotobacterium), designer plant tissue, or designer plant cells, DNA constructs encoding genes of a designer butanol- and/or related higher alcohols-production pathway(s), as well as the designer algae, designer oxyphotobacteria (including designer cyanobacteria), designer plants, designer plant tissues, and designer plant cells created. The various aspects of the present invention are described in further detail hereinbelow.

Host Photosynthetic Organisms

[0050] According to the present invention, a designer organism or cell for the photosynthetic butanol and/or related higher alcohols production of the invention can be created utilizing as host, any plant (including alga and oxyphotobacterium), plant tissue, or plant cells that have a photosynthetic capability, i.e., an active photosynthetic apparatus and enzymatic pathway that captures light energy through photosynthesis, using this energy to convert inorganic substances into organic matter. Preferably, the host organism should have an adequate photosynthetic CO_2 fixation rate, for example, to support photosynthetic butanol (and/or related higher alcohols) production from CO_2 and H_2O at least about 1,450 kg butanol per acre per year, more preferably, 7,270 kg butanol per acre per year, or even more preferably, 72,700 kg butanol per acre per year.

[0051] In a preferred embodiment, an aquatic plant is utilized to create a designer plant. Aquatic plants, also called hydrophytic plants, are plants that live in or on aquatic environments, such as in water (including on or under the water surface) or permanently saturated soil. As used herein, aquatic plants include, for example, algae, blue-green algae (cyanobacteria and oxychlorobacteria), submersed aquatic herbs (*Hydrilla verticillate, Elodea densa, Hippuris vulgaris, Aponogeton Boivinianus Aponogeton Rigidifolius, Aponogeton Longiplumulosus, Didiplis Diandra, Vesicularia Dubyana, Hygrophilia Augustifolia, Micranthemum Umbrosum, Eichhornia Azurea, Saururus Cernuus, Cryptocoryne Lingua, Hydrotriche Hottoniiflora Eustralis Stellata, Vallisneria Rubra, Hygrophila Salicifolia, Cyperus Helferi, Cryptocoryne Petchii, Vallisneria americana, Vallisneria Torta, Hydrotriche Hottoniiflora, Crassula Helmsii, Limnophila Sessiliflora, Potamogeton Perfoliatus, Rotala Wallichii, Cryptocoryne Becketii, Blyxa Aubertii, Hygrophila Difformmis*), duckweeds (*Spirodela polyrrhiza, Wolffia globosa, Lemna trisulca, Lemna gibba, Lemna minor, Landoltia punctata*), water cabbage (*Pistia stratiotes*), buttercups (*Ranunculus*), water caltrop (*Trapa natans* and *Trapa bicornis*), water lily (*Nymphaea lotus*, Nymphaeaceae and Nelumbonaceae), water hyacinth (*Eichhornia crassipes*), *Bolbitis heudelotii, Cabomba* sp., seagrasses (*Heteranthera Zosterifolia*, Posidoniaceae, Zosteraceae, Hydrocharitaceae, and Cymodoceaceae). Butanol (and/or related higher alcohols) produced from an aquatic plant can diffuse into water, permitting normal growth of the plants and more robust production of butanol from the plants. Liquid cultures of aquatic plant tissues (including, but not limited to, multicellular algae) or cells (including, but not limited to, unicellular algae) are also highly preferred for use, since the butanol (and/or related higher alcohols) molecules produced from a designer butanol (and/or related higher alcohols) production pathway(s) can readily diffuse out of the cells or tissues into the liquid water medium, which can serve as a large pool to store the product

butanol (and/or related higher alcohols) that can be subsequently harvested by filtration and/or distillation/evaporation techniques.

[0052] Although aquatic plants or cells are preferred host organisms for use in the methods of the present invention, tissue and cells of non-aquatic plants, which are photosynthetic and can be cultured in a liquid culture medium, can also be used to create designer tissue or cells for photosynthetic butanol (and/or related higher alcohols) production. For example, the following tissue or cells of non-aquatic plants can also be selected for use as a host organism in this invention: the photoautotrophic shoot tissue culture of wood apple tree *Feronia limonia*, the chlorophyllous callus-cultures of corn plant *Zea mays*, the green root cultures of Asteraceae and Solanaceae species, the tissue culture of sugarcane stalk parenchyma, the tissue culture of bryophyte *Physcomitrella patens*, the photosynthetic cell suspension cultures of soybean plant (*Glycine max*), the photoautotrophic and photomixotrophic culture of green Tobacco (*Nicofiana tabacum* L.) cells, the cell suspension culture of *Gisekia pharmaceoides* (a C_4 plant), the photosynthetic suspension cultured lines of *Amaranthus powellii* Wats., *Datura innoxia* Mill., *Gossypium hirsutum* L., and *Nicotiana tabacum*×*Nicotiana glutinosa* L. fusion hybrid.

[0053] By "liquid medium" is meant liquid water plus relatively small amounts of inorganic nutrients (e.g., N, P, K etc, commonly in their salt forms) for photoautotrophic cultures; and sometimes also including certain organic substrates (e.g., sucrose, glucose, or acetate) for photomixotrophic and/or photoheterotrophic cultures.

[0054] In an especially preferred embodiment, the plant utilized in the butanol (and/or related higher alcohols) production method of the present invention is an alga or a blue-green alga. The use of algae and/or blue-green algae has several advantages. They can be grown in an open pond at large amounts and low costs. Harvest and purification of butanol (and/or related higher alcohols) from the water phase is also easily accomplished by distillation/evaporation or membrane separation.

[0055] Algae suitable for use in the present invention include both unicellular algae and multi-unicellular algae. Multicellular algae that can be selected for use in this invention include, but are not limited to, seaweeds such as *Ulva latissima* (sea lettuce), *Ascophyllum nodosum, Codium fragile, Fucus vesiculosus, Eucheuma denticulatum, Gracilaria gracilis, Hydrodictyon reticulatum, Laminaria japonica, Undaria pinntifida, Saccharina japonica, Porphyra yezoensis*, and *Porphyra tenera*. Suitable algae can also be chosen from the following divisions of algae: green algae (Chlorophyta), red algae (Rhodophyta), brown algae (Phaeophyta), diatoms (Bacillariophyta), and blue-green algae (Oxyphotobacteria including Cyanophyta and Prochlorophytes). Suitable orders of green algae include Ulvales, Ulotrichales, Volvocales, Chlorellales, Schizogoniales, Oedogoniales, Zygnematales, Cladophorales, Siphonales, and Dasycladales. Suitable genera of Rhodophyta are *Porphyra, Chondrus, Cyanidioschyzon, Porphyridium, Gracilaria, Kappaphycus, Gelidium* and *Agardhiella*. Suitable genera of Phaeophyta are *Laminaria, Undaria, Macrocystis, Sargassum* and *Dictyosiphon*. Suitable genera of Cyanophyta (also known as Cyanobacteria) include (but not limited to) *Phoridium, Synechocystis, Syncechococcus, Oscillatoria*, and *Anabaena*. Suitable genera of Prochlorophytes (also known as oxychlorobacteria) include (but not limited to) *Prochloron, Prochlorothrix*, and *Prochlorococcus*. Suitable genera of Bacillariophyta are *Cyclotella, Cylindrotheca, Navicula, Thalassiosira*, and *Phaeodactylum*. Preferred species of algae for use in the present invention include *Chlamydomonas reinhardtii, Platymonas subcordiformis, Chlorella fusca, Chlorella sorokiniana, Chlorella vulgaris, 'Chlorella' ellipsoidea, Chlorella* spp., *Dunaliella salina, Dunaliella viridis, Dunaliella bardowil, Haematococcus pluvialis; Parachlorella kessleri, Betaphycus gelatinum, Chondrus crispus, Cyanidioschyzon merolae, Cyanidium caldarium, Galdieria sulphuraria, Gelidiella acerosa, Gracilaria changii, Kappaphycus alvarezii, Porphyra miniata, Ostreococcus tauri, Porphyra yezoensis, Porphyridium* sp., *Palmaria palmata, Gracilaria* spp., *Isochrysis galbana, Kappaphycus* spp., *Laminaria japonica, Laminaria* spp., *Monostroma* spp., *Nannochloropsis oculata, Porphyra* spp., *Porphyridium* spp., *Undaria pinnatifida, Ulva lactuca, Ulva* spp., *Undaria* spp., *Phaeodactylum Tricornutum, Navicula saprophila, Crypthecodinium cohnii, Cylindrotheca fusiformis, Cyclotella cryptica, Euglena gracilis, Amphidinium* sp., *Symbiodinium microadriaticum, Macrocystis pyrifera, Ankistrodesmus braunii*, and *Scenedesmus obliquus*.

[0056] Preferred species of blue-green algae (oxyphotobacteria including cyanobacteria and oxychlorobacteria) for use in the present invention include *Thermosynechococcus elongatus* BP-1, *Nostoc* sp. PCC 7120, *Synechococcus elongatus* PCC 6301, *Syncechococcus* sp. strain PCC 7942, *Syncechococcus* sp. strain PCC 7002, *Syncechocystis* sp. strain PCC 6803, *Prochlorococcus marinus* MED4, *Prochlorococcus marinus* MIT 9313, *Prochlorococcus marinus* NATL1A, *Prochlorococcus* SS120, *Spirulina platensis* (*Arthrospira platensis*), *Spirulina pacifica, Lyngbya majuscule, Anabaena* sp., *Synechocystis* sp., *Synechococcus elongates, Synechococcus* (MC-A), *Trichodesmium* sp., *Richelia intracellularis, Synechococcus* WH7803, *Synechococcus* WH8102, *Nostoc punctiforme, Syncechococcus* sp. strain PCC 7943, Synechocyitis PCC 6714 phycocyanin-deficient mutant PD-1, *Cyanothece* strain 51142, *Cyanothece* sp. CCY0110, *Oscillatoria limosa, Lyngbya majuscula, Symploca muscorum, Gloeobacter violaceus, Prochloron didemni, Prochlorothrix hollandica, Synechococcus* (MC-A), *Trichodesmium* sp., *Richelia intracellularis, Prochlorococcus marinus, Prochlorococcus* SS120, *Synechococcus* WH8102, *Lyngbya majuscula, Symploca muscorum, Synechococcus bigranulatus*, cryophilic *Oscillatoria* sp., *Phormidium* sp., *Nostoc* sp.-1, *Calothrix parietina*, thermophilic *Synechococcus bigranulatus, Synechococcus lividus*, thermophilic *Mastigocladus laminosus, Chlorogloeopsis fritschii* PCC 6912, *Synechococcus vulcanus, Synechococcus* sp. strain MA4, *Synechococcus* sp. strain MA19, and *Thermosynechococcus elongatus*.

[0057] Proper selection of host photosynthetic organisms for their genetic backgrounds and certain special features is also beneficial. For example, a photosynthetic-butanol-producing designer alga created from cryophilic algae (psychrophiles) that can grow in snow and ice, and/or from cold-tolerant host strains such as *Chlamydomonas* cold strain CCMG1619, which has been characterized as capable of performing photosynthetic water splitting as cold as 4° C. (Lee, Blankinship and Greenbaum (1995), "Temperature effect on production of hydrogen and oxygen by *Chlamydomonas* cold strain CCMP1619 and wild type 137c," *Applied Biochemistry and Biotechnology* 51/52:379-386), permits photobiological butanol production even in cold seasons or regions such as Canada. Meanwhile, a designer alga

created from a thermophilic/thermotolerant photosynthetic organism such as thermophilic algae *Cyanidium caldarium* and *Galdieria sulphuraria* and/or thermophilic cyanobacteria (blue-green algae) such as *Thermosynechococcus elongatus* BP-1 and *Synechococcus bigranulatus* may permit the practice of this invention to be well extended into the hot seasons or areas such as Mexico and the Southwestern region of the United States including Nevada, California, Arizona, New Mexico and Texas, where the weather can often be hot. Furthermore, a photosynthetic-butanol-producing designer alga created from a marine alga, such as *Platymonas subcordiformis*, permits the practice of this invention using seawater, while the designer alga created from a freshwater alga such as *Chlamydomonas reinhardtii* can use freshwater. Additional optional features of a photosynthetic butanol (and/or related higher alcohols) producing designer alga include the benefits of reduced chlorophyll-antenna size, which has been demonstrated to provide higher photosynthetic productivity (Lee, Mets, and Greenbaum (2002). "Improvement of photosynthetic efficiency at high light intensity through reduction of chlorophyll antenna size," *Applied Biochemistry and Biotechnology,* 98-100: 37-48) and butanol-tolerance (and/or related higher alcohols-tolerance) that allows for more robust and efficient photosynthetic production of butanol (and/or related higher alcohols) from CO_2 and H_2O. By use of a phycocyanin-deficient mutant of *Synechocystis* PCC 6714, it has been experimentally demonstrated that photoinhibition can be reduced also by reducing the content of light-harvesting pigments (Nakajima, Tsuzuki, and Ueda (1999) "Reduced photoinhibition of a phycocyanin-deficient mutant of *Synechocystis* PCC 6714", *Journal of Applied Phycology* 10: 447-452). These optional features can be incorporated into a designer alga, for example, by use of a butanol-tolerant and/or chlorophyll antenna-deficient mutant (e.g., *Chlamydomonas reinhardtii* strain DS521) as a host organism, for gene transformation with the designer butanol-production-pathway genes. Therefore, in one of the various embodiments, a host alga is selected from the group consisting of green algae, red algae, brown algae, blue-green algae (oxyphotobacteria including cyanobacteria and prochlorophytes), diatoms, marine algae, freshwater algae, unicellular algae, multicellular algae, seaweeds, cold-tolerant algal strains, heat-tolerant algal strains, light-harvesting-antenna-pigment-deficient mutants, butanol-tolerant algal strains, higher alcohols-tolerant algal strains, and combinations thereof.

Creating a Designer Butanol-Production Pathway in a Host

Selecting Appropriate Designer Enzymes

[0058] One of the key features in the present invention is the creation of a designer butanol-production pathway to tame and work with the natural photosynthetic mechanisms to achieve the desirable synthesis of butanol directly from CO_2 and H_2O. The natural photosynthetic mechanisms include (1) the process of photosynthetic water splitting and proton gradient-coupled electron transport through the thylakoid membrane, which produces the reducing power (NADPH) and energy (ATP), and (2) the Calvin cycle, which reduces CO_2 by consumption of the reducing power (NADPH) and energy (ATP).

[0059] In accordance with the present invention, a series of enzymes are used to create a designer butanol-production pathway that takes an intermediate product of the Calvin cycle and converts the intermediate product into butanol as illustrated in FIG. **1**. A "designer butanol-production-pathway enzyme" is hereby defined as an enzyme that serves as a catalyst for at least one of the steps in a designer butanol-production pathway. According to the present invention, a number of intermediate products of the Calvin cycle can be utilized to create designer butanol-production pathway(s); and the enzymes required for a designer butanol-production pathway are selected depending upon from which intermediate product of the Calvin cycle the designer butanol-production pathway branches off from the Calvin cycle.

[0060] In one example, a designer pathway is created that takes glyceraldehydes-3-phosphate and converts it into butanol by using, for example, a set of enzymes consisting of, as shown with the numerical labels 01-12 in FIG. **1**, glyceraldehyde-3-phosphate dehydrogenase 01, phosphoglycerate kinase 02, phosphoglycerate mutase 03, enolase 04, pyruvate kinase 05, pyruvate-ferredoxin oxidoreductase 06, thiolase 07, 3-hydroxybutyryl-CoA dehydrogenase 08, crotonase 09, butyryl-CoA dehydrogenase 10, butyraldehyde dehydrogenase 11, and butanol dehydrogenase 12. In this glyceraldehydes-3-phosphate-branched designer pathway, for conversion of two molecules of glyceraldehyde-3-phosphate to butanol, two NADH molecules are generated from NAD^+ at the step from glyceraldehyde-3-phosphate to 1,3-diphosphoglycerate catalyzed by glyceraldehyde-3-phosphate dehydrogenase 01; meanwhile two molecules of NADH are converted to NAD^+: one at the step catalyzed by 3-hydroxybutyryl-CoA dehydrogenase 08 in reducing acetoacetyl-CoA to 3-hydroxybutyryl-CoA and another at the step catalyzed by butyryl-CoA dehydrogenase 10 in reducing crotonyl-CoA to butyryl-CoA. Consequently, in this glyceraldehydes-3-phosphate-branched designer pathway (01-12), the number of NADH molecules consumed is balanced with the number of NADH molecules generated. Furthermore, both the pathway step catalyzed by butyraldehyde dehydrogenase 11 (in reducing butyryl-CoA to butyraldehyde) and the terminal step catalyzed by butanol dehydrogenase 12 (in reducing butyraldehyde to butanol) can use NADPH, which can be regenerated by the photosynthetic water splitting and proton gradient-coupled electron transport process. Therefore, this glyceraldehydes-3-phosphate-branched designer butanol-production pathway can operate continuously.

[0061] In another example, a designer pathway is created that takes the intermediate product, 3-phosphoglycerate, and converts it into butanol by using, for example, a set of enzymes consisting of (as shown with the numerical labels 03-12 in FIG. **1**) phosphoglycerate mutase 03, enolase 04, pyruvate kinase 05, pyruvate-ferredoxin oxidoreductase 06, thiolase 07, 3-hydroxybutyryl-CoA dehydrogenase 08, crotonase 09, butyryl-CoA dehydrogenase 10, butyraldehyde dehydrogenase 11, and butanol dehydrogenase 12. It is worthwhile to note that the last ten enzymes (03-12) of the glyceraldehydes-3-phosphate-branched designer butanol-producing pathway (01-12) are identical with those utilized in the 3-phosphoglycerate-branched designer pathway (03-12). In other words, the designer enzymes (01-12) of the glyceraldehydes-3-phosphate-branched pathway permit butanol production from both the point of 3-phosphoglycerate and the point glyceraldehydes 3-phosphate in the Calvin cycle. These two pathways, however, have different characteristics. Unlike the glyceraldehyde-3-phosphate-branched butanol-production pathway, the 3-phosphoglycerate-branched pathway which consists of the activities of only ten enzymes (03-12) could not itself generate any NADH that is required for use at

two places: one at the step catalyzed by 3-hydroxybutyryl-CoA dehydrogenase 08 in reducing acetoacetyl-CoA to 3-hydroxybutyryl-CoA, and another at the step catalyzed by butyryl-CoA dehydrogenase 10 in reducing crotonyl-CoA to butyryl-CoA. That is, if (or when) a 3-hydroxybutyryl-CoA dehydrogenase and/or a butyryl-CoA dehydrogenase that can use strictly only NADH but not NADPH is employed, it would require a supply of NADH for the 3-phosphoglycerate-branched pathway (03-12) to operate. Consequently, in order for the 3-phosphoglycerate-branched butanol-production pathway to operate, it is important to use a 3-hydroxybutyryl-CoA dehydrogenase 08 and a butyryl-CoA dehydrogenase 10 that can use NADPH which can be supplied by the photo-driven electron transport process. Therefore, it is a preferred practice to use a 3-hydroxybutyryl-CoA dehydrogenase and a butyryl-CoA dehydrogenase that can use NADPH or both NADPH and NADH (i.e., NAD(P)H) for this 3-phosphoglycerate-branched designer butanol-production pathway (03-12 in FIG. **1**). Alternatively, when a 3-hydroxybutyryl-CoA dehydrogenase and a butyryl-CoA dehydrogenase that can use only NADH are employed, it is preferably here to use an additional embodiment that can confer an NADPH/NADH conversion mechanism (to supply NADH by converting NADPH to NADH, see more detail later in the text) in the designer organism to facilitate photosynthetic production of butanol through the 3-phosphoglycerate-branched designer pathway.

[0062] In still another example, a designer pathway is created that takes fructose-1,6-diphosphate and converts it into butanol by using, as shown with the numerical labels 20-33 in FIG. **1**, a set of enzymes consisting of aldolase 20, triose phosphate isomerase 21, glyceraldehyde-3-phosphate dehydrogenase 22, phosphoglycerate kinase 23, phosphoglycerate mutase 24, enolase 25, pyruvate kinase 26, pyruvate-$NADP^+$ oxidoreductase (or pyruvate-ferredoxin oxidoreductase) 27, thiolase 28, 3-hydroxybutyryl-CoA dehydrogenase 29, crotonase 30, butyryl-CoA dehydrogenase 31, butyraldehyde dehydrogenase 32, and butanol dehydrogenase 33, with aldolase 20 and triose phosphate isomerase 21 being the only two additional enzymes relative to the glyceraldehydes-3-phosphate-branched designer pathway. The use of a pyruvate-$NADP^+$ oxidoreductase 27 (instead of pyruvate-ferredoxin oxidoreductase) in catalyzing the conversion of a pyruvate molecule to acetyl-CoA enables production of an NADPH, which can be used in some other steps of the butanol-production pathway. The addition of yet one more enzyme in the designer organism, phosphofructose kinase 19, permits the creation of another designer pathway which branches off from the point of fructose-6-phosphate of the Calvin cycle for the production of butanol. Like the glyceraldehyde-3-phosphate-branched butanol-production pathway, both the fructose-1,6-diphosphate-branched pathway (20-33) and the fructose-6-phosphate-branched pathway (19-33) can themselves generate NADH for use in the pathway at the step catalyzed by 3-hydroxybutyryl-CoA dehydrogenase 29 to reduce acetoacetyl-CoA to 3-hydroxybutyryl-CoA and at the step catalyzed by butyryl-CoA dehydrogenase 31 to reduce crotonyl-CoA to butyryl-CoA. In each of these designer butanol-production pathways, the numbers of NADH molecules consumed are balanced with the numbers of NADH molecules generated; and both the butyraldehyde dehydrogenase 32 (catalyzing the step in reducing butyryl-CoA to butyraldehyde) and the butanol dehydrogenase 33 (catalyzing the terminal step in reducing butyraldehyde to butanol) can all use NADPH, which can be regenerated by the photosynthetic water splitting and proton gradient-coupled electron transport process. Therefore, these designer butanol-production pathways can operate continuously.

[0063] Table 1 lists examples of the enzymes including those identified above for construction of the designer butanol-production pathways. Throughout this specification, when reference is made to an enzyme, such as, for example, any of the enzymes listed in Table 1, it includes their isozymes, functional analogs, and designer modified enzymes and combinations thereof. These enzymes can be selected for use in construction of the designer butanol-production pathways (such as those illustrated in FIG. **1**). The "isozymes or functional analogs" refer to certain enzymes that have the same catalytic function but may or may not have exactly the same protein structures. The most essential feature of an enzyme is its active site that catalyzes the enzymatic reaction. Therefore, certain enzyme-protein fragment(s) or subunit(s) that contains such an active catalytic site may also be selected for use in this invention. For various reasons, some of the natural enzymes contain not only the essential catalytic structure but also other structure components that may or may not be desirable for a given application. With techniques of bioinformatics-assisted molecular designing, it is possible to select the essential catalytic structure(s) for use in construction of a designer DNA construct encoding a desirable designer enzyme. Therefore, in one of the various embodiments, a designer enzyme gene is created by artificial synthesis of a DNA construct according to bioinformatics-assisted molecular sequence design. With the computer-assisted synthetic biology approach, any DNA sequence (thus its protein structure) of a designer enzyme may be selectively modified to achieve more desirable results by design. Therefore, the terms "designer modified sequences" and "designer modified enzymes" are hereby defined as the DNA sequences and the enzyme proteins that are modified with bioinformatics-assisted molecular design. For example, when a DNA construct for a designer chloroplast-targeted enzyme is designed from the sequence of a mitochondrial enzyme, it is a preferred practice to modify some of the protein structures, for example, by selectively cutting out certain structure component(s) such as its mitochondrial transit-peptide sequence that is not suitable for the given application, and/or by adding certain peptide structures such as an exogenous chloroplast transit-peptide sequence (e.g., a 135-bp Rubisco small-subunit transit peptide (RbcS2)) that is needed to confer the ability in the chloroplast-targeted insertion of the designer protein. Therefore, one of the various embodiments flexibly employs the enzymes, their isozymes, functional analogs, designer modified enzymes, and/or the combinations thereof in construction of the designer butanol-production pathway (s).

[0064] As shown in Table 1, many genes of the enzymes identified above have been cloned and/or sequenced from various organisms. Both genomic DNA and/or mRNA sequence data can be used in designing and synthesizing the designer DNA constructs for transformation of a host alga, oxyphotobacterium, plant, plant tissue or cells to create a designer organism for photobiological butanol production (FIG. **1**). However, because of possible variations often associated with various source organisms and cellular compartments with respect to a specific host organism and its chloroplast/thylakoid environment where the butanol-production pathway(s) is designed to work with the Calvin cycle, certain

molecular engineering art work in DNA construct design including codon-usage optimization and sequence modification is often necessary for a designer DNA construct (FIG. **2**) to work well. For example, in creating a butanol-producing designer eukaryotic alga, if the source sequences are from cytosolic enzymes (sequences), a functional chloroplast-targeting sequence may be added to provide the capability for a designer unclear gene-encoded enzyme to insert into a host chloroplast to confer its function for a designer butanol-production pathway. Furthermore, to provide the switchability for a designer butanol-production pathway, it is also important to include a functional inducible promoter sequence such as the promoter of a hydrogenase (Hyd1) or nitrate reductase (Nia1) gene, or nitrite reductase (nirA) gene in certain designer DNA construct(s) as illustrated in FIG. **2**A to control the expression of designer gene(s). In addition, as mentioned before, certain functional derivatives or fragments of these enzymes (sequences), chloroplast-targeting transit peptide sequences, and inducible promoter sequences can also be selected for use in full, in part or in combinations thereof, to create the designer organisms according to various embodiments of this invention. The arts in creating and using the designer organisms are further described hereinbelow.

Targeting the Designer Enzymes to the Stroma Region of Chloroplasts

[0065] Some of the designer enzymes discussed above, such as, pyruvate-ferredoxin oxidoreductase, thiolase, 3-hydroxybutyryl-CoA dehydrogenase, crotonase, butyryl-CoA dehydrogenase, butyraldehyde dehydrogenase, and butanol dehydrogenase are known to function in certain special bacteria such as *Clostridium*; but wild-type plant chloroplasts generally do not possess these enzymes to function with the Calvin cycle. Therefore, in one of the various embodiments in creating a butanol-producing eukaryotic designer organism, designer nucleic acids encoding for these enzymes are expressed in the chloroplast(s) of a host cell. This can be accomplished by delivery of designer butanol-production-pathway gene(s) into the chloroplast genome of the eukaryotic host cell typically using a genegun. In certain extent, the molecular genetics of chloroplasts are similar to that of cyanobacteria. After being delivered into the chloroplast, a designer DNA construct that contains a pair of proper recombination sites as illustrated in FIG. **2**F can be incorporated into the chloroplast genome through a natural process of homologous DNA double recombination.

[0066] In another embodiment, nucleic acids encoding for these enzymes are genetically engineered such that the enzymes expressed are inserted into the chloroplasts to operate with the Calvin cycle there. Depending on the genetic background of a particular host organism, some of the designer enzymes discussed above such as phosphoglycerate mutase and enolase may exist at some background levels in its native form in a wild-type chloroplast. For various reasons including often the lack of their controllability, however, some of the chloroplast background enzymes may or may not be sufficient to serve as a significant part of the designer butanol-production pathway(s). Furthermore, a number of useful inducible promoters happen to function in the nuclear genome. For example, both the hydrogenase (Hyd1) promoter and the nitrate reductase (Nia1) promoter that can be used to control the expression of the designer butanol-production pathways are located in the nuclear genome of *Chlamydomonas reinhardtii*, of which the genome has recently been sequenced. Therefore, in one of the various embodiments, it is preferred to use nuclear-genome-encodable designer genes to confer a switchable butanol-production pathway. Consequently, nucleic acids encoding for these enzymes also need to be genetically engineered with proper sequence modification such that the enzymes are controllably expressed and are inserted into the chloroplasts to create a designer butanol-production pathway.

[0067] According to one of the various embodiments, it is best to express the designer butanol-producing-pathway enzymes only into chloroplasts (at the stroma region), exactly where the action of the enzymes is needed to enable photosynthetic production of butanol. If expressed without a chloroplast-targeted insertion mechanism, the enzymes would just stay in the cytosol and not be able to directly interact with the Calvin cycle for butanol production. Therefore, in addition to the obvious distinctive features in pathway designs and associated approaches, another significant distinction is that one of the various embodiments innovatively employs a chloroplast-targeted mechanism for genetic insertion of many designer butanol-production-pathway enzymes into chloroplast to directly interact with the Calvin cycle for photobiological butanol production.

[0068] With a chloroplast stroma-targeted mechanism, the cells will not only be able to produce butanol but also to grow and regenerate themselves when they are returned to certain conditions under which the designer pathway is turned off, such as under aerobic conditions when designer hydrogenase promoter-controlled butanol-production-pathway genes are used. Designer algae, plants, or plant cells that contain normal mitochondria should be able to use the reducing power (NADH) from organic reserves (and/or some exogenous organic substrate such as acetate or sugar) to power the cells immediately after returning to aerobic conditions. Consequently, when the designer algae, plants, or plant cells are returned to aerobic conditions after use under anaerobic conditions for photosynthetic butanol production, the cells will stop making the butanol-producing-pathway enzymes and start to restore the normal photoautotrophic capability by synthesizing new and functional chloroplasts. Therefore, it is possible to use such genetically engineered designer alga/plant organisms for repeated cycles of photoautotrophic growth under normal aerobic conditions and efficient production of butanol directly from CO_2 and H_2O under certain specific designer butanol-producing conditions such as under anaerobic conditions and/or in the presence of nitrate when a Nia1 promoter-controlled butanol-production pathway is used.

[0069] The targeted insertion of designer butanol-production-pathway enzymes can be accomplished through use of a DNA sequence that encodes for a stroma "signal" peptide. A stroma-protein signal (transit) peptide directs the transport and insertion of a newly synthesized protein into stroma. In accordance with one of the various embodiments, a specific targeting DNA sequence is preferably placed in between the promoter and a designer butanol-production-pathway enzyme sequence, as shown in a designer DNA construct (FIG. **2**A). This targeting sequence encodes for a signal (transit) peptide that is synthesized as part of the apoprotein of an enzyme in the cytosol. The transit peptide guides the insertion of an apoprotein of a designer butanol-production-pathway enzyme from cytosol into the chloroplast. After the apopro-

tein is inserted into the chloroplast, the transit peptide is cleaved off from the apoprotein, which then becomes an active enzyme.

[0070] A number of transit peptide sequences are suitable for use for the targeted insertion of the designer butanol-production-pathway enzymes into chloroplast, including but not limited to the transit peptide sequences of: the hydrogenase apoproteins (such as HydA1 (Hyd1) and HydA2, GenBank accession number AJ308413, AF289201, AY090770), ferredoxin apoprotein (Frx1, accession numbers L10349, P07839), thioredoxin m apoprotein (Trx2, X62335), glutamine synthase apoprotein (Gs2, Q42689), LhcII apoproteins (AB051210, AB051208, AB051205), PSII-T apoprotein (PsbT), PSII-S apoprotein (PsbS), PSII-W apoprotein (PsbW), CF_0CF_1 subunit-δapoprotein (AtpC), CF_0CF_1 subunit-6 apoprotein (AtpD, U41442), $CFoCF_1$ subunit-II apoprotein (AtpG), photosystem I (PSI) apoproteins (such as, of genes PsaD, PsaE, PsaF, PsaG, PsaH, and PsaK), Rubisco SSU apoproteins (such as RbcS2, X04472). Throughout this specification, when reference is made to a transit peptide sequence, such as, for example, any of the transit peptide sequence described above, it includes their functional analogs, modified designer sequences, and combinations thereof. A "functional analog" or "modified designer sequence" in this context refers to a peptide sequence derived or modified (by, e.g., conservative substitution, moderate deletion or addition of amino acids, or modification of side chains of amino acids) based on a native transit peptide sequence, such as those identified above, that has the same function as the native transit peptide sequence, i.e., effecting targeted insertion of a desired enzyme.

[0071] In certain specific embodiments, the following transit peptide sequences are used to guide the insertion of the designer butanol-production-pathway enzymes into the stroma region of the chloroplast: the Hyd1 transit peptide (having the amino acid sequence: msalvlkpca avsirgsscr arqvaprapl aastvrvala tleaparrlg nvacaa (SEQ ID NO: 54)), the RbcS2 transit peptides (having the amino acid sequence: maaviakssv saavarpars svrpmaalkp avkaapvaap aqanq (SEQ ID NO: 55)), ferredoxin transit peptide (having the amino acid sequence: mamamrs (SEQ ID NO: 56)), the CF_0CF_1 subunit-δ transit peptide (having the amino acid sequence: mlaaksiagp rafkasavra apkagrrtvv vma (SEQ ID NO: 57)), their analogs, functional derivatives, designer sequences, and combinations thereof.

Use of a Genetic Switch to Control the Expression of a Designer Butanol-Producing Pathway.

[0072] Another key feature of the invention is the application of a genetic switch to control the expression of the designer butanol-producing pathway(s), as illustrated in FIG. **1**. This switchability is accomplished through the use of an externally inducible promoter so that the designer transgenes are inducibly expressed under certain specific inducing conditions. Preferably, the promoter employed to control the expression of designer genes in a host is originated from the host itself or a closely related organism. The activities and inducibility of a promoter in a host cell can be tested by placing the promoter in front of a reporting gene, introducing this reporter construct into the host tissue or cells by any of the known DNA delivery techniques, and assessing the expression of the reporter gene.

[0073] In a preferred embodiment, the inducible promoter used to control the expression of designer genes is a promoter that is inducible by anaerobiosis, i.e., active under anaerobic conditions but inactive under aerobic conditions. A designer alga/plant organism can perform autotrophic photosynthesis using CO_2 as the carbon source under aerobic conditions, and when the designer organism culture is grown and ready for photosynthetic butanol production, anaerobic conditions will be applied to turn on the promoter and the designer genes that encode a designer butanol-production pathway(s).

[0074] A number of promoters that become active under anaerobic conditions are suitable for use in the present invention. For example, the promoters of the hydrogenase genes (HydA1 (Hyd1) and HydA2, GenBank accession number: AJ308413, AF289201, AY090770) of *Chlamydomonas reinhardtii*, which is active under anaerobic conditions but inactive under aerobic conditions, can be used as an effective genetic switch to control the expression of the designer genes in a host alga, such as *Chlamydomonas reinhardtii*. In fact, *Chlamydomonas* cells contain several nuclear genes that are coordinately induced under anaerobic conditions. These include the hydrogenase structural gene itself (Hyd1), the Cyc6 gene encoding the apoprotein of Cytochrome C_6, and the Cpx1 gene encoding coprogen oxidase. The regulatory regions for the latter two have been well characterized, and a region of about 100 bp proves sufficient to confer regulation by anaerobiosis in synthetic gene constructs (Quinn, Barraco, Ericksson and Merchant (2000). "Coordinate copper- and oxygen-responsive Cyc6 and Cpx1 expression in *Chlamydomonas* is mediated by the same element." *J Biol Chem* 275: 6080-6089). Although the above inducible algal promoters may be suitable for use in other plant hosts, especially in plants closely related to algae, the promoters of the homologous genes from these other plants, including higher plants, can be obtained and employed to control the expression of designer genes in those plants.

[0075] In another embodiment, the inducible promoter used in the present invention is an algal nitrate reductase (Nia1) promoter, which is inducible by growth in a medium containing nitrate and repressed in a nitrate-deficient but ammonium-containing medium (Loppes and Radoux (2002) "Two short regions of the promoter are essential for activation and repression of the nitrate reductase gene in *Chlamydomonas reinhardtii*," *Mol Genet Genomics* 268: 42-48). Therefore, the Nia1 (gene accession number AF203033) promoter can be selected for use to control the expression of the designer genes in an alga according to the concentration levels of nitrate and ammonium in a culture medium. Additional inducible promoters that can also be selected for use in the present invention include, for example, the heat-shock protein promoter HSP70A (accession number: DQ059999, AY456093, M98823; Schroda, Blocker, Beek (2000) The HSP70A promoter as a tool for the improved expression of transgenes in *Chlamydomonas. Plant Journal* 21:121-131), the promoter of CabII-1 gene (accession number M24072), the promoter of Ca1 gene (accession number P20507), and the promoter of Ca2 gene (accession number P24258).

[0076] In the case of blue-green algae (oxyphotobacteria including cyanobacteria and oxychlorobacteria), there are also a number of inducible promoters that can be selected for use in the present invention. For example, the promoters of the anaerobic-responsive bidirectional hydrogenase hox genes of *Nostoc* sp. PCC 7120 (GenBank: BA000019), *Prochlorothrix hollandica* (GenBank: U88400; hoxUYH operon promoter), *Synechocystis* sp. strain PCC 6803 (CyanoBase: sll1220 and sll1223), *Synechococcus elongatus*

PCC 6301 (CyanoBase: syc1235_c), *Arthrospira platensis* (GenBank: ABC26906), *Cyanothece* sp. CCY0110 (GenBank: ZP_01727419) and *Synechococcus* sp. PCC 7002 (GenBank: AAN03566), which are active under anaerobic conditions but inactive under aerobic conditions (Sjoholm, Oliveira, and Lindblad (2007) "Transcription and regulation of the bidirectional hydrogenase in the Cyanobacterium *Nostoc* sp. strain PCC 7120," *Applied and Environmental Microbiology,* 73(17): 5435-5446), can be used as an effective genetic switch to control the expression of the designer genes in a host oxyphotobacterium, such as *Nostoc* sp. PCC 7120, *Synechocystis* sp. strain PCC 6803, *Synechococcus elongatus* PCC 6301, *Cyanothece* sp. CCY0110, *Arthrospira platensis*, or *Synechococcus* sp. PCC 7002.

[0077] In another embodiment in creating switchable butanol-production designer organisms such as switchable designer oxyphotobacteria, the inducible promoter selected for use is a nitrite reductase (nirA) promoter, which is inducible by growth in a medium containing nitrate and repressed in a nitrate-deficient but ammonium-containing medium (Qi, Hao, Ng, Slater, Baszis, Weiss, and Valentin (2005) "Application of the *Synechococcus* nirA promoter to establish an inducible expression system for engineering the *Synechocystis* tocopherol pathway," *Applied and Environmental Microbiology,* 71(10): 5678-5684; Maeda, Kawaguchi, Ohe, and Omata (1998) "cis-Acting sequences required for NtcB-dependent, nitrite-responsive positive regulation of the nitrate assimilation operon in the Cyanobacterium *Synechococcus* sp. strain PCC 7942," *Journal of Bacteriology,* 180(16):4080-4088). Therefore, the nirA promoter sequences can be selected for use to control the expression of the designer genes in a number of oxyphotobacteria according to the concentration levels of nitrate and ammonium in a culture medium. The nirA promoter sequences that can be selected and modified for use include (but not limited to) the nirA promoters of the following oxyphotobacteria: *Synechococcus elongatus* PCC 6301 (GenBank: AP008231, region 355890-255950), *Synechococcus* sp. (GenBank: X67680.1, D16303.1, D12723.1, and D00677), *Synechocystis* sp. PCC 6803 (GenBank: NP_442378, BA000022, AB001339, D63999-D64006, D90899-D90917), *Anabaena* sp. (GenBank: X99708.1), *Nostoc* sp. PCC 7120 (GenBank: BA000019.2 and AJ319648), *Plectonema boryanum* (GenBank: D31732.1), *Synechococcus elongatus* PCC 7942 (GenBank: P39661, CP000100.1), *Thermosynechococcus elongatus* BP-1 (GenBank: BAC08901, NP_682139), *Phormidium laminosum* (GenBank: CAA79655, Q51879), *Mastigocladus laminosus* (GenBank: ABD49353, ABD49351, ABD49349, ABD49347), *Anabaena variabilis* ATCC 29413 (GenBank: YP_325032), *Prochlorococcus marinus* str. MIT 9303 (GenBank: YP_001018981), *Synechococcus* sp. WH 8103 (GenBank: AAC17122), *Synechococcus* sp. WH 7805 (GenBank: ZP_01124915), and *Cyanothece* sp. CCY0110 (GenBank: ZP_01727861).

[0078] In yet another embodiment, an inducible promoter selected for use is the light- and heat-responsive chaperone gene groE promoter, which can be induced by heat and/or light [Kojima and Nakamoto (2007) "A novel light- and heat-responsive regulation of the groE transcription in the absence of HrcA or CIRCE in cyanobacteria," FEBS Letters 581: 1871-1880). A number of groE promoters such as the groES and groEL (chaperones) promoters are available for use as an inducible promoter in controlling the expression of the designer butanol-production-pathway enzymes. The groE promoter sequences that can be selected and modified for use in one of the various embodiments include (but not limited to) the groES and/or groEL promoters of the following oxyphotobacteria: *Synechocystis* sp. (GenBank: D12677.1), *Synechocystis* sp. PCC 6803 (GenBank: BA000022.2), *Synechococcus elongatus* PCC 6301 (GenBank: AP008231.1), *Synechococcus* sp (GenBank: M58751.1), *Synechococcus elongatus* PCC 7942 (GenBank: CP000100.1), *Nostoc* sp. PCC 7120 (GenBank: BA000019.2), *Anabaena variabilis* ATCC 29413 (GenBank: CP000117.1), *Anabaena* sp. L-31 (GenBank: AF324500); *Thermosynechococcus elongatus* BP-1 (CyanoBase: t110185, t110186), *Synechococcus vulcanus* (GenBank: D78139), *Oscillatoria* sp. NKBG091600 (GenBank: AF054630), *Prochlorococcus marinus* MIT9313 (GenBank: BX572099), *Prochlorococcus marinus* str. MIT 9303 (GenBank: CP000554), *Prochlorococcus marinus* str. MIT 9211 (GenBank: ZP_01006613), *Synechococcus* sp. WH8102 (GenBank: BX569690), *Synechococcus* sp. CC9605 (GenBank: CP000110), *Prochlorococcus marinus* subsp. *marinus* str. CCMP1375 (GenBank: AE017126), and *Prochlorococcus marinus* MED4 (GenBank: BX548174).

[0079] Additional inducible promoters that can also be selected for use in the present invention include: for example, the metal (zinc)-inducible smt promoter of *Synechococcus* PCC 7942 (Erbe, Adams, Taylor and Hall (1996) "Cyanobacteria carrying an smt-lux transcriptional fusion as biosensors for the detection of heavy metal cations," *Journal of Industrial Microbiology,* 17:80-83); the iron-responsive idiA promoter of *Synechococcus elongatus* PCC 7942 (Michel, Pistorius, and Golden (2001) "Unusual regulatory elements for iron deficiency induction of the idiA gene of *Synechococcus elongatus* PCC 7942" *Journal of Bacteriology,* 183(17): 5015-5024); the redox-responsive cyanobacterial crhR promoter (Patterson-Fortin, Colvin and Owttrim (2006) "A LexA-related protein regulates redox-sensitive expression of the cyanobacterial RNA helicase, crhR", *Nucleic Acids Research,* 34(12):3446-3454); the heat-shock gene hsp16.6 promoter of *Synechocystis* sp. PCC 6803 (Fang and Barnum (2004) "Expression of the heat shock gene hsp16.6 and promoter analysis in the Cyanobacterium, *Synechocystis* sp. PCC 6803," *Current Microbiology* 49:192-198); the small heat-shock protein (Hsp) promoter such as *Synechococcus vulcanus* gene hspA promoter (Nakamoto, Suzuki, and Roy (2000) "Constitutive expression of a small heat-shock protein confers cellular thermotolerance and thermal protection to the photosynthetic apparatus in cyanobacteria," FEBS Letters 483:169-174); the CO_2-responsive promoters of oxyphotobacterial carbonic-anhydrase genes (GenBank: EAZ90903, EAZ90685, ZP_01624337, EAW33650, ABB17341, AAT41924, CAO89711, ZP_00111671, YP_400464, AAC44830; and CyanoBase: all2929, PMT1568 slr0051, slr1347, and syc0167_c); the nitrate-reductase-gene (narB) promoters (such as GenBank accession numbers: BAC08907, NP_682145, AAO25121; ABI46326, YP_732075, BAB72570, NP_484656); the green/red light-responsive promoters such as the light-regulated cpcB2A2 promoter of *Fremyella diplosiphon* (Casey and Grossman (1994) "In vivo and in vitro characterization of the light-regulated cpcB2A2 promoter of *Fremyella diplosiphont*" *Journal of Bacteriology,* 176(20):6362-6374); and the UV-light responsive promoters of cyanobacterial genes lexA, recA and ruvB (Domain, Houot, Chauvat, and Cassier-Chauvat (2004) "Function and regulation of the cyanobacterial

genes lexA, recA and ruvB: LexA is critical to the survival of cells facing inorganic carbon starvation," *Molecular Microbiology,* 53(1):65-80).

[0080] Furthermore, in one of the various embodiments, certain "semi-inducible" or constitutive promoters can also be selected for use in combination of an inducible promoter (s) for construction of a designer butanol-production pathway (s) as well. For example, the promoters of oxyphotobacterial Rubisco operon such as the rbcL genes (GenBank: X65960, ZP_01728542, Q3M674, BAF48766, NP_895035, 0907262A; CyanoBase: PMT1205, PMM0550, Pro0551, tll1506, SYNW1718, glr2156, alr1524, slr0009), which have certain light-dependence but could be regarded almost as constitutive promoters, can also be selected for use in combination of an inducible promoter(s) such as the nirA, hox, and/or groE promoters for construction of the designer butanol-production pathway(s) as well.

[0081] Throughout this specification, when reference is made to inducible promoter, such as, for example, any of the inducible promoters described above, it includes their analogs, functional derivatives, designer sequences, and combinations thereof. A "functional analog" or "modified designer sequence" in this context refers to a promoter sequence derived or modified (by, e.g., substitution, moderate deletion or addition or modification of nucleotides) based on a native promoter sequence, such as those identified hereinabove, that retains the function of the native promoter sequence.

DNA Constructs and Transformation into Host Organisms

[0082] DNA constructs are generated in order to introduce designer butanol-production-pathway genes to a host alga, plant, plant tissue or plant cells. That is, a nucleotide sequence encoding a designer butanol-production-pathway enzyme is placed in a vector, in an operable linkage to a promoter, preferably an inducible promoter, and in an operable linkage to a nucleotide sequence coding for an appropriate chloroplast-targeting transit-peptide sequence. In a preferred embodiment, nucleic acid constructs are made to have the elements placed in the following 5' (upstream) to 3' (downstream) orientation: an externally inducible promoter, a transit targeting sequence, and a nucleic acid encoding a designer butanol-production-pathway enzyme, and preferably an appropriate transcription termination sequence. One or more designer genes (DNA constructs) can be placed into one genetic vector. An example of such a construct is depicted in FIG. **2**A. As shown in the embodiment illustrated in FIG. **2**A, a designer butanol-production-pathway transgene is a nucleic acid construct comprising: a) a PCR forward primer; b) an externally inducible promoter; c) a transit targeting sequence; d) a designer butanol-production-pathway-enzyme-encoding sequence with an appropriate transcription termination sequence; and e) a PCR reverse primer.

[0083] In accordance with various embodiments, any of the components a) through e) of this DNA construct are adjusted to suit for certain specific conditions. In practice, any of the components a) through e) of this DNA construct are applied in full or in part, and/or in any adjusted combination to achieve more desirable results. For example, when an algal hydrogenase promoter is used as an inducible promoter in the designer butanol-production-pathway DNA construct, a transgenic designer alga that contains this DNA construct will be able to perform autotrophic photosynthesis using ambient-air CO_2 as the carbon source and grows normally under aerobic conditions, such as in an open pond. When the algal culture is grown and ready for butanol production, the designer transgene(s) can then be expressed by induction under anaerobic conditions because of the use of the hydrogenase promoter. The expression of designer gene(s) produces a set of designer butanol-production-pathway enzymes to work with the Calvin cycle for photobiological butanol production (FIG. **1**).

[0084] The two PCR primers are a PCR forward primer (PCR FD primer) located at the beginning (the 5' end) of the DNA construct and a PCR reverse primer (PCR RE primer) located at the other end (the 3' end) as shown in FIG. **2**A. This pair of PCR primers is designed to provide certain convenience when needed for relatively easy PCR amplification of the designer DNA construct, which is helpful not only during and after the designer DNA construct is synthesized in preparation for gene transformation, but also after the designer DNA construct is delivered into the genome of a host alga for verification of the designer gene in the transformants. For example, after the transformation of the designer gene is accomplished in a *Chlamydomonas reinhardtii*-arg7 host cell using the techniques of electroporation and argininosuccinate lyase (arg7) complementation screening, the resulted transformants can be then analyzed by a PCR DNA assay of their nuclear DNA using this pair of PCR primers to verify whether the entire designer butanol-production-pathway gene (the DNA construct) is successfully incorporated into the genome of a given transformant. When the nuclear DNA PCR assay of a transformant can generate a PCR product that matches with the predicted DNA size and sequence according to the designer DNA construct, the successful incorporation of the designer gene(s) into the genome of the transformant is verified.

[0085] Therefore, the various embodiments also teach the associated method to effectively create the designer transgenic algae, plants, or plant cells for photobiological butanol production. This method, in one of embodiments, includes the following steps: a) Selecting an appropriate host alga, plant, plant tissue, or plant cells with respect to their genetic backgrounds and special features in relation to butanol production; b) Introducing the nucleic acid constructs of the designer genes into the genome of said host alga, plant, plant tissue, or plant cells; c) Verifying the incorporation of the designer genes in the transformed alga, plant, plant tissue, or plant cells with DNA PCR assays using the said PCR primers of the designer DNA construct; d) Measuring and verifying the designer organism features such as the inducible expression of the designer butanol-pathway genes for photosynthetic butanol production from carbon dioxide and water by assays of mRNA, protein, and butanol-production characteristics according to the specific designer features of the DNA construct(s) (FIG. **2**A).

[0086] The above embodiment of the method for creating the designer transgenic organism for photobiological butanol production can also be repeatedly applied for a plurality of operational cycles to achieve more desirable results. In various embodiments, any of the steps a) through d) of this method described above are adjusted to suit for certain specific conditions. In various embodiments, any of the steps a) through d) of the method are applied in full or in part, and/or in any adjusted combination.

[0087] Examples of designer butanol-production-pathway genes (DNA constructs) are shown in the sequence listings. SEQ ID NO: 1 presents a detailed DNA construct of a designer Butanol Dehydrogenase gene (1809 bp) that includes a PCR FD primer (sequence 1-20), a 262-bp nitrate

reductase Nia1 promoter (21-282), a 135-bp RbcS2 transit peptide (283-417), an enzyme-encoding sequence (418-1566) selected and modified from a *Clostridium saccharoperbutylacetonicum* Butanol Dehydrogenase sequence (AB257439), a 223-bp RbcS2 terminator (1567-1789), and a PCR RE primer (1790-1809). The 262-bp Nia1 promoter (DNA sequence 21-282) is used as an example of an inducible promoter to control the expression of a designer butanol-production-pathway Butanol Dehydrogenase gene (DNA sequence 418-1566). The 135-bp RbcS2 transit peptide (DNA sequence 283-417) is used as an example to guide the insertion of the designer enzyme (DNA sequence 418-1566) into the chloroplast of the host organism. The RbcS2 terminator (DNA sequence 1567-1789) is employed so that the transcription and translation of the designer gene is properly terminated to produce the designer apoprotein (RbcS2 transit peptide-Butanol Dehydrogenase) as desired. Because the Nia1 promoter is a nuclear DNA that can control the expression only for nuclear genes, the synthetic butanol-production-pathway gene in this example is designed according to the codon usage of *Chlamydomonas* nuclear genome. Therefore, in this case, the designer enzyme gene is transcribed in nucleus. Its mRNA is naturally translocated into cytosol, where the mRNA is translated to an apoprotein that consists of the RbcS2 transit peptide (corresponding to DNA sequence 283-417) with its C-terminal end linked together with the N-terminal end of the Butanol Dehydrogenase protein (corresponding to DNA sequence 418-1566). The transit peptide of the apoprotein guides its transportation across the chloroplast membranes and into the stroma area, where the transit peptide is cut off from the apoprotein. The resulting Butanol Dehydrogenase then resumes its function as an enzyme for the designer butanol-production pathway in chloroplast. The two PCR primers (sequences 1-20 and 1790-1809) are selected and modified from the sequence of a Human actin gene and can be paired with each other. Blasting the sequences against *Chlamydomonas* GenBank found no homologous sequences of them. Therefore, they can be used as appropriate PCR primers in DNA PCR assays for verification of the designer gene in the transformed alga.

[0088] SEQ ID NO: 2 presents example 2 for a designer Butyraldehyde Dehydrogenase DNA construct (2067 bp) that includes a PCR FD primer (sequence 1-20), a 262-bp nitrate reductase Nia1 promoter (21-282), a 135-bp RbcS2 transit peptide (283-417), a Butyraldehyde Dehydrogenase-encoding sequence (418-1824) selected and modified from a *Clostridium saccharoperbutylacetonicum* Butyraldehyde Dehydrogenase sequence (AY251646), a 223-bp RbcS2 terminator (1825-2047), and a PCR RE primer (2048-2067). This DNA construct is similar to example 1, SEQ ID NO: 1, except that a Butyraldehyde Dehydrogenase-encoding sequence (418-1824) selected and modified from a *Clostridium saccharoperbutylacetonicum* Butyraldehyde Dehydrogenase sequence (AY251646) is used.

[0089] SEQ ID NO: 3 presents example 3 for a designer Butyryl-CoA Dehydrogenase construct (1815 bp) that includes a PCR FD primer (sequence 1-20), a 262-bp nitrate reductase promoter (21-282), a 9-bp Xho I NdeI site (283-291), a 135-bp RbcS2 transit peptide (292-426), a Butyryl-CoA Dehydrogenase encoding sequence (427-1563) selected/modified from the sequences of a *Clostridium beijerinckii* Butyryl-CoA Dehydrogenase (AF494018), a 9-bp XbaI site (1564-1572), a 223-bp RbcS2 terminator (1573-1795), and a PCR RE primer (1796-1815) at the 3' end. This DNA construct is similar to example 1, SEQ ID NO: 1, except that a Butyryl-CoA Dehydrogenase encoding sequence (427-1563) selected/modified from the sequences of a *Clostridium beijerinckii* Butyryl-CoA Dehydrogenase (AF494018) is used and restriction sites of Xho I NdeI and XbaI are added to make the key components such as the targeting sequence (292-426) and the designer enzyme sequence (427-1563) as a modular unit that can be flexible replaced when necessary to save cost of gene synthesis and enhance work productivity. Please note, the enzyme does not have to be *Clostridium beijerinckii* Butyryl-CoA Dehydrogenase; a number of butyryl-CoA dehydrogenase enzymes (such as those listed in Table 1) including their isozymes, designer modified enzymes, and functional analogs from other sources such as *Butyrivibrio fibrisolvens*, Butyrate producing bacterium L2-50, *Thermoanaerobacterium thermosaccharolyticum*, can also be selected for use.

[0090] SEQ ID NO: 4 presents example 4 for a designer Crotonase DNA construct (1482 bp) that includes a PCR FD primer (sequence 1-20), a 262-bp nitrate reductase promoter (21-282), a 9-bp Xho I NdeI site (283-291) a 135-bp RbcS2 transit peptide (292-426), a Crotonase-encoding sequence (427-1209) selected/modified from the sequences of a *Clostridium beijerinckii* Crotonase (Genbank: AF494018), a 21-bp Lumio-tag-encoding sequence (1210-1230), a 9-bp XbaI site (1231-1239) containing a stop codon, a 223-bp RbcS2 terminator (1240-1462), and a PCR RE primer (1463-1482) at the 3' end. This DNA construct is similar to example 3, SEQ ID NO: 3, except that a Crotonase-encoding sequence (427-1209) selected/modified from the sequences of a *Clostridium beijerinckii* Crotonase (Genbank: AF494018) is used and a 21-bp Lumio-tag-encoding sequence (1210-1230) is added at the C-terminal end of the enolase sequence. The 21-bp Lumio-tag sequence (1210-1230) is employed here to encode a Lumio peptide sequence Gly-Cys-Cys-Pro-Gly-Cys-Cys, which can become fluorescent when treated with a Lumio reagent that is now commercially available from Invitrogen [https://catalog.invitrogen.com]. Lumio molecular tagging technology is based on an EDT (1,2-ethanedithiol) coupled biarsenical derivative (the Lumio reagent) of fluorescein that binds to an engineered tetracysteine sequence (Keppetipola, Coffman, and et al (2003). Rapid detection of in vitro expressed proteins using Lumio™ technology, *Gene Expression,* 25.3:7-11). The tetracysteine sequence consists of Cys-Cys-Xaa-Xaa-Cys-Cys, where Xaa is any non-cysteine amino acid such as Pro or Gly in this example. The EDT-linked Lumio reagent allows free rotation of the arsenic atoms that quenches the fluorescence of fluorescein. Covalent bond formation between the thiols of the Lumio's arsenic groups and the tetracysteines prevents free rotation of arsenic atoms that releases the fluorescence of fluorescein (Griffin, Adams, and Tsien (1998), "Specific covalent labeling of recombinant protein molecules inside live cells", *Science,* 281:269-272). This also permits the visualization of the tetracysteine-tagged proteins by fluorescent molecular imaging. Therefore, use of the Lumio tag in this manner enables monitoring and/or tracking of the designer Crotonase when expressed to verify whether the designer butanol-production pathway enzyme is indeed delivered into the chloroplast of a host organism as designed. The Lumio tag (a short 7 amino acid peptide) that is linked to the C-terminal end of the Crotonase protein in this example should have minimal effect on the function of the designer enzyme, but enable the designer enzyme molecule to be visualized when treated with the

Lumio reagent. Use of the Lumio tag is entirely optional. If the Lumio tag somehow affects the designer enzyme function, this tag can be deleted in the DNA sequence design.

[0091] SEQ ID NO: 5 presents example 5 for a designer 3-Hydroxybutyryl-CoA Dehydrogenase DNA construct (1367 bp) that includes a PCR FD primer (sequence 1-20), a 84-bp nitrate reductase promoter (21-104), a 9-bp Xho I NdeI site (105-113) a 135-bp RbcS2 transit peptide (114-248), a 3-Hydroxybutyryl-CoA Dehydrogenase-encoding sequence (249-1094) selected/modified from a *Clostridium beijerinckii* 3-Hydroxybutyryl-CoA Dehydrogenase sequence (Genbank: AF494018), a 21-bp Lumio-tag sequence (1095-1115), a 9-bp XbaI site (1116-1124), a 223-bp RbcS2 terminator (1125-1347), and a PCR RE primer (1348-1367). This DNA construct is similar to example 4, SEQ ID NO: 4, except that an 84-bp nitrate reductase promoter (21-104) and a 3-Hydroxybutyryl-CoA Dehydrogenase-encoding sequence (249-1094) selected/modified from a *Clostridium beijerinckii* 3-Hydroxybutyryl-CoA Dehydrogenase sequence (Genbank: AF494018) are used. The 84-bp nitrate-reductase promoter is artificially created by joining two partially homologous sequence regions (−231 to −201 and -77 to −25 with respect to the start site of transcription) of the native *Chlamydomonas reinhardtii* Nia1 promoter. Experimental studies have demonstrated that the 84-bp sequence is more active than the native Nia1 promoter (Loppes and Radoux (2002) "Two short regions of the promoter are essential for activation and repression of the nitrate reductase gene in *Chlamydomonas reinhardtii," Mol Genet Genomics* 268: 42-48). Therefore, this is also an example where functional synthetic sequences, analogs, functional derivatives and/or designer modified sequences such as the synthetic 84-bp sequence can be selected for use according to various embodiments in this invention.

[0092] SEQ ID NO: 6 presents example 6 for a designer Thiolase DNA construct (1721 bp) that includes a PCR FD primer (sequence 1-20), a 84-bp nitrate reductase promoter (21-104), a 9-bp Xho I NdeI site (105-113) a 135-bp RbcS2 transit peptide (114-248), a Thiolase-encoding sequence (248-1448) selected/modified from a *Butyrivibrio fibrisolvens* Thiolase sequence (AB190764), a 21-bp Lumio-tag sequence (1449-1469), a 9-bp XbaI site (1470-1478), a 223-bp RbcS2 terminator (1479-1701), and a PCR RE primer (1702-1721). This DNA construct is also similar to example 4, SEQ ID NO: 4, except that a Thiolase-encoding-encoding sequence (249-1448) and an 84-bp synthetic Nia1 promoter (21-104) are used. This is another example that functional synthetic sequences can also be selected for use in designer DNA constructs.

[0093] SEQ ID NO: 7 presents example 7 for a designer Pyruvate-Ferredoxin Oxidoreductase DNA construct (4211 bp) that includes a PCR FD primer (sequence 1-20), a 2×84-bp nitrate reductase promoter (21-188), a 9-bp Xho I NdeI site (189-197) a 135-bp RbcS2 transit peptide (198-332), a Pyruvate-Ferredoxin Oxidoreductase-encoding sequence (333-3938) selected/modified from the sequences of a *Mastigamoeba balamuthi* Pyruvate-ferredoxin oxidoreductase (GenBank: AY101767), a 21-bp Lumio-tag sequence (3939-3959), a 9-bp XbaI site (3960-3968), a 223-bp RbcS2 terminator (3969-4191), and a PCR RE primer (4192-4211). This DNA construct is also similar to example 4, SEQ ID NO: 4, except a designer 2×84-bp Nia1 promoter and a Pyruvate-Ferredoxin Oxidoreductase-encoding sequence (333-3938) selected/modified from the sequences of a *Mastigamoeba balamuthi* Pyruvate-ferredoxin oxidoreductase (GenBank: AY101767) are used. The 2×84-bp Nia1 promoter is constructed as a tandem duplication of the 84-bp synthetic Nia1 promoter sequence presented in SEQ ID NO: 6 above. Experimental tests have shown that the 2×84-bp synthetic Nia1 promoter is even more powerful than the 84-bp sequence which is more active than the native Nia1 promoter (Loppes and Radoux (2002) "Two short regions of the promoter are essential for activation and repression of the nitrate reductase gene in *Chlamydomonas reinhardtii," Mol Genet Genomics* 268: 42-48). Use of this type of inducible promoter sequences with various promoter strengths can also help in adjusting the expression levels of the designer enzymes for the butanol-production pathway(s).

[0094] SEQ ID NO: 8 presents example 8 for a designer Pyruvate Kinase DNA construct (2021 bp) that includes a PCR FD primer (sequence 1-20), a 84-bp nitrate reductase promoter (21-104), a 9-bp Xho I NdeI site (105-113) a 135-bp RbcS2 transit peptide (114-248), a pyruvate kinase-encoding sequence (249-1748) selected/modified from a *Saccharomyces cerevisiae* Pyruvate Kinase sequence (GenBank: AY949876), a 21-bp Lumio-tag sequence (1749-1769), a 9-bp XbaI site (1770-1778), a 223-bp RbcS2 terminator (1779-2001), and a PCR RE primer (2002-2021). This DNA construct is similar to example 6, SEQ ID NO: 6, except that a pyruvate kinase-encoding sequence (249-1748) is used.

[0095] SEQ ID NO: 9 presents example 9 for a designer Enolase gene (1815 bp) consisting of a PCR FD primer (sequence 1-20), a 262-bp nitrate reductase promoter (21-282), a 9-bp Xho I NdeI site (283-291) a 135-bp RbcS2 transit peptide (292-426), a enolase-encoding sequence (427-1542) selected/modified from the sequences of a *Chlamydomonas reinhardtii* cytosolic enolase (Genbank: X66412, P31683), a 21-bp Lumio-tag-encoding sequence (1507-1527), a 9-bp XbaI site (1543-1551) containing a stop codon, a 223-bp RbcS2 terminator (1552-1795), and a PCR RE primer (1796-1815) at the 3' end. This DNA construct is similar to example 3, SEQ ID NO: 3, except that an enolase-encoding sequence (427-1542) selected/modified from the sequences of a *Chlamydomonas reinhardtii* cytosolic enolase is used.

[0096] SEQ ID NO: 10 presents example 10 for a designer Phosphoglycerate-Mutase DNA construct (2349 bp) that includes a PCR FD primer (sequence 1-20), a 262-bp nitrate reductase promoter (21-282), a 9-bp Xho I NdeI site (283-291), a 135-bp RbcS2 transit peptide (292-426), a phosphoglycerate-mutase encoding sequence (427-2097) selected/modified from the sequences of a *Chlamydomonas reinhardtii* cytosolic phosphoglycerate mutase (JGI Chlre2 protein ID 161689, Genbank: AF268078), a 9-bp XbaI site (2098-2106), a 223-bp RbcS2 terminator (2107-2329), and a PCR RE primer (2330-2349) at the 3' end. This DNA construct is similar to example 3, SEQ ID NO: 3, except that a phosphoglycerate-mutase encoding sequence (427-2097) selected/modified from the sequences of a *Chlamydomonas reinhardtii* cytosolic phosphoglycerate mutase is used.

[0097] SEQ ID NO: 11 presents example 11 for a designer Phosphoglycerate Kinase DNA construct (1908 bp) that includes a PCR FD primer (sequence 1-20), a 262-bp nitrate reductase Nia1 promoter (21-282), a phosphoglycerate-kinase-encoding sequence (283-1665) selected from a *Chlamydomonas reinhardtii* chloroplast phosphoglycerate-kinase sequence including its chloroplast signal peptide and mature enzyme sequence (GenBank: U14912), a 223-bp RbcS2 terminator (1666-1888), and a PCR RE primer (1889-1908).

This DNA construct is similar to example 1, SEQ ID NO: 1, except a phosphoglycerate-kinase-encoding sequence (283-1665) selected from a *Chlamydomonas reinhardtii* chloroplast phosphoglycerate-kinase sequence including its chloroplast signal peptide and mature enzyme sequence is used. Therefore, this is also an example where the sequence of a nuclear-encoded chloroplast enzyme such as the *Chlamydomonas reinhardtii* chloroplast phosphoglycerate kinase can also be used in design and construction of a designer butanol-production pathway gene when appropriate with a proper inducible promoter such as the Nia1 promoter (DNA sequence 21-282).

[0098] SEQ ID NO: 12 presents example 12 for a designer Glyceraldehyde-3-Phosphate Dehydrogenase gene (1677 bp) that includes a PCR FD primer (sequence 1-20), a 262-bp nitrate reductase Nia1 promoter (21-282), a 135-bp RbcS2 transit peptide (283-417), an enzyme-encoding sequence (418-1434) selected and modified from a *Mesostigma viride* cytosolic glyceraldehyde-3-phosphate dehydrogenase (mRNA) sequence (GenBank accession number DQ873404), a 223-bp RbcS2 terminator (1435-1657), and a PCR RE primer (1658-1677). This DNA construct is similar to example 1, SEQ ID NO: 1, except that an enzyme-encoding sequence (418-1434) selected and modified from a *Mesostigma viride* cytosolic glyceraldehyde-3-phosphate dehydrogenase (mRNA) sequence (GenBank accession number DQ873404) is used.

[0099] SEQ ID NO: 13 presents example 13 for a designer HydA1-promoter-linked Phosphoglycerate Mutase DNA construct (2351 bp) that includes a PCR FD primer (sequence 1-20), a 282-bp HydA1 promoter (21-302), a 135-bp RbcS2 transit peptide (303-437), a phosphoglycerate-mutase encoding sequence (438-2108) selected/modified from the sequences of a *Chlamydomonas reinhardtii* cytosolic phosphoglycerate mutase (JGI Chlre2 protein ID 161689, Genbank: AF268078), a 223-bp RbcS2 terminator (2109-2331), and a PCR RE primer (2332-2351). This designer DNA construct is quite similar to example 1, SEQ ID NO:1, except that a 282-bp HydA1 promoter (21-302) and a phosphoglycerate-mutase encoding sequence (438-2108) selected/modified from the sequences of a *Chlamydomonas reinhardtii* cytosolic phosphoglycerate mutase are used. The 282-bp HydA1 promoter (21-302) has been proven active by experimental assays at the inventor's laboratory. Use of the HydA1 promoter (21-302) enables activation of designer enzyme expression by using anaerobic culture-medium conditions.

[0100] With the same principle of using an inducible anaerobic promoter and a chloroplast-targeting sequence as that shown in SEQ ID NO: 13 (example 13), SEQ ID NOS: 14-23 show designer-gene examples 14-23. Briefly, SEQ ID NO: 14 presents example 14 for a designer HydA1-promoter-linked Enolase DNA construct (1796 bp) that includes a PCR FD primer (sequence 1-20), a 282-bp HydA1 promoter (21-302), a 135-bp RbcS2 transit peptide (303-437), a Enolase-encoding sequence (438-1553) selected/modified from the sequences of a *Chlamydomonas reinhardtii* cytosolic enolase (Genbank: X66412, P31683), a 223-bp RbcS2 terminator (1554-1776), and a PCR RE primer (1777-1796).

[0101] SEQ ID NO: 15 presents example 15 for a designer HydA1-promoter-controlled Pyruvate-Kinase DNA construct that includes a PCR FD primer (sequence 1-20), a 282-bp HydA1 promoter (21-302), a 135-bp RbcS2 transit peptide (303-437), a Pyruvate Kinase-encoding sequence (438-1589) selected/modified from a *Chlamydomonas reinhardtii* cytosolic pyruvate kinase sequence (JGI Chlre3 protein ID 138105), a 223-bp RbcS2 terminator (1590-1812), and a PCR RE primer (1813-1832).

[0102] SEQ ID NO:16 presents example 16 for a designer HydA1-promoter-linked Pyruvate-ferredoxin oxidoreductase DNA construct (4376 bp) that includes a PCR FD primer (sequence 1-20), a 282-bp HydA1 promoter (21-302), a 135-bp RbcS2 transit peptide (303-437), a Pyruvate-ferredoxin oxidoreductase-encoding sequence (438-4133) selected/modified from a *Desulfovibrio africanus* Pyruvate-ferredoxin oxidoreductase sequence (GenBank Accession Number Y09702), a 223-bp RbcS2 terminator (4134-4356), and a PCR RE primer (4357-4376).

[0103] SEQ ID NO:17 presents example 17 for a designer HydA1-promoter-linked Pyruvate-$NADP^+$ oxidoreductase DNA construct (6092 bp) that includes a PCR FD primer (sequence 1-20), a 282-bp HydA1 promoter (21-302), a 135-bp RbcS2 transit peptide (303-437), a Pyruvate-$NADP^+$ oxidoreductase-encoding sequence (438-5849) selected/modified from a *Euglena gracilis* Pyruvate-$NADP^+$ oxidoreductase sequence (GenBank Accession Number AB021127), a 223-bp RbcS2 terminator (5850-6072), and a PCR RE primer (6073-6092).

[0104] SEQ ID NO:18 presents example 18 for a designer HydA1-promoter-linked Thiolase DNA construct (1856 bp) that includes a PCR FD primer (sequence 1-20), a 282-bp HydA1 promoter (21-302), a 135-bp RbcS2 transit peptide (303-437), a Thiolase-encoding sequence (438-1613) selected/modified from the sequences of a *Thermoanaerobacterium thermosaccharolyticum* Thiolase (GenBank Z92974), a 223-bp RbcS2 terminator (1614-1836), and a PCR RE primer (1837-1856).

[0105] SEQ ID NO:19 presents example 19 for a designer HydA1-promoter-linked 3-Hydroxybutyryl-CoA dehydrogenase DNA construct (1550 bp) that includes a PCR FD primer (sequence 1-20), a 282-bp HydA1 promoter (21-302), a 135-bp RbcS2 transit peptide (303-437), a 3-Hydroxybutyryl-CoA dehydrogenase-encoding sequence (438-1307) selected/modified from the sequences of a *Thermoanaerobacterium thermosaccharolyticum* 3-Hydroxybutyryl-CoA dehydrogenase (GenBank Z92974), a 223-bp RbcS2 terminator (1308-1530), and a PCR RE primer (1531-1550).

[0106] SEQ ID NO:20 presents example 20 for a designer HydA1-promoter-linked Crotonase DNA construct (1457 bp) that includes a PCR FD primer (sequence 1-20), a 282-bp HydA1 promoter (21-302), a 135-bp RbcS2 transit peptide (303-437), a Crotonase-encoding sequence (438-1214) selected/modified from the sequences of a *Thermoanaerobacterium thermosaccharolyticum* Crotonase (GenBank Z92974), a 223-bpRbcS2 terminator (1215-1437), and a PCR RE primer (1438-1457).

[0107] SEQ ID NO:21 presents example 21 for a designer HydA1-promoter-linked Butyryl-CoA dehydrogenase DNA construct (1817 bp) that includes a PCR FD primer (sequence 1-20), a 282-bp HydA1 promoter (21-302), a 135-bp RbcS2 transit peptide (303-437), a Butyryl-CoA dehydrogenase-encoding sequence (438-1574) selected/modified from the sequences of a *Thermoanaerobacterium thermosaccharolyticum* Butyryl-CoA dehydrogenase (GenBank Z92974), a 223-bp RbcS2 terminator (1575-1797), and a PCR RE primer (1798-1817).

[0108] SEQ ID NO: 22 presents example 22 for a designer HydA1-promoter-linked Butyraldehyde dehydrogenase DNA construct (2084 bp) that includes a PCR FD primer

(sequence 1-20), a 282-bp HydA1 promoter (21-302), a 135-bp RbcS2 transit peptide (303-437), a Butyraldehyde dehydrogenase-encoding sequence (438-1841) selected/modified from the sequences of a *Clostridium saccharoperbutylacetonicum* Butyraldehyde dehydrogenase (GenBank AY251646), a 223-bp RbcS2 terminator (1842-2064), and a PCR RE primer (2065-2084).

[0109] SEQ ID NO: 23 presents example 23 for a designer HydA1-promoter-linked Butanol dehydrogenase DNA construct (1733 bp) that includes a PCR FD primer (sequence 1-20), a 282-bp HydA1 promoter (21-302), a 135-bp RbcS2 transit peptide (303-437), a Butanol dehydrogenase-encoding sequence (438-1490) selected/modified from the sequences of a *Clostridium beijerinckii* Butanol dehydrogenase (GenBank AF157307), a 223-bp RbcS2 terminator (1491-1713), and a PCR RE primer (1714-1733).

[0110] With the same principle of using a 2×84 synthetic Nia1 promoter and a chloroplast-targeting mechanism as mentioned previously, SEQ ID NOS:24-26 show more examples of designer-enzyme DNA-constructs. Briefly, SEQ ID NO: 24 presents example 24 for a designer Fructose-Diphosphate-Aldolase DNA construct that includes a PCR FD primer (sequence 1-20), a 2×84-bp NR promoter (21-188), a Fructose-Diphosphate Aldolase-encoding sequence (189-1313) selected/modified from a *C. reinhardtii* chloroplast fructose-1,6-bisphosphate aldolase sequence (GenBank: X69969), a 223-bpRbcS2 terminator (1314-1536), and a PCR RE primer (1537-1556).

[0111] SEQ ID NO: 25 presents example 24 for a designer Triose-Phosphate-Isomerase DNA construct that includes a PCR FD primer (sequence 1-20), a 2×84-bp NR promoter (21-188), a Triose-Phosphate Isomerase-encoding sequence (189-1136) selected and modified from a *Arabidopsis thaliana* chloroplast triosephosphate-isomerase sequence (GenBank: AF247559), a 223-bp RbcS2 terminator (1137-1359), and a PCR RE primer (1360-1379).

[0112] SEQ ID NO: 26 presents example 26 for a designer Phosphofructose-Kinase DNA construct that includes a PCR FD primer (sequence 1-20), a 2×84-bp NR promoter (21-188), a 135-bp RbcS2 transit peptide (189-323), a Phosphofructose Kinase-encoding sequence (324-1913) selected/modified from *Arabidopsis thaliana* 6-phosphofructokinase sequence (GenBank: NM_001037043), a 223-bp RbcS2 terminator (1914-2136), and a PCR RE primer (2137-2156).

[0113] The nucleic acid constructs, such as those presented in the examples above, may include additional appropriate sequences, for example, a selection marker gene, and an optional biomolecular tag sequence (such as the Lumio tag described in example 4, SEQ ID NO: 4). Selectable markers that can be selected for use in the constructs include markers conferring resistances to kanamycin, hygromycin, spectinomycin, streptomycin, sulfonyl urea, gentamycin, chloramphenicol, among others, all of which have been cloned and are available to those skilled in the art. Alternatively, the selective marker is a nutrition marker gene that can complement a deficiency in the host organism. For example, the gene encoding argininosuccinate lyase (arg7) can be used as a selection marker gene in the designer construct, which permits identification of transformants when *Chlamydomonas reinhardtii* arg7-(minus) cells are used as host cells.

[0114] Nucleic acid constructs carrying designer genes can be delivered into a host alga, blue-green alga, plant, or plant tissue or cells using the available gene-transformation techniques, such as electroporation, PEG induced uptake, and ballistic delivery of DNA, and *Agrobacterium*-mediated transformation. For the purpose of delivering a designer construct into algal cells, the techniques of electroporation, glass bead, and biolistic genegun can be selected for use as preferred methods; and an alga with single cells or simple thallus structure is preferred for use in transformation. Transformants can be identified and tested based on routine techniques.

[0115] The various designer genes can be introduced into host cells sequentially in a step-wise manner, or simultaneously using one construct or in one transformation. For example, the ten DNA constructs shown in SEQ ID NO: 13-16 (or 17) and 18-23 for the ten-enzyme 3-phosphoglycerate-branched butanol-production pathway can be placed into a genetic vector such as p389-Arg7 with a single selection marker (Arg7). Therefore, by use of a plasmid in this manner, it is possible to deliver all the ten DNA constructs (designer genes) into an arginine-requiring *Chlamydomonas reinhardtii*-arg7 host (CC-48) in one transformation for expression of the 3-phosphoglycerate-branched butanol-production pathway (03-12 in FIG. **1**). When necessary, a transformant containing the ten DNA constructs can be further transformed to get more designer genes into its genomic DNA with an additional selection marker such as streptomycin. By using combinations of various designer-enzymes DNA constructs such as those presented in SEQ ID NO: 1-26 in genetic transformation with an appropriate host organism, various butanol-production pathways such as those illustrated in FIG. **1** can be constructed. For example, the designer DNA constructs of SEQ ID NO: 1-12 can be selected for construction of the glyceraldehydes-3-phosphate-branched butanol-production pathway (01-12 in FIG. **1**); The designer DNA constructs of SEQ ID NO: 1-12, 24, and 25 can be selected for construction of the fructose-1,6-diphosphate-branched butanol-production pathway (20-33); and the designer DNA constructs of SEQ ID NO: 1-12 and 24-26 can be selected for construction of the fructose-6-phosphate-branched butanol-production pathway (19-33).

Additional Host Modifications to Enhance Photosynthetic Butanol Production

An NADPH/NADH Conversion Mechanism

[0116] According to the photosynthetic butanol production pathway(s), to produce one molecule of butanol from $4CO_2$ and $5H_2O$ is likely to require 14 ATP and 12 NADPH, both of which are generated by photosynthetic water splitting and photophosphorylation across the thylakoid membrane. In order for the 3-phosphoglycerate-branched butanol-production pathway (03-12 in FIG. **1**) to operate, it is a preferred practice to use a butanol-production-pathway enzyme(s) that can use NADPH that is generated by the photo-driven electron transport process. *Clostridium saccharoperbutylacetonicum* butanol dehydrogenase (GenBank accession number: AB257439) and butyaldehyde dehydrogenase (GenBank: AY251646) are examples of a butanol-production-pathway enzyme that is capable of accepting either NADP(H) or NAD(H). Such a butanol-production-pathway enzyme that can use both NADPH and NADH (i.e., NAD(P)H) can also be selected for use in this 3-phosphoglycerate-branched and any of the other designer butanol-production pathway(s) (FIG. **1**) as well. *Clostridium beijerinckii* Butyryl-CoA dehydrogenase (GenBank: AF494018) and 3-Hydroxybutyryl-CoA dehydrogenase (GenBank: AF494018) are examples of a

butanol-production-pathway enzyme that can accept only NAD(H). When a butanol-production-pathway enzyme that can only use NADH is employed, it may require an NADPH/NADH conversion mechanism in order for this 3-phosphoglycerate-branched butanol-production pathway to operate well. However, depending on the genetic backgrounds of a host organism, a conversion mechanism between NADPH and NADH may exist in the host so that NADPH and NADH may be interchangeably used in the organism. In addition, it is known that NADPH could be converted into NADH by a NADPH-phosphatase activity (Pattanayak and Chatterjee (1998) "Nicotinamide adenine dinucleotide phosphate phosphatase facilitates dark reduction of nitrate: regulation by nitrate and ammonia," *Biologia Plantarium* 41(1):75-84) and that NAD can be converted to NADP by a NAD kinase activity (Muto, Miyachi, Usuda, Edwards and Bassham (1981) "Light-induced conversion of nicotinamide adenine dinucleotide to nicotinamide adenine dinucleotide phosphate in higher plant leaves," *Plant Physiology* 68(2):324-328; Matsumura-Kadota, Muto, Miyachi (1982) "Light-induced conversion of NAD^+ to $NADP^+$ in *Chlorella* cells," *Biochimica Biophysica Acta* 679(2):300-300). Therefore, when enhanced NADPH/NADH conversion is desirable, the host may be genetically modified to enhance the NADPH phosphatase and NAD kinase activities. Thus, in one of the various embodiments, the photosynthetic butanol-producing designer plant, designer alga or plant cell further contains additional designer transgenes (FIG. **2**B) to inducibly express one or more enzymes to facilitate the NADPH/NADH interconversion, such as the NADPH phosphatase and NAD kinase (GenBank: XM_001609395, XM_001324239), in the stroma of algal chloroplast.

[0117] Another embodiment that can provide an NADPH/NADH conversion mechanism is by properly selecting an appropriate branching point at the Calvin cycle for a designer butanol-production pathway to branch from. To confer this NADPH/NADH conversion mechanism by pathway design according to this embodiment, it is a preferred practice to branch a designer butanol-production pathway at or after the point of glyceraldehydes-3-phosphate of the Calvin cycle as shown in FIG. **1**. In these pathway designs, the NADPH/NADH conversion is achieved essentially by a two-step mechanism: 1) Use of the step with the Calvin-cycle's glyceraldehyde-3-phosphate dehydrogenase, which uses NADPH in reducing1,3-diphosphoglycerate to glyceraldehydes-3-phosphate; and 2) use of the step with the designer pathway's NAD^+-dependent glyceraldehyde-3-phosphate dehydrogenase 01, which produces NADH in oxidizing glyceraldehyde-3-phosphate to 1,3-diphosphoglycerate. The net result of the two steps described above is the conversion of NADPH to NADH, which can supply the needed reducing power in the form of NADH for the designer butanol-production pathway(s). For step 1), use of the Calvin-cycle's NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase naturally in the host organism is usually sufficient. Consequently, introduction of a designer NAD^+-dependent glyceraldehyde-3-phosphate dehydrogenase 01 to work with the Calvin-cycle's NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase may confer the function of an NADPH/NADH conversion mechanism, which is needed for the 3-phosphoglycerate-branched butanol-production pathway (03-12 in FIG. **1**) to operate well. For this reason, the designer NAD^+-dependent glyceraldehyde-3-phosphate-dehydrogenase DNA construct (example 12, SEQ ID NO:12) is used also as an NADPH/NADH-conversion designer gene (FIG. **2**B) to support the 3-phosphoglycerate-branched butanol-production pathway (03-12 in FIG. **1**) in one of the various embodiments. This also explains why it is important to use a NAD^+-dependent glyceraldehyde-3-phosphate dehydrogenase 01 to confer this two-step NADPH/NADH conversion mechanism for the designer butanol-production pathway (s). Therefore, in one of the various embodiments, it is also a preferred practice to use a NAD^+-dependent glyceraldehyde-3-phosphate dehydrogenase, its isozymes, functional derivatives, analogs, designer modified enzymes and/or combinations thereof in the designer butanol-production pathway(s) as illustrated in FIG. **1**.

iRNA Techniques to Further Tame Photosynthesis Regulation Mechanism

[0118] In another embodiment of the present invention, the host plant or cell is further modified to tame the Calvin cycle so that the host can directly produce liquid fuel butanol instead of synthesizing starch (glycogen in the case of oxyphotobacteria), celluloses and lignocelluloses that are often inefficient and hard for the biorefinery industry to use. According to the one of the various embodiments, inactivation of starch-synthesis activity is achieved by suppressing the expression of any of the key enzymes, such as, starch synthase (glycogen synthase in the case of oxyphotobacteria) 13, glucose-1-phosphate (G-1-P) adenylyltransferase 14, phosphoglucomutase 15, and hexose-phosphate-isomerase 16 of the starch-synthesis pathway which connects with the Calvin cycle (FIG. **1**).

[0119] Introduction of a genetically transmittable factor that can inhibit the starch-synthesis activity that is in competition with designer butanol-production pathway(s) for the Calvin-cycle products can further enhance photosynthetic butanol production. In a specific embodiment, a genetically encoded-able inhibitor (FIG. **2**C) to the competitive starch-synthesis pathway is an interfering RNA (iRNA) molecule that specifically inhibits the synthesis of a starch-synthesis-pathway enzyme, for example, starch synthase 16, glucose-1-phosphate (G-1-P) adenylyltransferase 15, phosphoglucomutase 14, and/or hexose-phosphate-isomerase 13 as shown with numerical labels 13-16 in FIG. **1**. The DNA sequences encoding starch synthase iRNA, glucose-1-phosphate (G-1-P) adenylyltransferase iRNA, a phosphoglucomutase iRNA and/or a G-P-isomerase iRNA, respectively, can be designed and synthesized based on RNA interference techniques known to those skilled in the art (Liszewski (Jun. 1, 2003) Progress in RNA interference, *Genetic Engineering News, Vol.* 23, number 11, pp. 1-59). Generally speaking, an interfering RNA (iRNA) molecule is anti-sense but complementary to a normal mRNA of a particular protein (gene) so that such iRNA molecule can specifically bind with the normal mRNA of the particular gene, thus inhibiting (blocking) the translation of the gene-specific mRNA to protein (Fire, Xu, Montgomery, Kostas, Driver, Mello (1998) "Potent and specific genetic interference by double-stranded RNA in *Caenorhabditis elegans". Nature* 391(6669):806-11; Dykxhoorn, Novina, Sharp (2003) "Killing the messenger: short RNAs that silence gene expression", *Nat Rev Mol Cell Biol.* 4(6):457-67).

[0120] Examples of a designer starch-synthesis iRNA DNA construct (FIG. **2**C) are shown in SEQ ID NO: 27 and 28 listed. Briefly, SEQ ID NO: 27 presents example 27 for a designer Nia1-promoter-controlled Starch-Synthase-iRNA DNA construct (860 bp) that includes a PCR FD primer

(sequence 1-20), a 262-bp Nia1 promoter (21-282), a Starch-Synthase iRNA sequence (283-617) consisting of start codon atg and a reverse complement sequence of two unique sequence fragments of a *Chlamydomonas reinhardtii* starch-synthase-mRNA sequence (GenBank: AF026422), a 223-bp RbcS2 terminator (618-850), and a PCR RE primer (851-860). Because of the use of a Nia1 promoter (21-282), this designer starch-synthesis iRNA gene is designed to be expressed only when needed to enhance photobiological butanol production in the presence of its specific inducer, nitrate (NO_3^-), which can be added into the culture medium as a fertilizer for induction of the designer organisms. The Starch-Synthase iRNA sequence (283-617) is designed to bind with the normal mRNA of the starch synthase gene, thus blocking its translation into a functional starch synthase. The inhibition of the starch/glycogen synthase activity at 16 in this manner is to channel more photosynthetic products of the Calvin cycle into the Calvin-cycle-branched butanol-production pathway(s) such as the glyceraldehydes-3-phosphate-branched butanol-production pathway 01-12 as illustrated in FIG. **1**.

[0121] SEQ ID NO: 28 presents example 28 for a designer HydA1-promoter-controlled Starch-Synthase-iRNA DNA construct (1328 bp) that includes a PCR FD primer (sequence 1-20), a 282-bp HydA1 promoter (21-302), a designer Starch-Synthase iRNA sequence (303-1085), a 223-bp RbcS2 terminator (1086-1308), and a PCR RE primer (1309-1328). The designer Starch-Synthase-iRNA sequence (303-1085) comprises of: a 300-bp sense fragment (303-602) selected from the first 300-bp unique coding sequence of a *Chlamydomonas reinhardtii* starch synthase mRNA sequence (GenBank: AF026422), a 183-bp designer intron-like loop (603-785), and a 300-bp antisense sequence (786-1085) complement to the first 300-bp coding sequence of a *Chlamydomonas reinhardtii* starch-synthase-mRNA sequence (GenBank: AF026422). This designer Starch-Synthase-iRNA sequence (303-1085) is designed to inhibit the synthesis of starch synthase by the following two mechanisms. First, the 300-bp antisense complement iRNA sequence (corresponding to DNA sequence 786-1085) binds with the normal mRNA of the starch synthase gene, thus blocking its translation into a functional starch synthase. Second, the 300-bp antisense complement iRNA sequence (corresponding to DNA sequence 786-1085) can also bind with the 300-bp sense counterpart (corresponding to DNA sequence 303-602) in the same designer iRNA molecule, forming a hairpin-like double-stranded RNA structure with the 183-bp designer intron-like sequence (603-785) as a loop. Experimental studies have shown that this type of hairpin-like double-stranded RNA can also trigger post-transcriptional gene silencing (Fuhrmann, Stahlberg, Govorunova, Rank and Hegemann (2001) *Journal of Cell Science* 114:3857-3863). Because of the use of a HydA1 promoter (21-302), this designer starch-synthesis-iRNA gene is designed to be expressed only under anaerobic conditions when needed to enhance photobiological butanol production by channeling more photosynthetic products of the Calvin cycle into the butanol-production pathway (s) such as 01-12, 03-12, and/or 20-33 as illustrated in FIG. **1**.

Designer Starch-Degradation and Glycolysis Genes

[0122] In yet another embodiment of the present invention, the photobiological butanol production is enhanced by incorporating an additional set of designer genes (FIG. **2**D) that can facilitate starch/glycogen degradation and glycolysis in combination with the designer butanol-production gene(s) (FIG. **2**A). Such additional designer genes for starch degradation include, for example, genes coding for 17: amylase, starch phosphorylase, hexokinase, phosphoglucomutase, and for 18: glucose-phosphate-isomerase (G-P-isomerase) as illustrated in FIG. **1**. The designer glycolysis genes encode chloroplast-targeted glycolysis enzymes: glucosephosphate isomerase 18, phosphofructose kinase 19, aldolase 20, triose phosphate isomerase 21, glyceraldehyde-3-phosphate dehydrogenase 22, phosphoglycerate kinase 23, phosphoglycerate mutase 24, enolase 25, and pyruvate kinase 26. The designer starch-degradation and glycolysis genes in combination with any of the butanol-production pathways shown in FIG. **1** can form additional pathway(s) from starch/glycogen to butanol (17-33). Consequently, co-expression of the designer starch-degradation and glycolysis genes with the butanol-production-pathway genes can enhance photobiological production of butanol as well. Therefore, this embodiment represents another approach to tame the Calvin cycle for enhanced photobiological production of butanol. In this case, some of the Calvin-cycle products flow through the starch synthesis pathway (13-16) followed by the starch/glycogen-to-butanol pathway (17-33) as shown in FIG. **1**. In this case, starch/glycogen acts as a transient storage pool of the Calvin-cycle products before they can be converted to butanol. This mechanism can be quite useful in maximizing the butanol-production yield in certain cases. For example, at high sunlight intensity such as around noon, the rate of Calvin-cycle photosynthetic CO_2 fixation can be so high that may exceed the maximal rate capacity of a butanol-production pathway(s); use of the starch-synthesis mechanism allows temporary storage of the excess photosynthetic products to be used later for butanol production as well.

[0123] FIG. **1** also illustrates the use of a designer starch/glycogen-to-butanol pathway with designer enzymes (as labeled from 17 to 33) in combination with a Calvin-cycle-branched designer butanol-production pathway(s) such as the glyceraldehydes-3-phosphate-branched butanol-production pathway 01-12 for enhanced photobiological butanol production. Similar to the benefits of using the Calvin-cycle-branched designer butanol-production pathways, the use of the designer starch/glycogen-to-butanol pathway (17-33) can also help to convert the photosynthetic products to butanol before the sugars could be converted into other complicated biomolecules such as lignocellulosic biomasses which cannot be readily used by the biorefinery industries. Therefore, appropriate use of the Calvin-cycle-branched designer butanol-production pathway(s) (such as 01-12, 03-12, and/or 20-33) and/or the designer starch/glycogen-to-butanol pathway (17-33) may represent revolutionary inter alia technologies that can effectively bypass the bottleneck problems of the current biomass technology including the "lignocellulosic recalcitrance" problem.

[0124] Another feature is that a Calvin-cycle-branched designer butanol-production pathway activity (such as 01-12, 03-12, and/or 20-33) can occur predominantly during the days when there is light because it uses an intermediate product of the Calvin cycle which requires supplies of reducing power (NADPH) and energy (ATP) generated by the photosynthetic water splitting and the light-driven proton-translocation-coupled electron transport process through the thylakoid membrane system. The designer starch/glycogen-to-butanol pathway (17-33) which can use the surplus sugar that has been stored as starch/glycogen during photosynthesis can

operate not only during the days, but also at nights. Consequently, the use of a Calvin-cycle-branched designer butanol-production pathway (such as 01-12, 03-12, and/or 20-33) together with a designer starch/glycogen-to-butanol pathway (s) (17-33) as illustrated in FIG. **1** enables production of butanol both during the days and at nights.

[0125] Because the expression for both the designer starch/glycogen-to-butanol pathway(s) and the Calvin-cycle-branched designer butanol-production pathway(s) is controlled by the use of an inducible promoter such as an anaerobic hydrogenase promoter, this type of designer organisms is also able to grow photoautotrophically under aerobic (normal) conditions. When the designer photosynthetic organisms are grown and ready for photobiological butanol production, the cells are then placed under the specific inducing conditions such as under anaerobic conditions [or an ammonium-to-nitrate fertilizer use shift, if designer Nia1/nirA promoter-controlled butanol-production pathway(s) is used] for enhanced butanol production, as shown in FIGS. **1** and **3**.

[0126] Examples of designer starch (glycogen)-degradation genes are shown in SEQ ID NO: 29-33 listed. Briefly, SEQ ID NO:29 presents example 29 for a designer Amylase DNA construct (1889 bp) that includes a PCR FD primer (sequence 1-20), a 2×84-bp NR promoter (21-188), a 9-bp Xho I NdeI site (189-197), a 135-bp RbcS2 transit peptide (198-332), an Amylase-encoding sequence (333-1616) selected and modified from a Barley alpha-amylase (GenBank: J04202A my46 expression tested in aleurone cells), a 21-bp Lumio-tag sequence (1617-1637), a 9-bp XbaI site (1638-1646), a 223-bp RbcS2 terminator (1647-1869), and a PCR RE primer (1870-1889).

[0127] SEQ ID NO: 30 presents example 30 for a designer Starch-Phosphorylase DNA construct (3089 bp) that includes a PCR FD primer (sequence 1-20), a 2×84-bp NR promoter (21-188), a 135-bp RbcS2 transit peptide (189-323), a Starch Phosphorylase-encoding sequence (324-2846) selected and modified from a Citrus root starch-phosphorylase sequence (GenBank: AY098895, expression tested in citrus root), a 223-bp RbcS2 terminator (2847-3069), and a PCR RE primer (3070-3089).

[0128] SEQ ID NO: 31 presents example 31 for a designer Hexose-Kinase DNA construct (1949 bp) that includes a PCR FD primer (sequence 1-20), a 2×84-bp NR promoter (21-188), a 135-bp RbcS2 transit peptide (189-323), a Hexose Kinase-encoding sequence (324-1706) selected and modified from *Ajellomyces capsulatus* hexokinase mRNA sequence (Genbank: XM_001541513), a 223-bp RbcS2 terminator (1707-1929), and a PCR RE primer (1930-1949).

[0129] SEQ ID NO: 32 presents example 32 for a designer Phosphoglucomutase DNA construct (2249 bp) that includes a PCR FD primer (sequence 1-20), a 2×84-bp NR promoter (21-188), a 135-bp RbcS2 transit peptide (189-323), a Phosphoglucomutase-encoding sequence (324-2006) selected and modified from *Pichia stipitis* phosphoglucomutase sequence (GenBank: XM_001383281), a 223-bp RbcS2 terminator (2007-2229), and a PCR RE primer (2230-2249).

[0130] SEQ ID NO: 33 presents example 33 for a designer Glucosephosphate-Isomerase DNA construct (2231 bp) that includes a PCR FD primer (sequence 1-20), a 2×84-bp NR promoter (21-188), a 135-bp RbcS2 transit peptide (189-323), a Glucosephosphate Isomerase-encoding sequence (324-1988) selected and modified from a *S. cerevisiae* phosphoglucoisomerase sequence (GenBank: M21696), a 223-bp RbcS2 terminator (1989-2211), and a PCR RE primer (2212-2231).

[0131] The designer starch-degradation genes such as those shown in SEQ ID NO: 29-33 can be selected for use in combination with various designer butanol-production-pathway genes for construction of various designer starch-degradation butanol-production pathways such as the pathways shown in FIG. **1**. For example, the designer genes shown in SEQ ID NOS: 1-12, 24-26, and 29-33 can be selected for construction of a Nia1 promoter-controlled starch-to-butanol production pathway that comprises of the following designer enzymes: amylase, starch phosphorylase, hexokinase, phosphoglucomutase, glucosephosphate isomerase, phosphofructose kinase, fructose diphosphate aldolase, triose phosphate isomerase, glyceraldehyde-3-phosphate dehydrogenase, phosphoglycerate kinase, phosphoglycerate mutase, enolase, pyruvate kinase, pyruvate-$NADP^+$ oxidoreductase (or pyruvate-ferredoxin oxidoreductase), thiolase, 3-hydroxybutyryl-CoA dehydrogenase, crotonase, butyryl-CoA dehydrogenase, butyraldehyde dehydrogenase, and butanol dehydrogenase. This starch/glycogen-to-butanol pathway 17-33 may be used alone and/or in combinations with other butanol-production pathway(s) such as the 3-phosphoglycerate-branched butanol-production pathway 03-12 as illustrated in FIG. **1**.

Distribution of Designer Butanol-Production Pathways Between Chloroplast and Cytoplasm

[0132] In yet another embodiment of the present invention, photobiological butanol productivity is enhanced by a selected distribution of the designer butanol-production pathway(s) between chloroplast and cytoplasm in a eukaryotic plant cell. That is, not all the designer butanol-production pathway(s) (FIG. **1**) have to operate in the chloroplast; when needed, part of the designer butanol-production pathway(s) can operate in cytoplasm as well. For example, in one of the various embodiments, a significant part of the designer starch-to-butanol pathway activity from dihydroxyacetone phosphate to butanol (21-33) is designed to occur at the cytoplasm while the steps from starch to dihydroxyacetone phosphate (17-20) are in the chloroplast. In this example, the linkage between the chloroplast and cytoplasm parts of the designer pathway is accomplished by use of the triose phosphate-phosphate translocator, which facilitates translocation of dihydroxyacetone across the chloroplast membrane. By use of the triose phosphate-phosphate translocator, it also enables the glyceraldehyde-3-phospahte-branched designer butanol-production pathway to operate not only in chloroplast, but also in cytoplasm as well. The cytoplasm part of the designer butanol-production pathway can be constructed by use of designer butanol-production pathway genes (DNA constructs of FIG. **2**A) with their chloroplast-targeting sequence omitted as shown in FIG. **2**E.

Designer Oxyphotobacteria with Designer Butanol-Production Pathways in Cytoplasm

[0133] In prokaryotic photosynthetic organisms such as blue-green algae (oxyphotobacteria including cyanobacteria and oxychlorobacteria), which typically contain photosynthetic thylakoid membrane but no chloroplast structure, the Calvin cycle is located in the cytoplasm. In this special case, the entire designer butanol-production pathway(s) (FIG. **1**) including (but not limited to) the glyceraldehyde-3-phosphate branched butanol-production pathway (01-12), the

3-phosphpglycerate-branched butanol-production pathway (03-12), the fructose-1,6-diphosphate-branched pathway (20-33), the fructose-6-phosphate-branched pathway (19-33), and the starch (or glycogen)-to-butanol pathways (17-33) are adjusted in design to operate with the Calvin cycle in the cytoplasm of a blue-green alga. The construction of the cytoplasm designer butanol-production pathways can be accomplished by use of designer butanol-production pathway genes (DNA construct of FIG. **2**A) with their chloroplast-targeting sequence all omitted. When the chloroplast-targeting sequence is omitted in the designer DNA construct(s) as illustrated in FIG. **2**E, the designer gene(s) is transcribed and translated into designer enzymes in the cytoplasm whereby conferring the designer butanol-production pathway(s). The designer gene(s) can be incorporated into the chromosomal and/or plasmid DNA in host blue-green algae (oxyphotobacteria including cyanobacteria and oxychlorobacteria) by using the techniques of gene transformation known to those skilled in the art. It is a preferred practice to integrate the designer genes through an integrative transformation into the chromosomal DNA that can usually provide better genetic stability for the designer genes. In oxyphotobacteria such as cyanobacteria, integrative transformation can be achieved through a process of homologous DNA double recombination into the host's chromosomal DNA using a designer DNA construct as illustrated in FIG. **2**F, which typically, from the 5' upstream to the 3' downstream, consists of: recombination site 1, a designer butanol-production-pathway gene(s), and recombination site 2. This type of DNA constructs (FIG. **2**F) can be delivered into oxyphotobacteria (blue-green algae) with a number of available genetic transformation techniques including electroporation, natural transformation, and/or conjugation. The transgenic designer organisms created from blue-green algae are also called designer blue-green algae (designer oxyphotobacteria including designer cyanobacteria and designer oxychlorobacteria).

[0134] Examples of designer oxyphotobacterial butanol-production-pathway genes are shown in SEQ ID NO: 34-45 listed. Briefly, SEQ ID NO:34 presents example 34 for a designer oxyphotobacterial Butanol Dehydrogenase DNA construct (1709 bp) that includes a PCR FD primer (sequence 1-20), a 400-bp nitrite reductase (nirA) promoter from *Thermosynechococcus elongatus* BP-1 (21-420), an enzyme-encoding sequence (421-1569) selected and modified from a *Clostridium saccharoperbutylacetonicum* Butanol Dehydrogenase sequence (AB257439), a 120-bp rbcS terminator from *Thermosynechococcus elongatus* BP-1 (1570-1689), and a PCR RE primer (1690-1709) at the 3' end.

[0135] SEQ ID NO:35 presents example 35 for a designer oxyphotobacterial Butyraldehyde Dehydrogenase DNA construct (1967 bp) that includes a PCR FD primer (sequence 1-20), a 400-bp *Thermosynechococcus elongatus* BP-1 nitrite reductase nirA promoter (21-420), an enzyme-encoding sequence (421-1827) selected and modified from a *Clostridium saccharoperbutylacetonicum* Butyraldehyde Dehydrogenase sequence (AY251646), a 120-bp rbcS terminator from *Thermosynechococcus* (1828-1947), and a PCR RE primer (1948-1967).

[0136] SEQ ID NO:36 presents example 36 for a designer oxyphotobacterial Butyryl-CoA Dehydrogenase DNA construct (1602 bp) that includes a PCR FD primer (sequence 1-20), a 305-bp *Thermosynechococcus elongatus* BP-1 nitrate reductase promoter (21-325), a Butyryl-CoA Dehydrogenase encoding sequence (326-1422) selected/modified from the sequences of a *Clostridium beijerinckii* Butyryl-CoA Dehydrogenase (AF494018), a 120-bp *Thermosynechococcus* rbcS terminator (1423-1582), and a PCR RE primer (1583-1602).

[0137] SEQ ID NO:37 presents example 37 for a designer oxyphotobacterial Crotonase DNA construct (1248 bp) that includes a PCR FD primer (sequence 1-20), a 305-bp *Thermosynechococcus elongatus* BP-1 nitrate reductase promoter (21-325), a Crotonase-encoding sequence (326-1108) selected/modified from the sequences of a *Clostridium beijerinckii* Crotonase (GenBank: AF494018), 120-bp *Thermosynechococcus elongatus* BP-1 rbcS terminator (1109-1228), and a PCR RE primer (1229-1248).

[0138] SEQ ID NO:38 presents example 38 for a designer oxyphotobacterial 3-Hydroxybutyryl-CoA Dehydrogenase DNA construct (1311 bp) that include of a PCR FD primer (sequence 1-20), a 305-bp nirA promoter from (21-325), a 3-Hydroxybutyryl-CoA Dehydrogenase-encoding sequence (326-1171) selected/modified from a *Clostridium beijerinckii* 3-Hydroxybutyryl-CoA Dehydrogenase sequence Crotonase (GenBank: AF494018), a 120-bp *Thermosynechococcus* rbcS terminator (1172-1291), and a PCR RE primer (1292-1311).

[0139] SEQ ID NO:39 presents example 39 for a designer oxyphotobacterial Thiolase DNA construct (1665 bp) that includes a PCR FD primer (sequence 1-20), a 305-bp *Thermosynechococcus* nirA promoter (21-325), a Thiolase-encoding sequence (326-1525) selected from a *Butyrivibrio fibrisolvens* Thiolase sequence (AB190764), a 120-bp *Thermosynechococcus* rbcS terminator (1526-1645), and a PCR RE primer (1646-1665).

[0140] SEQ ID NO:40 presents example 40 for a designer oxyphotobacterial Pyruvate-Ferredoxin Oxidoreductase DNA construct (4071 bp) that includes a PCR FD primer (sequence 1-20), a 305-bp nirA promoter from *Thermosynechococcus elongatus* BP-1 (21-325), a Pyruvate-Ferredoxin Oxidoreductase-encoding sequence (326-3931) selected/modified from the sequences of a *Mastigamoeba balamuthi* Pyruvate-ferredoxin oxidoreductase (GenBank: AY101767), a 120-bp rbcS terminator from *Thermosynechococcus elongatus* BP-1 (3932-4051), and a PCR RE primer (4052-4071).

[0141] SEQ ID NO:41 presents example 41 for a designer oxyphotobacterial Pyruvate Kinase DNA construct (1806 bp) that includes a PCR FD primer (sequence 1-20), a 305-bp nirA promoter from *Thermosynechococcus* (21-325), a pyruvate kinase-encoding sequence (326-1666) selected/modified from a *Thermoproteus tenax* pyruvate kinase (GenBank: AF065890), a 120-bp *Thermosynechococcus* rbcS terminator (1667-1786), and a PCR RE primer (1787-1806).

[0142] SEQ ID NO:42 presents example 42 for a designer oxyphotobacterial Enolase DNA construct (1696 bp) that includes a PCR FD primer (sequence 1-20), a 231-bp nirA promoter from *Thermosynechococcus* (21-251), a enolase-encoding sequence (252-1556) selected/modified from the sequences of a *Chlamydomonas* cytosolic enolase (GenBank: X66412, P31683), a 120-bp rbcS terminator from *Thermosynechococcus* (1557-1676), and a PCR RE primer (1677-1696).

[0143] SEQ ID NO:43 presents example 43 for a designer oxyphotobacterial Phosphoglycerate-Mutase DNA construct (2029 bp) that includes a PCR FD primer (sequence 1-20), a 231-bp nirA promoter from *Thermosynechococcus elongatus* BP-1 (21-251), a phosphoglycerate-mutase encoding sequence (252-1889) selected/modified from the sequences

of a *Pelotomaculum thermopropionicum* SI phosphoglycerate mutase (GenBank: YP_001213270), a 120-bp *Thermosynechococcus* rbcS terminator (1890-2009), and a PCR RE primer (2010-2029).

[0144] SEQ ID NO:44 presents example 44 for a designer oxyphotobacterial Phosphoglycerate Kinase DNA construct (1687 bp) that includes a PCR FD primer (sequence 1-20), a 231-bp nirA promoter from *Thermosynechococcus elongatus* BP-1 (21-251), a phosphoglycerate-kinase-encoding sequence (252-1433) selected from *Pelotomaculum thermopropionicum* SI phosphoglycerate kinase (BAF60903), a 234-bp *Thermosynechococcus elongatus* BP-1 rbcS terminator (1434-1667), and a PCR RE primer (1668-1687).

[0145] SEQ ID NO:45 presents example 45 for a designer oxyphotobacterial Glyceraldehyde-3-Phosphate Dehydrogenase DNA construct (1514 bp) that includes a PCR FD primer (sequence 1-20), a 305-bp *Thermosynechococcus elongatus* BP-1 nirA promoter (21-325), an enzyme-encoding sequence (326-1260) selected and modified from *Blastochloris viridis* NAD-dependent Glyceraldehyde-3-phosphate dehydrogenase (CAC80993), a 234-bp rbcS terminator from *Thermosynechococcus elongatus* BP-1 (1261-1494), and a PCR RE primer (1495-1514).

[0146] The designer oxyphotobacterial genes such as those shown in SEQ ID NO: 34-45 can be selected for use in full or in part, and/or in combination with various other designer butanol-production-pathway genes for construction of various designer oxyphotobacterial butanol-production pathways such as the pathways shown in FIG. **1**. For example, the designer genes shown in SEQ ID NOS: 34-45 can be selected for construction of an oxyphotobacterial nirA promoter-controlled and glyceraldehyde-3-phosphate-branched butanol-production pathway (01-12) that comprises of the following designer enzymes: NAD-dependent glyceraldehyde-3-phosphate dehydrogenase 01, phosphoglycerate kinase 02, phosphoglycerate mutase 03, enolase 04, pyruvate kinase 05, pyruvate-ferredoxin oxidoreductase (or pyruvate-$NADP^+$ oxidoreductase) 06, thiolase 07, 3-hydroxybutyryl-CoA dehydrogenase 08, crotonase 09, butyryl-CoA dehydrogenase 10, butyraldehyde dehydrogenase 11, and butanol dehydrogenase 12. Use of these designer oxyphotobacterial butanol-production-pathway genes (SEQ ID NOS: 34-45) in a thermophilic and/or thermotolerant cyanobacterium may represent a thermophilic and/or thermotolerant butanol-producing oxyphotobacterium. Fox example, use of these designer genes (SEQ ID NOS: 34-45) in a thermophilic/thermotolerant cyanobacterium such as *Thermosynechococcus elongatus* BP-1 may represent a designer thermophilic/thermotolerant butanol-producing cyanobacterium such as a designer butanol-producing *Thermosynechococcus.*

Further Host Modifications to Help Ensure Biosafety

[0147] The present invention also provides biosafety-guarded photosynthetic biofuel (e.g., butanol and/or related higher alcohols) production methods based on cell-division-controllable designer transgenic plants (such as algae and oxyphotobacteria) or plant cells. For example, the cell-division-controllable designer photosynthetic organisms (FIG. **3**) are created through use of a designer biosafety-control gene (s) (FIG. **2**G) in conjunction with the designer butanol-production-pathway gene(s) (FIGS. **2**A-**2**F) such that their cell division and mating function can be controllably stopped to provide better biosafety features.

[0148] In one of the various embodiments, a fundamental feature is that a designer cell-division-controllable photosynthetic organism (such as an alga, plant cell, or oxyphotobacterium) contains two key functions (FIG. **3**A): a designer biosafety mechanism(s) and a designer biofuel-production pathway(s). As shown in FIG. **3**B, the designer biosafety feature(s) is conferred by a number of mechanisms including: (1) the inducible insertion of designer proton-channels into cytoplasm membrane to permanently disable any cell division and mating capability, (2) the selective application of designer cell-division-cycle regulatory protein or interference RNA (iRNA) to permanently inhibit the cell division cycle and preferably keep the cell at the G_1 phase or G_0 state, and (3) the innovative use of a high-CO_2-requiring host photosynthetic organism for expression of the designer biofuel-production pathway(s). Examples of the designer biofuel-production pathway(s) include the designer butanol-production pathway(s), which work with the Calvin cycle to synthesize biofuel such as butanol directly from carbon dioxide (CO_2) and water (H_2O). The designer cell-division-control technology can help ensure biosafety in using the designer organisms for photosynthetic biofuel production. Accordingly, this embodiment provides, inter alia, biosafety-guarded methods for producing biofuel (e.g., butanol and/or related higher alcohols) based on a cell-division-controllable designer biofuel-producing alga, cyanobacterium, oxychlorobacterium, plant or plant cells.

[0149] In one of the various embodiments, a cell-division-controllable designer butanol-producing eukaryotic alga or plant cell is created by introducing a designer proton-channel gene (FIG. **2**H) into a host alga or plant cell (FIG. **3**B). SEQ ID NO: 46 presents example 46 for a detailed DNA construct of a designer Nia1-promoter-controlled proton-channel gene (609 bp) that includes a PCR FD primer (sequence 1-20), a 262-bp nitrate reductase Nia1 promoter (21-282), a Melittin proton-channel encoding sequence (283-366), a 223-bp RbcS2 terminator (367-589), and a PCR RE primer (590-609).

[0150] The expression of the designer proton-channel gene (FIG. **2**H) is controlled by an inducible promoter such as the nitrate reductase (Nia1) promoter, which can also be used to control the expression of a designer biofuel-production-pathway gene(s). Therefore, before the expression of the designer gene(s) is induced, the designer organism can grow photoautotrophically using CO_2 as the carbon source and H_2O as the source of electrons just like wild-type organism. When the designer organism culture is grown and ready for photobiological production of biofuels, the cell culture is then placed under a specific inducing condition (such as by adding nitrate into the culture medium if the nitrate reductase (Nia1) promoter is used as an inducible promoter) to induce the expression of both the designer proton-channel gene and the designer biofuel-production-pathway gene(s). The expression of the proton-channel gene is designed to occur through its transcription in the nucleus and its translation in the cytosol. Because of the specific molecular design, the expressed proton channels are automatically inserted into the cytoplasm membrane, but leave the photosynthetic thylakoid membrane intact. The insertion of the designer proton channels into cytoplasm membrane collapses the proton gradient across the cytoplasm membrane so that the cell division and mating function are permanently disabled. However, the photosynthetic thylakoid membrane inside the chloroplast is kept intact (functional) so that the designer biofuel-production-

pathway enzymes expressed into the stroma region can work with the Calvin cycle for photobiological production of biofuels from CO_2 and H_2O. That is, when both the designer proton-channel gene and the designer biofuel-production-pathway gene(s) are turned on, the designer organism becomes a non-reproducible cell for dedicated photosynthetic production of biofuels. Because the cell division and mating function are permanently disabled (killed) at this stage, the designer-organism culture is no longer a living matter except its catalytic function for photochemical conversion of CO_2 and H_2O into a biofuel. It will no longer be able to mate or exchange any genetic materials with any other cells, even if it somehow comes in contact with a wild-type cell as it would be the case of an accidental release into the environments.

[0151] According to one of the various embodiments, the nitrate reductase (Nia1) promoter or nitrite reductase (nirA) promoter is a preferred inducible promoter for use to control the expression of the designer genes. In the presence of ammonium (but not nitrate) in culture medium, for example, a designer organism with Nia1-promoter-controlled designer proton-channel gene and biofuel-production-pathway gene (s) can grow photoauotrophically using CO_2 as the carbon source and H_2O as the source of electrons just like a wild-type organism. When the designer organism culture is grown and ready for photobiological production of biofuels, the expression of both the designer proton-channel gene and the designer biofuel-production-pathway gene(s) can then be induced by adding some nitrate fertilizer into the culture medium. Nitrate is widely present in soils and nearly all surface water on Earth. Therefore, even if a Nia1-promoter-controlled designer organism is accidentally released into the natural environment, it will soon die since the nitrate in the environment will trig the expression of a Nia1-promoter-controlled designer proton-channel gene which inserts proton-channels into the cytoplasm membrane thereby killing the cell. That is, a designer photosynthetic organism with Nia1-promoter-controlled proton-channel gene is programmed to die as soon as it sees nitrate in the environment. This characteristic of cell-division-controllable designer organisms with Nia1-promoter-controlled proton-channel gene provides an added biosafety feature.

[0152] The art in constructing proton-channel gene (FIG. **2**H) with a thylakoid-membrane targeting sequence has recently been disclosed [James W. Lee (2007). Designer proton-channel transgenic algae for photobiological hydrogen production, PCT International Publication Number: WO 2007/134340 A2]. In the present invention of creating a cell-division-controllable designer organism, the thylakoid-membrane-targeting sequence must be omitted in the proton-channel gene design. For example, the essential components of a Nia1-promoter-controlled designer proton-channel gene can simply be a Nia1 promoter linked with a proton-channel-encoding sequence (without any thylakoid-membrane-targeting sequence) so that the proton channel will insert into the cytoplasm membrane but not into the photosynthetic thylakoid membrane.

[0153] According to one of the various embodiments, it is a preferred practice to use the same inducible promoter such as the Nia1 promoter to control the expression of both the designer proton-channel gene and the designer biofuel-production pathway genes. In this way, the designer biofuel-production pathway(s) can be inducibly expressed simultaneously with the expression of the designer proton-channel gene that terminates certain cellular functions including cell division and mating.

[0154] In one of the various embodiments, an inducible promoter that can be used in this designer biosafety embodiment is selected from the group consisting of the hydrogenase promoters [HydA1 (Hyd1) and HydA2, accession number: AJ308413, AF289201, AY090770], the Cyc6 gene promoter, the Cpx1 gene promoter, the heat-shock protein promoter HSP70A, the CabII-1 gene (accession number M24072) promoter, the Ca1 gene (accession number P20507) promoter, the Ca2 gene (accession number P24258) promoter, the nitrate reductase (Nia1) promoter, the nitrite-reductase-gene (nirA) promoters, the bidirectional-hydrogenase-gene hox promoters, the light- and heat-responsive groE promoters, the Rubisco-operon rbcL promoters, the metal (zinc)-inducible smt promoter, the iron-responsive idiA promoter, the redox-responsive crhR promoter, the heat-shock-gene hsp16.6 promoter, the small heat-shock protein (Hsp) promoter, the CO_2-responsive carbonic-anhydrase-gene promoters, the green/red light responsive cpcB2A2 promoter, the UV-light responsive lexA, recA and ruvB promoters, the nitrate-reductase-gene (narB) promoters, and combinations thereof.

[0155] In another embodiment, a cell-division-controllable designer photosynthetic organism is created by use of a carbonic anhydrase deficient mutant or a high-CO_2-requiring mutant as a host organism to create the designer biofuel-production organism. High-CO_2-requiring mutants that can be selected for use in this invention include (but not limited to): *Chlamydomonas reinhardtii* carbonic-anhydrase-deficient mutant12-1C(CC-1219 ca1 mt-), *Chlamydomonas reinhardtii* cia3 mutant (*Plant Physiology* 2003, 132:2267-2275), the high-CO_2-requiring mutant M3 of *Synechococcus* sp. Strain PCC 7942, or the carboxysome-deficient cells of *Synechocystis* sp. PCC 6803 (*Plant biol* (Stuttg) 2005, 7:342-347) that lacks the CO_2-concentrating mechanism can grow photoautotrophically only under elevated CO_2 concentration level such as 0.2-3% CO_2.

[0156] Under atmospheric CO_2 concentration level (380 ppm), the carbonic anhydrase deficient or high-CO_2-requiring mutants commonly cannot survive. Therefore, the key concept here is that a high-CO_2-requiring designer biofuel-production organism that lacks the CO_2 concentrating mechanism will be grown and used for photobiological production of biofuels always under an elevated CO_2 concentration level (0.2-5% CO_2) in a sealed bioreactor with CO_2 feeding. Such a designer transgenic organism cannot survive when it is exposed to an atmospheric CO_2 concentration level (380 ppm=0.038% CO_2) because its CO_2-concetrating mechanism (CCM) for effective photosynthetic CO_2 fixation has been impaired by the mutation. Even if such a designer organism is accidentally released into the natural environment, its cell will soon not be able to divide or mate, but die quickly of carbon starvation since it cannot effectively perform photosynthetic CO_2 fixation at the atmospheric CO_2 concentration (380 ppm). Therefore, use of such a high-CO_2-requiring mutant as a host organism for the genetic transformation of the designer biofuel-production-pathway gene(s) represents another way in creating the envisioned cell-division-controllable designer organisms for biosafety-guarded photobiological production of biofuels from CO_2 and H_2O. No designer proton-channel gene is required here.

[0157] In another embodiment, a cell-division-controllable designer organism (FIG. **3**B) is created by use of a designer

cell-division-cycle regulatory gene as a biosafety-control gene (FIG. **2**G) that can control the expression of the cell-division-cycle (cdc) genes in the host organism so that it can inducibly turn off its reproductive functions such as permanently shutting off the cell division and mating capability upon specific induction of the designer gene.

[0158] Biologically, it is the expression of the natural cdc genes that controls the cell growth and cell division cycle in cyanobacteria, algae, and higher plant cells. The most basic function of the cell cycle is to duplicate accurately the vast amount of DNA in the chromosomes during the S phase (S for synthesis) and then segregate the copies precisely into two genetically identical daughter cells during the M phase (M for mitosis). Mitosis begins typically with chromosome condensation: the duplicated DNA strands, packaged into elongated chromosomes, condense into the much-more compact chromosomes required for their segregation. The nuclear envelope then breaks down, and the replicated chromosomes, each consisting of a pair of sister chromatids, become attached to the microtubules of the mitotic spindle. As mitosis proceeds, the cell pauses briefly in a state called metaphase, when the chromosomes are aligned at the equator of the mitotic spindle, poised for segregation. The sudden segregation of sister chromatids marks the beginning of anaphase during which the chromosomes move to opposite poles of the spindle, where they decondense and reform intact nuclei. The cell is then pinched into two by cytoplasmic division (cytokinesis) and the cell division is then complete. Note, most cells require much more time to grow and double their mass of proteins and organelles than they require to replicate their DNA (the S phase) and divide (the M phase). Therefore, there are two gap phases: a G_1 phase between M phase and S phase, and a G2 phase between S phase and mitosis. As a result, the eukaryotic cell cycle is traditionally divided into four sequential phases: G_1, S, G_2, and M. Physiologically, the two gap phases also provide time for the cell to monitor the internal and external environment to ensure that conditions are suitable and preparation are complete before the cell commits itself to the major upheavals of S phase and mitosis. The G_1 phase is especially important in this aspect. Its length can vary greatly depending on external conditions and extracellular signals from other cells. If extracellular conditions are unfavorable, for example, cells delay progress through G_1 and may even enter a specialized resting state known as G_0 (G zero), in which they remain for days, weeks, or even for years before resuming proliferation. Indeed, many cells remain permanently in G_0 state until they die.

[0159] In one of the various embodiments, a designer gene (s) that encodes a designer cdc-regulatory protein or a specific cdc-iRNA is used to inducibly inhibit the expression of certain cdc gene(s) to stop cell division and disable the mating capability when the designer gene(s) is trigged by a specific inducing condition. When the cell-division-controllable designer culture is grown and ready for photosynthetic production of biofuels, for example, it is a preferred practice to induce the expression of a specific designer cdc-iRNA gene (s) along with induction of the designer biofuel-production-pathway gene(s) so that the cells will permanently halt at the G_1 phase or G_0 state. In this way, the grown designer-organism cells become perfect catalysts for photosynthetic production of biofuels from CO_2 and H_2O while their functions of cell division and mating are permanently shut off at the G_1 phase or G_0 state to help ensure biosafety.

[0160] Use of the biosafety embodiments with various designer biofuel-production-pathways genes listed in SEQ ID NOS: 1-45 (and 58-165) can create various biosafety-guarded photobiological biofuel producers (FIGS. **3**A, **3**B, and **3**C). Note, SEQ ID NOS: 46 and 1-12 (examples 1-12) represent an example for a cell-division-controllable designer eukaryotic organism such as a cell-division-controllable designer alga (e.g., *Chlamydomonas*) that contains a designer Nia1-promoter-controlled proton-channel gene (SEQ ID NO: 46) and a set of designer Nia1-promoter-controlled butanol-production-pathway genes (SEQ ID NOS: 1-12). Because the designer proton-channel gene and the designer biofuel-production-pathway gene(s) are all controlled by the same Nia1-promoter sequences, they can be simultaneously expressed upon induction by adding nitrate fertilizer into the culture medium to provide the biosafety-guarded photosynthetic biofuel-producing capability as illustrated in FIG. **3**B. Use of the designer Nia1-promoter-controlled butanol-production-pathway genes (SEQ ID NOS: 1-12) in a high CO_2-requiring host photosynthetic organism, such as *Chlamydomonas reinhardtii* carbonic-anhydrase-deficient mutant12-1C(CC-1219 ca1 mt-) or *Chlamydomonas reinhardtii* cia3 mutant, represents another example in creating a designer cell-division-controllable photosynthetic organism to help ensure biosafety.

[0161] This designer biosafety feature may be useful to the production of other biofuels such as biooils, biohydrogen, ethanol, and intermediate products as well. For example, this biosafety embodiment in combination with a set of designer ethanol-production-pathway genes such as those shown SEQ ID NOS: 47-53 can represent a cell-division-controllable ethanol producer (FIG. **3**C). Briefly, SEQ ID NO: 47 presents example 47 for a detailed DNA construct (1360 base pairs (bp)) of a nirA-promoter-controlled designer NAD-dependent Glyceraldehyde-3-Phosphate-Dehydrogenase gene including: a PCR FD primer (sequence 1-20), a 88-bp nirA promoter (21-108) selected from the *Synechococcus* sp. (freshwater cyanobacterium) nitrite-reductase-gene promoter sequence, an enzyme-encoding sequence (109-1032) selected and modified from a *Cyanidium caldarium* cytosolic NAD-dependent glyceraldehyde-3-phosphate-dehydrogenase sequence (GenBank accession number: CAC85917), a 308-bp Synechococcus rbcS terminator (1033-1340), and a PCR RE primer (1341-1360) at the 3' end.

[0162] SEQ ID NO: 48 presents example 48 for a designer nirA-promoter-controlled Phosphoglycerate Kinase DNA construct (1621 bp) that includes a PCR FD primer (sequence 1-20), a 88-bp *Synechococcus* sp. strain PCC 7942 nitrite-reductase nirA promoter (21-108), a phosphoglycerate-kinase-encoding sequence (109-1293) selected from a *Geobacillus kaustophilus* phosphoglycerate-kinase sequence (GenBank: BAD77342), a 308-bp *Synechococcus* rbcS terminator (1294-1601), and a PCR RE primer (1602-1621).

[0163] SEQ ID NO: 49 presents example 49 for a designer nirA-promoter-controlled Phosphoglycerate-Mutase DNA construct (1990 bp) that includes a PCR FD primer (sequence 1-20), a 88-bp *Synechococcus* sp. strain PCC 7942 nitrite-reductase nirA promoter (21-108), a 9-bp Xho I NdeI site (109-117), a phosphoglycerate-mutase encoding sequence (118-1653) selected from the sequences of a *Caldicellulosiruptor saccharolyticus* DSM 8903 phosphoglycerate mutase (GenBank: ABP67536), a 9-bp XbaI site (1654-1662), a 308-bp *Synechococcus* sp. strain PCC 7942 rbcS terminator (1663-1970), and a PCR RE primer (1971-1990).

[0164] SEQ ID NO: 50 presents example 50 for a designer nirA-promoter-controlled Enolase DNA construct (1765 bp) that includes a PCR FD primer (sequence 1-20), a 88-bp *Synechococcus* sp. strain PCC 7942 nitrite reductase nirA promoter (21-108), a 9-bp Xho I NdeI site (109-117), an enolase-encoding sequence (118-1407) selected from the sequence of a *Cyanothece* sp. CCY0110 enolase (GenBank: ZP_01727912), a 21-bp Lumio-tag-encoding sequence (1408-1428), a 9-bp XbaI site (1429-1437) containing a stop codon, a 308-bp *Synechococcus* rbcS terminator (1438-1745), and a PCR RE primer (1746-1765) at the 3' end.

[0165] SEQ ID NO: 51 presents example 51 for a designer nirA-promoter-controlled Pyruvate Kinase DNA construct (1888 bp) that includes a PCR FD primer (sequence 1-20), a 88-bp *Synechococcus* nitrite reductase nirA promoter (21-108), a 9-bp Xho I NdeI site (109-117), a Pyruvate-Kinase-encoding sequence (118-1530) selected from a *Selenomonas ruminantium* Pyruvate Kinase sequence (GenBank: AB037182), a 21-bp Lumio-tag sequence (1531-1551), a 9-bp XbaI site (1552-1560), a 308-bp *Synechococcus* rbcS terminator (1561-1868), and a PCR RE primer (1869-1888).

[0166] SEQ ID NO: 52 presents example 52 for a designer nirA-promoter-controlled Pyruvate Decarboxylase DNA construct (2188 bp) that includes a PCR FD primer (sequence 1-20), a 88-bp *Synechococcus* nitrite reductase nirA promoter (21-108), a 9-bp Xho I NdeI site (109-117), a Pyruvate-Decarboxylase-encoding sequence (118-1830) selected from the sequences of a *Pichia stipitis* pyruvate-decarboxylase sequence (GenBank: XM_001387668), a 21-bp Lumio-tag sequence (1831-1851), a 9-bp XbaI site (1852-1860), a 308-bp *Synechococcus* rbcS terminator (1861-2168), and a PCR RE primer (2169-2188) at the 3' end.

[0167] SEQ ID NO: 53 presents example 53 for a nirA-promoter-controlled designer NAD(P)H-dependent Alcohol Dehydrogenase DNA construct (1510 bp) that includes a PCR FD primer (sequence 1-20), a 88-bp *Synechococcus* nitrite-reductase nirA promoter (21-108), a NAD(P)H dependent Alcohol-Dehydrogenase-encoding sequence (109-1161) selected/modified (its mitochondrial signal peptide sequence removed) from the sequence of a *Kluyveromyces lactis* alcohol dehydrogenase (ADH3) gene (GenBank: X62766), a 21-bp Lumio-tag sequence (1162-1182), a 308-bp *Synechococcus* rbcS terminator (1183-1490), and a PCR RE primer (1491-1510) at the 3' end.

[0168] Note, SEQ ID NOS: 47-53 (DNA-construct examples 47-53) represent a set of designer nirA-promoter-controlled ethanol-production-pathway genes that can be used in oxyphotobacteria such as *Synechococcus* sp. strain PCC 7942. Use of this set of designer ethanol-production-pathway genes in a high-CO_2-requiring cyanobacterium such as the *Synechococcus* sp. Strain PCC 7942 mutant M3 represents another example of cell-division-controllable designer cyanobacterium for biosafety-guarded photosynthetic production of biofuels from CO_2 and H_2O.

More on Designer Calvin-Cycle-Channeled Production of Butanol and Related Higher Alcohols

[0169] The present invention further discloses designer Calvin-cycle-channeled and photosynthetic-NADPH (reduced nicotinamide adenine dinucleotide phosphate)-enhanced pathways, associated designer DNA constructs (designer genes) and designer transgenic photosynthetic organisms for photobiological production of butanol and related higher alcohols from carbon dioxide and water. In this context throughout this specification as mentioned before, a "higher alcohol" or "related higher alcohol" refers to an alcohol that comprises at least four carbon atoms, including both straight and branched higher alcohols such as 1-butanol and 2-methyl-1-butanol. The Calvin-cycle-channeled and photosynthetic-NADPH-enhanced pathways are constructed with designer enzymes expressed through use of designer genes in host photosynthetic organisms such as algae and oxyphotobacteria (including cyanobacteria and oxychlorobacteria) organisms for photobiological production of butanol and related higher alcohols. The said butanol and related higher alcohols are selected from the group consisting of: 1-butanol, 2-methyl-1-butanol, isobutanol, 3-methyl-1-butanol, 1-hexanol, 1-octanol, 1-pentanol, 1-heptanol, 3-methyl-1-pentanol, 4-methyl-1-hexanol, 5-methyl-1-heptanol, 4-methyl-1-pentanol, 5-methyl-1-hexanol, and 6-methyl-1-heptanol. The designer photosynthetic organisms such as designer transgenic algae and oxyphotobacteria (including cyanobacteria and oxychlorobacteria) comprise designer Calvin-cycle-channeled and photosynthetic NADPH-enhanced pathway gene(s) and biosafety-guarding technology for enhanced photobiological production of butanol and related higher alcohols from carbon dioxide and water.

[0170] Photosynthetic water splitting and its associated proton gradient-coupled electron transport process generates chemical energy intermediate in the form of adenosine triphosphate (ATP) and reducing power in the form of reduced nicotinamide adenine dinucleotide phosphate (NADPH). However, certain butanol-related metabolic pathway enzymes such as the NADH-dependent butanol dehydrogenase (GenBank accession numbers: YP_148778, NP_561774, AAG23613, ZP_05082669, ADO12118, ADC48983) can use only reduced nicotinamide adenine dinucleotide (NADH) but not NADPH. Therefore, to achieve a true coupling of a designer pathway with the Calvin cycle for photosynthetic production of butanol and related higher alcohols, it is a preferred practice to use an effective NADPH/NADH conversion mechanism and/or NADPH-using enzyme(s) (such as NADPH-dependent enzymes) in construction of a compatible designer pathway(s) to couple with the photosynthesis/Calvin-cycle process in accordance with the present invention.

[0171] According to one of the various embodiments, a number of various designer Calvin-cycle-channeled pathways can be created by use of an NADPH/NADH conversion mechanism in combination with certain amino-acids-metabolic pathways for production of butanol and higher alcohols from carbon dioxide and water. The Calvin-cycle-channeled and photosynthetic-NADPH-enhanced pathways are constructed typically with designer enzymes that are selectively expressed through use of designer genes in a host photosynthetic organism such as a host alga or oxyphotobacterium for production of butanol and higher alcohols. A list of exemplary enzymes that can be selected for use in construction of the Calvin-cycle-channeled and photosynthetic-NADPH-enhanced pathways are presented in Table 1. As shown in FIGS. **4-10**, the net results of the designer Calvin-cycle-channeled and photosynthetic NADPH-enhanced pathways in working with the Calvin cycle are production of butanol and related higher alcohols from carbon dioxide (CO_2) and water (H_2O) using photosynthetically generated ATP (Adenosine triphosphate) and NADPH (reduced nicotinamide adenine dinucleotide phosphate). A significant feature is the innovative utilization of an NADPH-dependent glyceraldehyde-3-phosphate

dehydrogenase 34 and a nicotinamide adenine dinucleotide (NAD)-dependent glyceraldehyde-3-phosphate dehydrogenase 35 to serve as a NADPH/NADH conversion mechanism that can convert certain amount of photosynthetically generated NADPH to NADH which can then be used by NADH-requiring pathway enzymes such as an NADH-dependent alcohol dehydrogenase 43 (examples of its encoding gene with GenBank accession numbers are: BAB59540, CAA89136, NP_148480) for production of butanol and higher alcohols.

[0172] More specifically, an NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase 34 (e.g., GenBank accession numbers: ADC37857, ADC87332, YP_003471459, ZP_04395517, YP_003287699, ZP_07004478, ZP_04399616) catalyzes the following reaction that uses NADPH in reducing 1,3-Diphosphoglycerate (1,3-DiPGA) to 3-Phosphoglyaldehyde (3-PGAld) and inorganic phosphate (Pi):

$$\text{1,3-DiPGA+NADPH+H}^{+}\rightarrow\text{3-PGAld+NADP}^{+}\text{+Pi} \quad [3]$$

Meanwhile, an NAD-dependent glyceraldehyde-3-phosphate dehydrogenase 35 (e.g., GenBank: ADM41489, YP_003095198, ADC36961, ZP_07003925, ACQ61431, YP_002285269, ADN80469, ACI60574) catalyzes the oxidation of 3-PGAld by oxidized nicotinamide adenine dinucleotide (NAD^{+}) back to 1,3-DiPGA:

$$\text{3-PGAld+NAD}^{+}\text{+Pi}\rightarrow\text{1,3-DiPGA+NADH+H}^{+} \quad [4]$$

The net result of the enzymatic reactions [3] and [4] is the conversion of photosynthetically generated NADPH to NADH, which various NADH-requiring designer pathway enzymes such as NADH-dependent alcohol dehydrogenase 43 can use in producing butanol and related higher alcohols. When there is too much NADH, this NADPH/NADH conversion system can run also reversely to balance the supply of NADH and NADPH. Therefore, it is a preferred practice to innovatively utilize this NADPH/NADH conversion system under control of a designer switchable promoter such as nirA (or Nia1 for eukaryotic system) promoter when/if needed to achieve robust production of butanol and related higher alcohols. Various designer Calvin-cycle-channeled pathways in combination of a NADPH/NADH conversion mechanism with certain amino-acids-metabolism-related pathways for photobiological production of butanol and related higher alcohols are further described hereinbelow.

TABLE 1

lists examples of enzymes for construction of designer Calvin-cycle-linked pathways for production of butanol and related higher alcohols.

Enzyme/callout number	Source (Organism)	GenBank Accession Number, JGI Protein ID or Citation
03: Phosphoglycerate mutase (phosphoglyceromutase)	*Oceanithermus profundus DSM 14977;* '*Nostoc azollae*' 0708; *Thermotoga lettingae* TMO; *Syntrophothermus lipocalidus* DSM 12680;	ADR35708; ADI65627, YP_003722750; YP_001470593, ABV33529; ADI02216, YP_003702781;
	Pelotomaculum thermopropionicum SI;	YP_001212148;
	Fervidobacterium nodosum Rt17-B1;	YP_001409891;
	Caldicellulosiruptor bescii DSM 6725;	YP_002573254, YP_002573195;
	Fervidobacterium nodosum Rt17-B1;	ABS60234;
	Thermotoga petrophila RKU-1;	ABQ47079, YP_001244998;
	Deferribacter desulfuricans SSM1;	YP_003496402, BAI80646;
	Cyanobium sp. PCC 7001;	ZP_05046421;
	Cyanothece sp. PCC 8802;	YP_003138980, YP_003138979;
	Chlamydomonas reinhardtii cytoplasm;	JGI Chlre2 protein ID 161689,
	Aspergillus fumigatus; *Coccidioides immitis*; *Leishmania braziliensis*;	GenBank: AF268078; XM_747847; XM_749597;
	Ajellomyces capsulatus;	XM_001248115; XM_001569263;
	Monocercomonoides sp.; *Aspergillus clavatus*; *Arabidopsis thaliana*; *Zea mays*	XM_001539892; DQ665859; XM_001270940; NM_117020; M80912
04: Enolase	*Syntrophothermus lipocalidus* DSM 12680; '*Nostoc azollae*' 0708;	ADI02602, YP_003703167; ADI63801;
	Thermotoga petrophila RKU-1;	ABQ46079;
	Spirochaeta thermophila DSM 6192;	YP_003875216, ADN02943;
	Cyanothece sp. PCC 7822;	YP_003886899, ADN13624;
	Hydrogenobacter thermophilus TK-6;	YP_003432637, BAI69436;
	Thermosynechococcus elongatus BP-1,	BAC08209;
	Prochlorococcus marinus str. MIT 9301; *Synechococcus* sp. WH 5701;	ABO16851; ZP_01083626;
	Trichodesmium erythraeum IMS101;	ABG51970;
	Anabaena variabilis ATCC 29413;	ABA23124;
	Nostoc sp. PCC 7120;	BAB75237;
	Chlamydomonas reinhardtii cytoplasm;	GenBank: X66412, P31683;
	Arabidopsis thaliana; *Leishmania Mexicana*; *Lodderomyces elongisporus*;	AK222035; DQ221745; XM_001528071; XM_001611873;
	Babesia bovis; *Sclerotinia sclerotiorum*;	XM_001594215; XM_001483612;
	Pichia guilliermondii;	AB221057; EF122486, U09450;
	Spirotrichonympha leidyi; *Oryza sativa;*	DQ845796; AB088633; U82438;
	Trimastix pyriformis; *Leuconostoc mesenteroides*; *Davidiella tassiana*;	D64113; U13799; AY307449; U17973
	Aspergillus oryzae;	

TABLE 1-continued

lists examples of enzymes for construction of designer Calvin-cycle-linked pathways for production of butanol and related higher alcohols.

Enzyme/callout number	Source (Organism)	GenBank Accession Number, JGI Protein ID or Citation
	Schizosaccharomyces pombe; *Brassica napus*; *Zea mays*	
05: Pyruvate kinase	*Syntrophothermus lipocalidus* DSM 12680; *Cyanothece* sp. PCC 8802; *Thermotoga lettingae* TMO; *Caldicellulosiruptor bescii* DSM 6725; *Geobacillus kaustophilus* HTA426; *Thermosynechococcus elongatus* BP-1; *Thermosipho melanesiensis* BI429; *Thermotoga petrophila* RKU-1; *Caldicellulosiruptor saccharolyticus* DSM 8903; *Cyanothece* sp. PCC 7425; *Acaryochloris marina* MBIC11017; *Cyanothece* sp. PCC 8801; *Microcystis aeruginosa* NIES-843; *Cyanothece* sp. PCC 7822; *cyanobacterium* UCYN-A; *Arthrospira maxima* CS-328; *Synechococcus* sp. PCC 7335; *Chlamydomonas reinhardtii* cytoplasm; *Arabidopsis thaliana*; *Saccharomyces cerevisiae*; *Babesia bovis*; *Sclerotinia sclerotiorum*; *Trichomonas vaginalis*; *Pichia guilliermondii*; *Pichia stipitis*; *Lodderomyces elongisporus*; *Coccidioides immitis*; *Trimastix pyriformis*; *Glycine max* (soybean)	ADI02459, YP_003703024; YP_002372431; YP_001471580, ABV34516; YP_002573139; YP_148872; NP_681306, BAC08068; YP_001306168, ABR30783; YP_001244312, ABQ46736; ABP67416, YP_001180607; ACL43749, YP_002482578; YP_001514814; YP_003138017; YP_001655408; YP_003890281; YP_003422225; ZP_03273505; ZP_05035056; JGI Chlre3 protein ID 138105; GenBank: AK229638; AY949876, AY949890, AY949888; XM_001612087; XM_001594710; XM_001329865; XM_001487289; XM_001384591; XM_001528210; XM_001240868; DQ845797; L08632
06a: Pyruvate-NADP$^+$ oxidoreductase	*Peranema trichophorum*; *Euglena gracilis*	GenBank: EF114757; AB021127, AJ278425
06b: Pyruvate-ferredoxin oxidoreductase	*Mastigamoeba balamuthi*; *Desulfovibrio africanus*; *Entamoeba histolytica*; *Trichomonas vaginalis*; *Cryptosporidium parvum*; *Cryptosporidium baileyi*; *Giardia lamblia*; *Entamoeba histolytica*; *Hydrogenobacter thermophilus*; *Clostridium pasteurianum*;	GenBank: AY101767; Y09702; U30149; XM_001582310, XM_001313670, XM_001321286, XM_001307087, XM_001311860, XM_001314776, XM_001307250; EF030517; EF030516; XM_764947; XM_651927; AB042412; Y17727
07: Thiolase	*Butyrivibrio fibrisolvens*; butyrate-producing *bacterium* L2-50; *Thermoanaerobacterium thermosaccharolyticum*;	GenBank: AB190764; DQ987697; Z92974;
08: 3-Hydroxybutyryl-CoA dehydrogenase	*Clostridium beijerinckii*; *Butyrivibrio fibrisolvens*; *Ajellomyces capsulatus*; *Aspergillus fumigatus*; *Aspergillus clavatus*; *Neosartorya fischeri*; Butyrate-producing *bacterium* L2-50; *Arabidopsis thaliana*; *Thermoanaerobacterium thermosaccharolyticum*;	GenBank: AF494018; AB190764; XM_001537366; XM_741533; XM_001274776; XM_001262361; DQ987697; BT001208; Z92974;
09: Crotonase	*Clostridium beijerinckii*; *Butyrivibrio fibrisolvens*; Butyrate-producing *bacterium* L2-50; *Thermoanaerobacterium thermosaccharolyticum*;	GenBank: AF494018; AB190764; DQ987697; Z92974
10: Butyryl-CoA dehydrogenase	*Clostridium beijerinckii*; *Butyrivibrio fibrisolvens*; Butyrate-producing *bacterium* L2-50; *Thermoanaerobacterium thermosaccharolyticum*;	GenBank: AF494018; AB190764; DQ987697; Z92974
11: Butyraldehyde dehydrogenase	*Clostridium saccharoperbutylacetonicum*	GenBank: AY251646
12a: NADH-dependent Butanol dehydrogenase	*Geobacillus kaustophilus* HTA426; *Clostridium perfringens* str. 13; *Carboxydothermus hydrogenoformans*; *Pseudovibrio* sp. JE062; *Clostridium carboxidivorans* P7; *Bacillus pseudofirmus* OF4; *Oceanobacillus iheyensis* HTE831;	YP_148778, BAD77210; NP_561774, BAB80564; AAG23613; ZP_05082669, EEA96294; ADO12118; ADC48983, YP_003425875; NP_693981, BAC15015;

TABLE 1-continued

lists examples of enzymes for construction of designer Calvin-cycle-linked pathways for production of butanol and related higher alcohols.

Enzyme/callout number	Source (Organism)	GenBank Accession Number, JGI Protein ID or Citation
	Slackia exigua ATCC 700122;	ZP_06159969, EEZ61452;
	Fusobacterium ulcerans ATCC 49185;	ZP_05633940;
	Listeria monocytogenes FSL J1-175;	ZP_05388801;
	Chlorobium chlorochromatii CaD3;	ABB28961;
	Clostridium perfringens D str. JGS1721;	ZP_02952811;
	Clostridium perfringens NCTC	ZP_02641897;
	8239; *Clostridium perfringens* CPE str.	ZP_02638128;
	F4969; Clostridium perfringens B str.	ZP_02634798;
	ATCC 3626;	EDT24774;
	Clostridium botulinum NCTC 2916;	ZP_02614964, ZP_02614746;
	Nostoc sp. PCC 7120;	NP_488606, BAB76265;
12b:	*Clostridium perfringens* str. 13;	NP_562172, BAB80962;
NADPH-dependent Butanol	*Clostridium saccharobutylicum*;	AAA83520;
dehydrogenase	*Subdoligranulum variabile* DSM 15176;	EFB77036;
	Butyrivibrio crossotus DSM 2876;	EFF67629, ZP_05792927;
	Oribacterium sp. oral taxon 078 str.	ZP_06597730, EFE92592;
	F0262; *Clostridium* sp. M62/1;	EFE12215, ZP_06346636;
	Clostridium hathewayi DSM 13479;	EFC98086, ZP_06115415;
	Subdoligranulum variabile DSM 15176;	ZP_05979561;
	Faecalibacterium prausnitzii A2-165;	ZP_05615704, EEU95840;
	Blautia hansenii DSM 20583;	ZP_05853889, EEX22072;
	Roseburia intestinalis L1-82,	ZP_04745071, EEU99657;
	Bacillus cereus Rock3-28;	ZP_04236939, EEL31374;
	Eubacterium rectale ATCC 33656;	YP_002938098, ACR75964;
	Clostridium sp. HGF2;	EFR36834;
	Atopobium rimae ATCC 49626;	ZP_03568088;
	Clostridium perfringens D str. JGS1721;	ZP_02952006;
	Clostridium perfringens NCTC 8239;	ZP_02642725;
	Clostridium butyricum 5521;	ZP_02950013, ZP_02950012;
	Clostridium carboxidivorans P7;	ZP_06856327;
	Clostridium botulinum E3 str. Alaska	YP_001922606, YP_001922335,
	E43; *Clostridium novyi* NT;	ACD52989; YP_878939;
	Clostridium botulinum B str. Eklund	YP_001887401;
	17B; *Thermococcus* sp. AM4;	EEB74113;
	Fusobacterium sp. D11;	EFD81183;
	Anaerococcus vaginalis ATCC 51170;	ZP_05473100, EEU12061;
	Clostridium perfringens CPE str.	EDT27639;
	F4969; *Clostridium perfringens* B str.	EDT24389;
	ATCC 3626;	
13:	*Chlamydomonas reinhardtii*; *Phaseolus*	GenBank: AF026422, AF026421,
Starch synthase	*vulgaris*; *Oryza sativa*; *Arabidopsis*	DQ019314, AF433156;
	thaliana; *Colocasia esculenta*;	AB293998; D16202, AB115917,
	Amaranthus cruentus; *Parachlorella*	AY299404; AF121673,
	kessleri; *Triticum aestivum*; *Sorghum*	AK226881; NM_101044;
	bicolor; *Astragalus membranaceus*;	AY225862, AY142712;
	Perilla frutescens; *Zea mays*; *Ipomoea*	DQ178026; AB232549; Y16340;
	batatas	AF168786; AF097922;
		AF210699; AF019297; AF068834
14:	*Arabidopsis thaliana*; *Zea mays*;	GenBank: NM_127730,
Glucose-1-phosphate	*Chlamydia trachomatis*; *Solanum*	NM_124205, NM_121927,
adenylyltransferase	*tuberosum* (potato); *Shigella flexneri*;	AY059862; EF694839,
	Lycopersicon esculentum	EF694838; AF087165; P55242;
		NP_709206; T07674
15:	*Oryza sativa* plastid; *Ajellomyces*	GenBank: AC105932, AF455812;
Phosphoglucomutase	*capsulatus*; *Pichia stipitis*;	XM_001536436; XM_001383281;
	Lodderomyces elongisporus; *Aspergillus*	XM_001527445; XM_749345;
	fumigatus; *Arabidopsis thaliana*;	NM_124561, NM_180508,
	Populus tomentosa; *Oryza sativa*; *Zea*	AY128901; AY479974;
	mays	AF455812; U89342, U89341
16:	*Staphylococcus carnosus* subsp.	YP_002633806, CAL27621;
Hexose-phosphate-isomerase	*carnosus* TM300;	
17:	*Hordeum vulgare aleuron* cells;	GenBank: J04202;
Alpha-amylase;	*Trichomonas vaginalis*; *Phanerochaete*	XM_001319100; EF143986;
	chrysosporium; *Chlamydomonas*	AY324649; NM_129551;
	reinhardtii; *Arabidopsis thaliana*;	X07896;
	Dictyoglomus thermophilum heat-stable	
	amylase gene;	
Beta-amylase;	*Arabidopsis thaliana*; *Hordeum vulgare*;	GenBank: NM_113297; D21349;
	Musa acuminate;	DQ166026;

TABLE 1-continued

lists examples of enzymes for construction of designer Calvin-cycle-linked pathways for production of butanol and related higher alcohols.

Enzyme/callout number	Source (Organism)	GenBank Accession Number, JGI Protein ID or Citation
Starch phosphorylase;	*Citrus* hybrid cultivar root; *Solanum tuberosum chloroplast*; *Arabidopsis thaliana*; *Triticum aestivum*; *Ipomoea batatas*;	GenBank: AY098895; P53535; NM_113857, NM_114564; AF275551; M64362
18: Glucose-phosphate (glucose-6-phosphate) isomerase	*Chlamydomonas reinhardtii*; *Saccharomyces cerevisiae*; *Pichia stipitis*; *Ajellomyces capsulatus*; *Spinacia oleracea* cytosol; *Oryza sativa* cytoplasm; *Arabidopsis thaliana*; *Zea mays*	JGI Chlre3 protein ID 135202; GenBank: M21696; XM_001385873; XM_001537043; T09154; P42862; NM_123638, NM_118595; U17225
19: Phosphofructose kinase	*Chlamydomonas reinhardtii*; *Arabidopsis thaliana*; *Ajellomyces capsulatus*; *Yarrowia lipolytica*; *Pichia stipitis*; *Dictyostelium discoideum*; *Tetrahymena thermophila*; *Trypanosoma brucei*; *Plasmodium falciparum*; *Spinacia oleracea*;	JGI Chlre2 protein ID 159495; GenBank: NM_001037043, NM_179694, NM_119066, NM_125551; XM_001537193; AY142710; XM_001382359, XM_001383014; XM_639070; XM_001017610; XM_838827; XM_001347929; DQ437575;
20: Fructose-diphosphate aldolase	*Chlamydomonas reinhardtii* chloroplast; *Fragaria* x *ananassa* cytoplasm; *Homo sapiens*; *Babesia bovis*; *Trichomonas vaginalis*; *Pichia stipitis*; *Arabidopsis thaliana*	GenBank: X69969; AF308587; NM_005165; XM_001609195; XM_001312327, XM_001312338; XM_001387466; NM_120057, NM_001036644
21: Triose phosphate isomerase	*Arabidopsis thaliana*; *Chlamydomonas reinhardtii*; *Sclerotinia sclerotiorum*; *Chlorella pyrenoidosa*; *Pichia guilliermondii*; *Euglena intermedia*; *Euglena longa*; *Spinacia oleracea*; *Solanum chacoense*; *Hordeum vulgare*; *Oryza sativa*	GenBank: NM_127687, AF247559; AY742323; XM_001587391; AB240149; XM_001485684; DQ459379; AY742325; L36387; AY438596; U83414; EF575877;
34: NADPH-dependent Glyceraldehyde-3-phosphate dehydrogenase	*Staphylococcus aureus* 04-02981;	ADC37857;
	Staphylococcus lugdunensis;	ADC87332;
	Staphylococcus lugdunensis HKU09;	YP_003471459;
	Vibrio cholerae BX 330286;	ZP_04395517;
	Vibrio sp. Ex25;	YP_003287699;
	Pseudomonas savastanoi pv.;	ZP_07004478, EFI00105;
	Vibrio cholerae B33;	ZP_04399616
	Grimontia hollisae CIP 101886;	ZP_06052988, EEY71738;
	Vibrio mimicus MB-451,	ZP_06041160;
	Vibrio coralliilyticus ATCC BAA-450;	ZP_05886203;
	Vibrio cholerae MJ-1236;	YP_002876243;
	Zea mays cytosolic NADP dependent;	NP_001105589;
	Apium graveolens;	AAF08296;
	Vibrio cholerae B33;	EEO17521;
	Vibrio cholerae TMA 21;	EEO13209;
	Vibrio cholerae bv. *albensis* VL426;	EEO01829;
	Vibrio orientalis CIP 102891;	ZP_05943395;
	Vibrio cholerae MJ-1236;	ACQ62447;
	Vibrio cholerae CT 5369-93;	ZP_06049761;
	Vibrio sp. RC586;	ZP_06079970;
	Vibrio furnissii CIP 102972;	ZP_05878983;
	Vibrio metschnikovii CIP 69.14;	ZP_05883187;
35: NAD-dependent Glyceraldehyde-3-phosphate dehydrogenase	*Edwardsiella tarda* FL6-60;	ADM41489;
	Flavobacteriaceae bacterium 3519-10;	YP_003095198;
	Staphylococcus aureus 04-02981;	ADC36961;
	Pseudomonas savastanoi pv. *savastanoi* NCPPB 3335;	ZP_07003925;
	Vibrio cholerae MJ-1236;	ACQ61431, YP_002878104;
	Streptococcus pyogenes NZ131;	YP_002285269;
	Helicobacter pylori 908;	ADN80469;
	Streptococcus pyogenes NZ131;	ACI60574;
	Staphylococcus lugdunensis HKU09;	ADC88142;
	Vibrio sp. Ex25;	ACY51070;
	Stenotrophomonas chelatiphaga;	ADK67090;
	Pseudoxanthomonas dokdonensis;	ADK67075;
	Stenotrophomonas maltophilia;	ADK67085, ACH90636;
	Vibrio cholerae B33; *Photobacterium damselae* subsp. *damselae* CIP 102761;	ZP_04401333; ZP_06155532;
	Vibrio sp. RC586;	ZP_06080908;
	Grimontia hollisae CIP 101886;	ZP_06052393;

TABLE 1-continued

lists examples of enzymes for construction of designer Calvin-cycle-linked pathways for production of butanol and related higher alcohols.

Enzyme/callout number	Source (Organism)	GenBank Accession Number, JGI Protein ID or Citation
	Vibrio furnissii CIP 102972;	EEX42220;
	Acidithiobacillus caldus ATCC 51756;	ZP_05292346;
	Nostoc sp. PCC 7120;	CAC41000;
	Vibrio cholerae BX 330286;	EEO22474;
	Vibrio cholerae TMA 21;	EEO13042;
	Nostoc sp. PCC 7120;	CAC41000;
	Pinus sylvestris;	CAA04942;
	Cheilanthes yavapensis;	ACO58643, ACO58642;
	Cheilanthes wootonii;	ACO58624, ACO58623;
	Astrolepis laevis;	CBH41484, CBH41483;
36:	*Hydrogenobacter thermophilus* TK-6;	YP_003433013, ADO45737,
(R)-Citramalate synthase	*Geobacter bemidjiensis* Bem;	BAI69812;
(EC 2.3.1.182)	*Geobacter sulfurreducens* KN400;	ACH38284;
	Methanobrevibacter ruminantium M1;	ADI84633;
	Leptospira biflexa serovar Patoc strain 'Patoc 1 (Paris)'; *Leptospira biflexa* serovar Monteralerio; *Leptospira interrogans* serovar Australis; *Leptospira interrogans* serovar *Pomona*; *Leptospira interrogans* serovar Autumnalis; *Leptospira interrogans* serovar Pyrogenes; *Leptospira interrogans* serovar Canicola; *Leptospira interrogans* serovar Lai;	CP001719; ABK13757; ABK13756; ABK13755; ABK13753; ABK13754; ABK13752; ABK13751; ABK13750; ABK13749;
	Acetohalobium arabaticum DSM 5501;	ADL11763,
	Leadbetterella byssophila DSM 17132;	YP_003998693;
	Bacteroides xylanisolvens XB1A;	CBK66631;
	Mucilaginibacter paludis DSM 18603;	EFQ72644;
	Prevotella ruminicola 23;	ADE82919;
	Flavobacterium johnsoniae UW101;	ABQ04337;
	Victivallis vadensis ATCC BAA-548;	ZP_06244204,
	Prevotella copri DSM 18205;	EFA99692;
	Alistipes shahii WAL 8301;	EFB36404, ZP_06251228;
	Methylobacter tundripaludum SV96;	CBK64953;
	Methanosarcina mazei Go1;	ZP_07654184; NP_632695;
37:	*Eubacterium eligens* ATCC 27750	YP_002930810, YP_002930809;
(R)-2-Methylmalate	*Methanocaldococcus jannaschii*;	P81291;
dehydratase (large and small	*Sebaldella termitidis* ATCC 33386;	ACZ06998;
subunits)	*Eubacterium eligens* ATCC 27750;	ACR72362, ACR72361,
(EC 4.2.1.35)		ACR72363, YP_002930808;
38:	*Thermotoga petrophila* RKU-1;	ABQ46641, ABQ46640;
3-Isopropylmalate	*Cyanothece* sp. PCC 7822;	YP_003886427, YP_003889452;
dehydratase (large + small	*Syntrophothermus lipocalidus* DSM 12680;	ADI02900, ADI02899,
subunits)		YP_003703465, ADI01294;
(EC 4.2.1.33)	*Caldicellulosiruptor saccharolyticus* DSM 8903;	ABP66933, ABP66934;
	Pelotomaculum thermopropionicum SI,	YP_001211082, YP_001211083;
	Caldicellulosiruptor bescii DSM 6725;	YP_002573950, YP_002573949;
	Caldicellulosiruptor saccharolyticus DSM 8903;	YP_001180124, YP_001180125;
	E. coli;	leuC, ECK0074, JW0071; leuD, ECK0073, JW0070;
	Spirochaeta thermophila DSM 6192;	YP_003875294, YP_003873373;
	Pelotomaculum thermopropionicum SI;	YP_001213069, YP_001213068;
	Hydrogenobacter thermophilus TK-6;	YP_003433547, YP_003432351;
	Deferribacter desulfuricans SSM1;	YP_003495505, YP_003495504;
	Anoxybacillus flavithermus WK1;	ACJ32977, ACJ32978;
	Thermosynechococcus elongatus BP-1;	BAC08461, BAC08786;
	Geobacillus kaustophilus HTA426;	BAD76941, BAD76940;
	Synechocystis sp. PCC 6803;	BAA18738, BAA18298;
	Chlamydomonas reinhardtii;	XP_001702135, XP_001696402;
39:	*Thermotoga petrophila* RKU-1;	ABQ46392, YP_001243968;
3-Isopropylmalate	*Cyanothece* sp. PCC 7822;	YP_003888480, ADN15205;
dehydrogenase	*Thermosynechococcus elongatus* BP-1;	BAC09152, NP_682390;
(EC 1.1.1.85)	*Syntrophothermus lipocalidus* DSM 12680;	ADI02898, YP_003703463;
	Caldicellulosiruptor bescii DSM 6725;	ADQ78220;
	Paludibacter propionicigenes WB4;	YP_002573948;
	Leadbetterella byssophila DSM 17132;	YP_003998692;
	Caldicellulosiruptor saccharolyticus	ABP66935;

TABLE 1-continued

lists examples of enzymes for construction of designer Calvin-cycle-linked pathways for production of butanol and related higher alcohols.

Enzyme/callout number	Source (Organism)	GenBank Accession Number, JGI Protein ID or Citation
	DSM 8903; *Thermus thermophilus*;	AAA16706, YP_001180126;
	Pelotomaculum thermopropionicum SI;	YP_001211084;
	Geobacillus kaustophilus HTA426;	YP_148510, BAD76942;
	Hydrogenobacter thermophilus TK-6;	YP_003433176;
	Spirochaeta thermophila DSM 6192;	YP_003873639;
	Deferribacter desulfuricans SSM1;	YP_003495917;
	Anoxybacillus flavithermus WK1;	YP_002314961;
	Volvox carteri f. nagariensis;	XP_002955062, EFJ43816;
	Chlamydomonas reinhardtii;	XP_001701074, XP_001701073;
	Ostreococcus tauri;	XP_003083133;
40:	*Thermotoga petrophila* RKU-1;	ABQ46395, YP_001243971;
2-Isopropylmalate synthase	*Cyanothece* sp. PCC 7822;	YP_003890122, ADN16847;
(EC 2.3.3.13)	*Cyanothece* sp. PCC 8802;	ACU99797;
	Nostoc punctiforme PCC 73102;	ACC82459;
	Pelotomaculum thermopropionicum SI;	YP_001211081;
	Hydrogenobacter thermophilus TK-6;	YP_003432474, BAI69273;
	E. coli; *Caldicellulosiruptor*	NP_414616, AAC73185;
	saccharolyticus DSM 8903;	ABP66753, YP_001179944;
	Syntrophothermus lipocalidus DSM	YP_003703466, ADI02901;
	12680; *Geobacillus kaustophilus*	YP_148511, BAD76943;
	HTA426; *Caldicellulosiruptor bescii*	YP_002572404;
	DSM 6725; *Anoxybacillus flavithermus*	YP_002314960, ACJ32975;
	WK1; *Deferribacter desulfuricans*	YP_003496874, BAI81118;
	SSM1; *Thermosynechococcus elongatus*	NP_682187, BAC08949;
	BP-1; *Spirochaeta thermophila* DSM	ADN03009, YP_003875282;
	6192; *Thermotoga lettingae* TMO;	YP_001469896, ABV32832;
	Volvox carteri f. nagariensis;	XP_002945733,
	Micromonas sp. RCC299;	EFJ52728;
	Micromonas pusilla CCMP1545;	ACO69978, XP_002508720;
	Chlamydomonas reinhardtii;	XP_003063010, EEH52949;
		XP_001696603, EDP08580;
41:	*Geobacillus kaustophilus* HTA426;	YP_148509, YP_148508;
isopropylmalate isomerase	*Anabaena variabilis* ATCC 29413;	YP_324467, YP_324466;
large/small subunits	*Synechocystis* sp. PCC 6803;	NP_442926, NP_441618;
(EC 4.2.1.33)	*Anoxybacillus flavithermus* WK1;	YP_002314962, YP_002314963;
	Thermosynechococcus elongatus BP-1;	NP_682024, NP_681699;
	Spirochaeta thermophila DSM 6192;	YP_003873372;
	Salmonella enterica subsp. *enterica*	CBG23133, CBG23132;
	serovar *Typhimurium* str. D23580;	
	Staphylococcus aureus A5937;	ZP_05702396;
	Francisella philomiragia subsp.	EET20545;
	philomiragia ATCC 25015;	AAA53236;
	Neisseria lactamica; *Francisella*	ABK88972;
	novicida U112; *Staphylococcus aureus*	EEV86047;
	A5937; *Staphylococcus aureus* subsp.	ZP_05607839;
	aureus 68-397; *Fusobacterium* sp.	EEO38992;
	2_1_31; *Francisella novicida* GA99-	EDN35429;
	3549; marine *bacterium* HP15;	ADP98363, ADP98362;
	Bacillus licheniformis ATCC 14580;	YP_092517, YP_092516;
	Rhodobacter sphaeroides 2.4.1;	YP_353947, YP_353945;
	Bordetella petrii DSM 12804;	YP_001631647, YP_001631646;
	Agrobacterium vitis S4;	YP_002551071, YP_002551071;
42:	*Lactococcus lactis*;	AAS49166;
2-keto acid decarboxylase	*Lactococcus lactis* subsp. *lactis KF147;*	ADA65057, YP_003353820;
(EC 4.1.1.72, etc)	*Lactococcus lactis* subsp. *Lactis*;	
	Kluyveromyces marxianus;	CAG34226;
	Kluyveromyces lactis;	AAA35267;
	Mycobacterium avium 104;	CAA59953;
	Mycobacterium ulcerans Agy99;	A0QBE6;
	Mycobacterium bovis;	A0PL16;
	Mycobacterium leprae;	Q7U140;
	Proteus mirabilis HI4320;	Q9CBD6;
	Staphylococcus aureus 04-02981;	YP_002150004;
	Acetobacter pasteurianus;	ADC36400;
	Saccharomyces cerevisiae;	AAM21208;
	Zymomonas mobilis subsp. *mobilis* CP4;	CAA39398;
	Mycobacterium tuberculosis;	AAA27696;

TABLE 1-continued

lists examples of enzymes for construction of designer Calvin-cycle-linked pathways for production of butanol and related higher alcohols.

Enzyme/callout number	Source (Organism)	GenBank Accession Number, JGI Protein ID or Citation
	Mycobacterium smegmatis str. MC2 155; *Mycobacterium bovis* BCG str. Pasteur 1173P2;	O53865; A0R480; A1KGY5;
43: Alcohol dehydrogenase (NAD dependent) (EC 1.1.1.1);	*Thermoplasma volcanium* GSS1; *Gluconacetobacter hansenii* ATCC 23769; *Saccharomyces cerevisiae*; *Aeropyrum pernix* K1; *Rhodobacterales bacterium* HTCC2083; *Bradyrhizobium japonicum* USDA 110; *Syntrophothermus lipocalidus* DSM 12680; *Fervidobacterium nodosum* Rt17-B1; *Desulfotalea psychrophila* LSv54; *Acetobacter pasteurianus* IFO 3283-03; *Gluconobacter oxydans* 621H; *Aeromonas hydrophila* subsp. *hydrophila* ATCC 7966; *Acetobacter pasteurianus* IFO 3283-01; *Streptomyces hygroscopicus* ATCC 53653;	BAB59540 ZP_06834544; CAA89136; NP_148480; ZP_05073895; NP_769420; ADI01021; YP_001411173; YP_065604; BAI03878; YP_192500; ABK38651; BAI00830; EFL29096;
44: Alcohol dehydrogenase (NADPH dependent) (EC 1.1.1.2);	*Pelotomaculum thermopropionicum* SI; *Fusobacterium* sp. 7_1; *Pichia pastoris* GS115; *Pichia pastoris* GS115; *Escherichia coli* str. K-12 substr. MG1655; *Clostridium hathewayi* DSM 13479; *Clostridium butyricum* 5521; *Fusobacterium ulcerans* ATCC 49185; *Fusobacterium* sp. D11; *Desulfovibrio desulfuricans* subsp. *desulfuricans* str. G20; *Clostridium novyi* NT; *Clostridium tetani* E88; *Aureobasidium pullulans*; *Scheffersomyces stipitis* CBS 6054, *Thermotoga lettingae* TMO; *Thermotoga petrophila* RKU-1; *Coprinopsis cinerea* okayama7#130; *Saccharomyces cerevisiae* EC1118; *Saccharomyces cerevisiae* JAY291;	YP_001211038, BAF58669; ZP_04573952, EEO43462; XP_002494014, XP_002490014; CAY71835, XP_002492217, CAY67733; yqhD, NP_417484, AAC76047; EFC99049; ZP_02948287 ZP_05632371; ZP_05440863; YP_389756; YP_878957; NP_782735; ADG56699; ABN66271, XP_001384300; YP_001471424; YP_001244106; XP_001834460; CAY82157; EEU07174;
45: Phosphoenolpyruvate carboxylase (EC 4.1.1.31)	*Thermaerobacter subterraneus* DSM 13965; *Cyanothece* sp. PCC 7822; *Thermus* sp.; *Rhodothermus marinus*; *Thermosynechococcus elongatus* BP-1; *Leadbetterella byssophila* DSM 17132; *Riemerella anatipestifer* DSM 15868; *Mucilaginibacter paludis* DSM 18603; *Truepera radiovictrix* DSM 17093; *Ferrimonas balearica* DSM 9799; *Meiothermus silvanus* DSM 9946; *Nocardiopsis dassonvillei* subsp. *dassonvillei* DSM 43111; *E. coli*, *Meiothermus ruber* DSM 1279; *Olsenella uli* DSM 7084; *Ktedonobacter racemifer* DSM 44963; *Rhodopirellula baltica* SH 1; *Oceanithermus profundus* DSM 14977; *marine bacterium* HP15; *Marivirga tractuosa* DSM 4126; *Mucilaginibacter paludis* DSM 18603; *Streptomyces coelicolor* A3(2); *Delftia acidovorans* SPH-1; *Actinobacillus pleuropneumoniae* serovar 13 str. N273; *Prochlorococcus marinus* str. MIT 9301; *Prochlorococcus marinus* str. NATL1A *Prochlorococcus marinus* str. MIT 9515; *Clostridium cellulovorans* 743B; *Neisseria meningitidis* Z2491; *Deinococcus geothermalis* DSM 11300; *Micromonospora* sp. L5;	EFR61439; YP_003887888; BAA07723; CAA67760; NP_682702, BAC09464; YP_003998059, ADQ17706; ADQ81501, YP_004045007; EFQ77722; YP_003706036; YP_003911597, ADN74523; YP_003685046; YP_003681843; ZP_07594313, ZP_07565817; ADD27759; YP_003801346, ADK68466; ZP_06967036, EFH90147; NP_866412, CAD78193; ADR36285; ADP96559; ADR23252; ZP_07746438; NP_627344; ABX34873; ZP_07544559; ABO18389; ABM76577; ABM72969; YP_003842669, ADL50905; CAM07667; ABF44963; ZP_06399624;

TABLE 1-continued

lists examples of enzymes for construction of designer Calvin-cycle-linked pathways for production of butanol and related higher alcohols.

Enzyme/callout number	Source (Organism)	GenBank Accession Number, JGI Protein ID or Citation
	Chlorobium phaeobacteroides DSM 266; *Arthrobacter* sp. FB24; *Rhodomicrobium vannielii* ATCC 17100; *Gordonia bronchialis* DSM 43247; *Thermus aquaticus* Y51MC23; *Burkholderia ambifaria* IOP40-10;	ABL64615; YP_830113; YP_004010507; YP_003273502; ZP_03496338; ZP_02894226;
46: Aspartate aminotransferase (EC 2.6.1.1)	*Thermotoga lettingae* TMO; *Synechococcus elongatus* PCC 6301; *Synechococcus elongatus* PCC 7942; *Thermosipho melanesiensis* BI429; *Thermotoga petrophila* RKU-1; *Thermus thermophilus*; *Anoxybacillus flavithermus* WK1; *Bacillus* sp.; *E. coli*, *Pelotomaculum thermopropionicum* SI; *Phormidium lapideum*; *Fervidobacterium nodosum* Rt17-B1; *Geobacillus kaustophilus* HTA426; *Thermosynechococcus elongatus* BP-1; *Anoxybacillus flavithermus* WK1; *Geobacillus kaustophilus* HTA426; *Spirochaeta thermophila* DSM 6192; *Caldicellulosiruptor bescii* DSM 6725; *Caldicellulosiruptor saccharolyticus* DSM 8903; *Arabidopsis thaliana*; *Glycine max*; *Lupinus angustifolius*; *Chlamydomonas reinhardtii*; *Micromonas pusilla* CCMP1545;	YP_001470126; YP_172275; YP_401562; YP_001306480; YP_001244588; BAA07487; YP_002315494; AAA22250; aspC: BAB34434; YP_001211971; BAB86290; YP_001410686, YP_001409589; YP_148025, YP_147632, YP_146225; NP_683147; ACJ34747; BAD77213, BAD76064; YP_003874653; YP_002572445; YP_001179582; AAA79371; AAA33942; CAA42430; XP_001696609; XP_003060871;
47: Aspartokinase (EC = 2.7.2.4)	*Thermotoga lettingae* TMO; *Cyanothece* sp. PCC 8802; *Thermotoga petrophila* RKU-1 *Hydrogenobacter thermophilus* TK-6; *Anoxybacillus flavithermus* WK1; *Bacillus* sp.; *Spirochaeta thermophila* DSM 6192; *Anoxybacillus flavithermus* WK1; *Geobacillus kaustophilus* HTA426; *Syntrophothermus lipocalidus* DSM 12680; *E. coli*; *Thermosynechococcus elongatus* BP-1; *Fervidobacterium nodosum* Rt17-B1; *Spirochaeta thermophila* DSM 6192; *Pelotomaculum thermopropionicum* SI; *Caldicellulosiruptor saccharolyticus* DSM 8903; *Caldicellulosiruptor bescii* DSM 6725; *Thermosipho melanesiensis* BI429; *Thermotoga lettingae* TMO; *Arabidopsis thaliana*; *Chlamydomonas reinhardtii*;	YP_001470361, ABV33297; YP_003136939; YP_001244864, YP_001243977; YP_003432105, BAI68904; ACJ35001; AAA22251; YP_003873788, ADN01515; ACJ34043, YP_002316986; BAD77480, YP_149048; ADI02230, YP_003702795; ZP_07594328, ZP_07565832; NP_682623, BAC09385; ABS59942, YP_001410786; YP_003873302, ADN01029; YP_001212149, YP_001211837; ABP66605; YP_002573821; YP_001307097, ABR31712; YP_001470985, ABV33921; CAA67376; XP_001698576, EDP08069, XP_001695256;
48: Aspartate-semialdehyde dehydrogenase	*Thermotoga lettingae* TMO; *Trichodesmium erythraeum* IMS101; *Prochlorococcus marinus* str. MIT 9303; *Thermotoga petrophila* RKU-1; *Caldicellulosiruptor saccharolyticus* DSM 8903; *Syntrophothermus lipocalidus* DSM 12680; *E. coli*; *Fervidobacterium nodosum* Rt17-B1 *Caldicellulosiruptor bescii* DSM 6725; *Thermosipho melanesiensis* BI429; *Spirochaeta thermophila* DSM 6192; *Pelotomaculum thermopropionicum* SI; *Hydrogenobacter thermophilus* TK-6; *Anoxybacillus flavithermus* WK1; *Geobacillus kaustophilus* HTA426; *Deferribacter desulfuricans* SSM1; *Thermosynechococcus elongatus* BP-1;	YP_001470981, ABV33917; ABG50031; ABM76828; ABQ47283, YP_001244859; ABP67176, YP_001180367; ADI01804, YP_003702369; YP_001460230, YP_001464895; YP_001409594, ABS59937; YP_002573009; YP_001307092, ABR31707; YP_003875128, ADN02855; YP_001211836, BAF59467; YP_003432252, BAI69051; YP_002316029, ACJ34044; YP_147128, BAD75560; YP_003496635, BAI80879; NP_680860, BAC07622; AAG23574, AAG23573;

TABLE 1-continued

lists examples of enzymes for construction of designer Calvin-cycle-linked pathways for production of butanol and related higher alcohols.

Enzyme/callout number	Source (Organism)	GenBank Accession Number, JGI Protein ID or Citation
	Carboxydothermus hydrogenoformans;	XP_001695059, EDP02211;
	Chlamydomonas reinhardtii;	ABH11018;
	Polytomella parva;	ACU30050;
	Glycine max;	ACG41594;
	Zea mays;	ABR26065;
	Oryza sativa Indica Group;	
49:	*Syntrophothermus lipocalidus* DSM	ADI02231, YP_003702796;
Homoserine dehydrogenase	12680; *Cyanothece* sp. PCC 7822;	YP_003887242;
	Caldicellulosiruptor bescii DSM 6725;	YP_002573819;
	Caldicellulosiruptor saccharolyticus	ABP66607, YP_001179798;
	DSM 8903; *E. coli*;	EFJ98002;
	Spirochaeta thermophila DSM 6192;	YP_003873441, ADN01168;
	Pelotomaculum thermopropionicum SI;	YP_001212151, BAF59782;
	Hydrogenobacter thermophilus TK-6;	YP_003431981, BAI68780;
	Anoxybacillus flavithermus WK1;	YP_002316756, ACJ34771;
	Geobacillus kaustophilus HTA426;	YP_148817, BAD77249;
	Deferribacter desulfuricans SSM1;	YP_003496401, BAI80645;
	Thermosynechococcus elongatus BP-1;	NP_681068, BAC07830;
	Glycine max;	ABG78600, AAZ98830;
	Chlamydomonas reinhardtii;	XP_001699712, EDP07408;
	Micromonas sp. RCC299;	ACO69662, XP_002508404;
50:	*Thermotoga petrophila* RKU-1;	YP_001243979, ABQ46403;
Homoserine kinase	*Cyanothece* sp. PCC 7822;	YP_003886645;
(EC 2.7.1.39)	*Caldicellulosiruptor bescii* DSM 6725;	YP_002573820;
	Caldicellulosiruptor saccharolyticus	ABP66606, YP_001179797;
	DSM 8903; *E. coli*;	AP_000667, BAB96580;
	Anoxybacillus flavithermus WK1;	YP_002316754, ACJ34769;
	Geobacillus kaustophilus HTA426;	YP_148815, BAD77247;
	Thermosynechococcus elongatus BP-1;	NP_682555, BAC09317;
	Pelotomaculum thermopropionicum SI;	YP_001212150, BAF59781;
	Hydrogenobacter thermophilus TK-6;	YP_003433124, BAI69923;
	Chlamydomonas reinhardtii;	XP_001701899, EDP06874;
	Prototheca wickerhamii;	ABC24954;
	Arabidopsis thaliana;	NP_179318, AAD33097;
	Glycine max;	ACU26535;
	Zea mays;	ACG46592;
51:	*Thermotoga petrophila* RKU-1;	YP_001243978, ABQ46402;
Threonine synthase	*Cyanothece* sp. PCC 7425;	YP_002485009;
(EC 4.2.99.2)	*Thermosipho melanesiensis* BI429;	YP_001306558, ABR31173;
	Syntrophothermus lipocalidus DSM	ADI02519, YP_003703084;
	12680; *E. coli*;	AP_000668, NP_414545;
	Pelotomaculum thermopropionicum SI;	YP_001213220;
	Anoxybacillus flavithermus WK1;	YP_002316755, ACJ34770;
	Caldicellulosiruptor bescii DSM 6725;	YP_002572552;
	Caldicellulosiruptor saccharolyticus	YP_001180015, ABP66824;
	DSM 8903; *Hydrogenobacter*	YP_003433070, YP_003433019,
	thermophilus TK-6; *Geobacillus*	BAI69869, BAI69818;
	kaustophilus HTA426;	YP_148816, YP_147614;
	Thermosynechococcus elongatus BP-1;	NP_682017, NP_681772,
	Spirochaeta thermophila DSM 6192;	BAC08534, BAC08779;
	Deferribacter desulfuricans SSM1;	YP_003873303, ADN01030;
	Geobacillus kaustophilus HTA426;	YP_003495358, BAI79602;
52:	*Geobacillus kaustophilus* HTA426;	BAD76058, BAD75876,
Threonine ammonia-lyase	*Prochlorococcus marinus* str. MIT	YP_147626, YP_147444;
(EC 4.3.1.19)	9202; *Synechococcus* sp. PCC 7335;	ZP_05137562; ZP_05035047;
	Thermotoga petrophila RKU-1;	ABQ46585, YP_001244161;
	Pelotomaculum thermopropionicum SI;	YP_001210652, BAF58283;
	Anoxybacillus flavithermus WK1;	YP_002315804, YP_002315746;
	Deferribacter desulfuricans SSM1;	YP_003497384, BAI81628;
	E. coli;	YP_001746093, ZP_07690697;
	Neisseria lactamica ATCC 23970;	EEZ76650, ZP_05986317;
	Citrobacter youngae ATCC 29220;	EFE07783, ZP_06571237;
	Neisseria polysaccharea ATCC 43768;	EFH23894, ZP_06863451;
	Providencia rettgeri DSM 1131;	EFE52186, ZP_06127162;
	Neisseria subflava NJ9703;	EFC51529, ZP_05985502;
	Mannheimia haemolytica PHL213;	ZP_04978734;
	Achromobacter piechaudii ATCC	ZP_06687730, ZP_06684811;
	43553; *Neisseria meningitidis* ATCC	ZP_07369980, EFM04207;
	13091; *Synechococcus* sp. CC9902;	
	Synechococcus sp. PCC 7002;	ABB26032;

TABLE 1-continued

lists examples of enzymes for construction of designer Calvin-cycle-linked pathways for production of butanol and related higher alcohols.

Enzyme/callout number	Source (Organism)	GenBank Accession Number, JGI Protein ID or Citation
	Synechococcus sp. WH 8109;	ACA99606;
	Cyanobium sp. PCC 7001;	ZP_05790446, EEX07646;
	Anabaena variabilis ATCC 29413;	EDY39077, ZP_05045768;
	Microcoleus chthonoplastes PCC 7420;	ABA20300;
	Chlamydomonas reinhardtii;	ZP_05029756; XP_001701816, EDP06791;
53: Acetolactate synthase (EC 2.2.1.6)	*Caldicellulosiruptor saccharolyticus* DSM 8903;	ABP66750, ABP66751, YP_001179942, ABP66455, YP_001179941, YP_001179646;
	Thermotoga petrophila RKU-1;	YP_001243976, YP_003345845, ADA66432, ADA66431, ABQ46399, YP_001243975, ABQ46400, YP_003345846;
	Thermosynechococcus elongatus BP-1;	NP_682614, BAC09376, NP_681670, BAC08432, NP_682086;
	Syntrophothermus lipocalidus DSM 12680;	ADI02904, YP_003703469, ADI02903, YP_003703468;
	Pelotomaculum thermopropionicum SI;	BAF58709, BAF58917, YP_001211286, YP_001211078;
	Geobacillus kaustophilus HTA426;	BAD76946, YP_148514, BAD76945, YP_148513:
	Caldicellulosiruptor bescii DSM 6725;	ACM59790, ACM59628, ACM59629, YP_002572563, YP_002572401, YP_002572402; YP_003432299, YP_003432300,
	Hydrogenobacter thermophilus TK-6;	BAI69099, BAI69098; YP_003874926, YP_003874927,
	Spirochaeta thermophila DSM 6192;	ADN02654, ADN02653, ACJ33615, YP_002314957,
	Anoxybacillus flavithermus WK1;	ACJ32972, ACJ32973, YP_002314958;
	Deferribacter desulfuricans SSM1;	YP_003496879, BAI81123, YP_003496878, BAI81122;
	Escherichia coli str. K-12 substr. W3110;	AP_004121, BAE77622, AP_004122, BAE77623, BAE77528, AP_004027, BAB96646, AP_000741; BAA12700;
	Saccharomyces cerevisiae,	EDN64495, CAA89744, EDV09697;
	Thermus aquaticus;	YP_001735999, ACB00744;
	Synechococcus sp. PCC 7002;	YP_002376012;
	Cyanothece sp. PCC 7424;	YP_324035;
	Anabaena variabilis ATCC 29413;	NP_487595, BAB75254;
	Nostoc sp. PCC 7120;	YP_001655615;
	Microcystis aeruginosa NIES-843;	NP_441297, BAA17984,
	Synechocystis sp. PCC 6803;	CAA66718, NP_441304, NP_442206, BAA10276 ;
	Synechococcus sp. JA-2-3B'a(2-13);	YP_478353;
	Synechococcus sp. JA-3-3Ab;	YP_475372, ABD00213, ABD00270, YP_475476, YP_475533;
	Chlamydomonas reinhardtii;	AAC03784, AAB88292, XP_001700185, EDO98300, XP_001695168, EDP01876;
	Volvox carteri;	AAC04854, AAB88296;
	Bacillus subtilis subsp. *subtilis* str. 168;	CAB07802 (AlsS);
	Bacillus licheniformis ATCC 14580;	AAU42663 (AlsS);
54: Ketol-acid reductoisomerase (EC 1.1.1.86)	*Syntrophothermus lipocalidus* DSM 12680; *Caldicellulosiruptor saccharolyticus* DSM 8903; E. coli;	ADI02902, YP_003703467; ABP66752, YP_001179943; AAA67577, YP_001460567;
	Thermotoga petrophila RKU-1;	ABQ46398, YP_001243974;
	Calditerrivibrio nitroreducens DSM 19672;	YP_004050904;
	Spirochaeta thermophila DSM 6192;	YP_003874858, ADN02585;
	Pelotomaculum thermopropionicum SI;	YP_001211079, BAF58710;
	Cyanothece sp. PCC 7822;	YP_003885458;
	Hydrogenobacter thermophilus TK-6;	YP_003433279, BAI70078;
	Anoxybacillus flavithermus WK1;	YP_002314959, ACJ32974;

TABLE 1-continued

lists examples of enzymes for construction of designer Calvin-cycle-linked pathways for production of butanol and related higher alcohols.

Enzyme/callout number	Source (Organism)	GenBank Accession Number, JGI Protein ID or Citation
	Caldicellulosiruptor bescii DSM 6725;	YP_002572403;
	Geobacillus kaustophilus HTA426;	YP_148512, BAD76944;
	Deferribacter desulfuricans SSM1;	YP_003496877, BAI81121;
	Thermosynechococcus elongatus BP-1;	NP_683044, BAC09806;
	Cyanothece sp. PCC 7425;	YP_002482078;
	Nostoc punctiforme PCC 73102;	ACC82013;
	Trichodesmium erythraeum IMS101;	ABG53327;
	Synechococcus sp. PCC 7335;	ZP_05036558;
	Microcoleus chthonoplastes PCC 7420;	ZP_05026584;
	Prochlorococcus marinus str. MIT	ABO18124;
	9301; *Cyanobium* sp. PCC 7001;	EDY39000;
	Arthrospira sp. PCC 8005;	ZP_07166132;
	Arabidopsis thaliana;	CAA48253, NP_001078309;
	Pisum sativum (pea);	CAA76854;
	Zea mays;	ACG35752;
	Chlamydomonas reinhardtii;	XP_001702649, EDP06428;
	Polytomella parva;	ABH11013;
55:	*Thermotoga petrophila* RKU-1;	YP_001243973, ABQ46397;
Dihydroxy-acid dehydratase	*Cyanothece* sp. PCC 7822;	YP_003887466;
(EC 4.2.1.9)	*Marivirga tractuosa* DSM 4126;	YP_004053736;
	Geobacillus kaustophilus HTA426;	YP_147899, BAD76331,
	Syntrophothermus lipocalidus DSM	YP_147822, BAD76254;
	12680;	ADI02905, YP_003703470;
	Spirochaeta thermophila DSM 6192;	YP_003874669, ADN02396;
	Anoxybacillus flavithermus WK1;	YP_002315593;
	Caldicellulosiruptor bescii DSM 6725;	YP_002572562;
	Caldicellulosiruptor saccharolyticus	YP_001179645, ABP66454;
	DSM 8903; *E. coli*;	ADR29155, YP_001460564;
	Deferribacter desulfuricans SSM1;	YP_003496880, BAI81124;
	Thermosynechococcus elongatus BP-1;	NP_681848, BAC08610;
	Hydrogenobacter thermophilus TK-6;	YP_003431766, BAI68565;
	Nostoc punctiforme PCC 73102;	ACC82168, ADN14191;
	'*Nostoc azollae*' 0708;	ADI62939;
	Arthrospira maxima CS-328;	EDZ97146;
	Prochlorococcus marinus str. MIT	AB017457;
	9301; *Cyanobium* sp. PCC 7001;	ZP_05044537, EDY37846;
	Synechococcus sp. PCC 7335;	ZP_05037932;
	Arthrospira platensis str. Paraca;	ZP_06383646;
	Microcystis aeruginosa NIES-843;	BAG02689;
	Chlamydomonas reinhardtii;	XP_001693179, EDP03205;
	Arabidopsis thaliana;	BAB03011;
	Oryza sativa Indica Group;	ABR25557;
	Glycine max;	ACU26534;
56:	*Schizosaccharomyces japonicus*	XP_002173231, EEB06938;
2-Methylbutyraldehyde	*yFS275;*	
reductase	*Pichia pastoris* GS115;	XP_002490018, CAY67737,
(EC 1.1.1.265)		XM_002489973;
	Saccharomyces cerevisiae S288c;	DAA12209, NP_010656 ,
		NM_001180676 ;
	Aspergillus fumigatus Af293;	XP_752003;
	Debaryomyces hansenii CBS767;	XP_002770138;
	Debaryomyces hansenii	CAR65507;
	Kluyveromyces lactis;	CAH02579;
	Lachancea thermotolerans CBS 6340;	XP_002554884;
	Lachancea thermotolerans;	CAR24447, CAR23718;
	Saccharomyces cerevisiae EC1118;	CAY78868;
	Saccharomyces cerevisiae JAY291;	EEU08013;
57:	*Saccharomyces cerevisiae* S288c;	DAA10635, NM_001183405,
3-Methylbutanal reductase		NP_014490;
(EC 1.1.1.265)	*Saccharomyces cerevisiae* EC1118;	CAY86141;
	Saccharomyces cerevisiae JAY291;	EEU07090;
07':	*Geobacillus kaustophilus* HTA426;	YP_147173, BAD75605;
3-Ketothiolase (reversible)	*Azohydromonas lata*;	
	Rhodoferax ferrireducens T118;	YP_523526;
	Allochromatium vinosum;	CAA01849, CAA01846;
	Dechloromonas aromatica RCB;	YP_286222;
	Rhodobacter sphaeroides ATCC 17029;	YP_001041914;
	Rhodobacter sphaeroides ATCC 17025;	YP_001166229;
	Bacillus sp. 256;	ABX11181;
	Silicibacter lacuscaerulensis ITI-1157;	ZP_05785678;

TABLE 1-continued

lists examples of enzymes for construction of designer Calvin-cycle-linked pathways for production of butanol and related higher alcohols.

Enzyme/callout number	Source (Organism)	GenBank Accession Number, JGI Protein ID or Citation
	Aspergillus fumigatus Af293;	XP_752635;
	Rhizobium etli;	AAK21958;
	Citreicella sp. SE45;	ZP_05784120, ZP_05781517;
	Silicibacter sp. TrichCH4B;	ZP_05742998;
	Azohydromonas lata;	AAC83659, AAD10275;
	Chromobacterium violaceum;	AAC69616;
	Dinoroseobacter shibae DFL 12;	ABV95064;
	Alcaligenes sp. SH-69;	AAP41838;
	Candida dubliniensis CD36;	CAX43351, XP_002418052;
	Pseudomonas sp. 14-3;	CAK18903;
	Aspergillus flavus NRRL3357;	XP_002375989;
	Aedes aegypti;	EAT37298, EAT37297, XP_001654752, XP_001654751;
	Scheffersomyces stipitis CBS 6054;	ABN68380, XP_001386409;
	Cyanothece sp. PCC 7424;	YP_002375827, ACK68959;
	Cyanothece sp. PCC 7822;	YP_003886602, ADN13327;
	Microcystis aeruginosa NIES-843;	BAG04828;
08': 3-Hydroxyacyl-CoA dehydrogenase	*Syntrophothermus lipocalidus* DSM 12680;	YP_003702743, ADI02178, ADI01287, ADI01071;
	Oceanithermus profundus DSM 14977;	ADR36325;
	Anoxybacillus flavithermus WK1;	YP_002317076, YP_002315864;
	Pelotomaculum thermopropionicum SI;	YP_001210823, BAF58454;
	Geobacillus kaustophilus HTA426;	YP_149248, YP_147889;
	Deferribacter desulfuricans SSM1;	YP_003497047, BAI81291;
	Glomerella graminicola M1.001;	EFQ32520, EFQ35765;
	Legionella pneumophila str. Corby;	YP_001250712, ABQ55366;
	Aspergillus fumigatus Af293;	XP_748706, XP_748351;
	Coprinopsis cinerea okayama7#130;	EAU80763;
	Botryotinia fuckeliana B05.10;	XP_001559519;
	Coccidioides posadasii; *E. coli*;	ABH10642; YP_001462756;
	Chelativorans sp. BNC1;	YP_675197;
	Nostoc punctiforme PCC 73102;	ACC81853, YP_001866796;
	Oscillatoria sp. PCC 6506;	ZP_07114022, CBN59220;
09': Enoyl-CoA dehydratase	*Bordetella petrii*;	CAP41574;
	Bordetella petrii DSM 12804;	YP_001629844;
	Anoxybacillus flavithermus WK1;	YP_002315700, YP_002314932;
	Geobacillus kaustophilus HTA426;	YP_148541, YP_147845,
	Geobacillus kaustophilus;	BAD76199; BAD18341;
	Syntrophothermus lipocalidus DSM 12680;	ADI02939, ADI02740, ADI02007, ADI01364;
	Acinetobacter sp. SE19;	AAG10018;
	Scheffersomyces stipitis CBS 6054;	ABN64617, XP_001382646;
	Laccaria bicolor S238N-H82;	EDR09131, XP_001888157;
	Alternaria alternate;	BAH83503,
	Ajellomyces dermatitidis ER-3;	EEQ91989;
	Aspergillus fumigatus Af293;	EAL93360, XP_755398;
	Cryptococcus neoformans var. *neoformans* JEC21; *E. Coli*;	XP_572730; ADN73405, YP_001458194;
	Aspergillus flavus NRRL3357;	XP_002377859;
	Laccaria bicolor S238N-H82;	EDR01115;
	Neosartorya fischeri NRRL 181;	EAW18645;
	Nostoc sp. '*Peltigera membranacea cyanobiont*';	ADA69246;
10': 2-Enoyl-CoA reductase	*Xanthomonas campestris* pv. *Campestris*; *Xanthomonas campestris* pv. *campestris* str. B100; *Xanthomonas campestris* pv. *musacearum*	CAP53709; YP_001905744; ZP_06489037;
	NCPPB4381; *Xanthomonas campestris* pv. *vasculorum* NCPPB702;	ZP_06487845;
	Aeromicrobium marinum DSM 15272;	ZP_07718056, EFQ82338;
	Rhodobacterales bacterium HTCC2083;	ZP_05074461, EDZ42121;
	Lysinibacillus fusiformis ZC1;	
	Mycobacterium smegmatis str. MC2 155;	ZP_07049092, EFI69525; YP_886510, ABK76225;
	Lysinibacillus sphaericus C3-41;	
	Coprinopsis cinerea okayama7#130;	YP_001699417, ACA41287;
	Arthroderma gypseum CBS 118893;	XP_002910885, EFI27391;
	Paracoccidioides brasiliensis Pb01;	EFR05506;
	Paracoccidioides brasiliensis Pb18;	XP_002796528, EEH39074;
	Ajellomyces capsulatus G186AR;	EEH43955;

TABLE 1-continued

lists examples of enzymes for construction of designer Calvin-cycle-linked pathways for production of butanol and related higher alcohols.

Enzyme/callout number	Source (Organism)	GenBank Accession Number, JGI Protein ID or Citation
	Ostreococcus tauri;	EEH03439;
	Jatropha curcas;	XP_003083795, CAL57762; ACS32302;
11': Acyl-CoA reductase (EC 1.2.1.50)	*Clostridium cellulovorans* 743B;	YP_003845606, ADL53842;
	Thermosphaera aggregans DSM 11486;	YP_003649571, ADG90619;
	Delftia acidovorans SPH-1;	
	Comamonas testosteroni KF-1;	YP_001565543, ABX37158;
	Bifidobacterium longum subsp. *infantis* ATCC 15697;	ZP_03543536; YP_002321654, ACJ51276;
	Clostridium papyrosolvens DSM 2782;	
	Acidovorax avenae subsp. *avenae* ATCC 19860;	ZP_05497968, EEU57047; ZP_06211782, EFA39209;
	Comamonas testosteroni KF-1;	
	Aminomonas paucivorans DSM 12260;	EED67822;
	Herpetosiphon aurantiacus ATCC 23779;	ZP_07740542, EFQ24431 ; ABX07240, YP_001547368;
	Clostridium beijerinckii NCIMB 8052;	
	Geobacillus sp. G11MC16;	ABR34265, YP_001309221;
	Clostridium lentocellum DSM 5427;	ZP_03148237, EDY05596;
	Leadbetterella byssophila DSM 17132;	ZP_06885967, EFG96716;
	Actinosynnema mirum DSM 43827;	YP_003997212, ADQ16859;
	Haliangium ochraceum DSM 14365;	YP_003101455, ACU37609 ;
	Photobacterium phosphoreum;	ACY16972, YP_003268865;
	Simmondsia chinensis;	AAT00788;
	Hevea brasiliensis;	AAD38039;
	Arabidopsis thaliana;	AAR88762; ABE65991;
12': Hexanol dehydrogenase	*Mycobacterium chubuense* NBB4;	ACZ56328;
12'': Octanol dehydrogenase EC 1.1.1.73	*Drosophila subobscura*;	ABO61862, ABO65263, CAD43362, CAD43361, CAD54410, CAD43360, CAD43359, CAD43358 CAD43357, CAD43356;
43': Short chain alcohol dehydrogenase	*Pyrococcus furiosus* DSM 3638;	AAC25556;
	Burkholderia vietnamiensis G4;	ABO56626;
	Geobacillus thermoleovorans;	BAA94092;
	Geobacillus kaustophilus HTA426;	YP_146837, BAD75269;
	Anoxybacillus flavithermus WK1;	YP_002314715, ACJ32730;
	Helicobacter pylori PeCan4;	YP_003927327, ADO07277;
	Mycobacterium chubuense NBB4;	ACZ56328;
	Mycobacterium avium subsp. *avium* ATCC 25291; *Aspergillus oryzae*;	ZP_05215778; BAE71320;
	cyanobacterium UCYN-A;	YP_003421738, ADB95357;
	Anabaena circinalis AWQC131C;	ABI75134;
	Cylindrospermopsis raciborskii T3;	ABI75108;
	Helicobacter pylori Sat464;	ADO05766;
	Helicobacter pylori Cuz20;	ADO04259;
	Mycobacterium intracellulare ATCC 13950; *Mycobacterium avium* subsp. *avium* ATCC 25291; *Gluconacetobacter hansenii* ATCC 23769; *Helicobacter pylori* Shi470;	ZP_05228059, ZP_05228058; ZP_05215779; ZP_06834730, EFG83978; YP_001910563, ACD48533;
	Mycobacterium avium 104;	YP_880627, ABK67217;
	Citrus sinensis;	ADH82118;
	Gossypium hirsutum;	ABD65462;
	Arabidopsis halleri;	ABZ02361, ABZ02360;
	Paracoccidioides brasiliensis Pb01;	XP_002792148, EEH34889;
	Pyrenophora tritici-repentis Pt-1C-BFP;	XP_001940779, EDU43498;
	Ajellomyces capsulatus H143;	EER38733;
	Scheffersomyces stipitis CBS 6054;	XP_001382930, ABN64901;
70: Membrane-bound hydrogenase (MBH)	*Ralstonia eutropha* H16;	NP_942643 (hoxK), NP_942644 (hoxG), YP_015633 (hoxZ); AAP85757 (hoxK), AAP85758
	Ralstonia eutropha H16;	(hoxG), AAA16463 (hoxZ); ABF08183 (hoxK), YP_583451
	Cupriavidus metallidurans CH34;	(hoxG), ABF08182 (hoxG); ADK12981, ADK12980;
	Thiocapsa roseopersicina,	ACJ15972;
	Thermococcus onnurineus NA1;	YP_004763067;

TABLE 1-continued

lists examples of enzymes for construction of designer Calvin-cycle-linked pathways for production of butanol and related higher alcohols.

Enzyme/callout number	Source (Organism)	GenBank Accession Number, JGI Protein ID or Citation
	Thermococcus sp. 4557;	YP_004763083;
	Thermococcus sp. 4557;	YP_004763081;
	Thermococcus sp. 4557;	AEK73406;
	Thermococcus sp. 4557;	AEK73404;
	Thermococcus sp. 4557;	NP_579163;
	Pyrococcus furiosus DSM 3638;	NP_579162;
	Pyrococcus furiosus DSM 3638;	YP_004624085;
	Pyrococcus yayanosii CH1;	YP_004624086;
	Pyrococcus yayanosii CH1;	YP_004624087;
	Pyrococcus yayanosii CH1;	NP_142896;
	Pyrococcus horikoshii OT3;	BAK19334;
	Hydrogenovibrio marinus;	CAA63615;
	Alcaligenes sp.;	CAA63616;
	Rubrivivax sp.;	BAF73677;
	Hydrogenobacter thermophilus TK-6;	ACS32538;
	Thermococcus gammatolerans EJ3;	ADN36337;
	Methanoplanus petrolearius DSM	YP_002958402;
	11571; *Thermococcus gammatolerans*	YP_004638463 (hoxZ);
	EJ3; *Oligotropha carboxidovorans*	AEI08136 (hoxZ);
	OM5; *Aquifex aeolicus* VF5;	NP_213456 (hoxZ);
	Centipeda periodontii DSM 2778;	ZP_08500995 (hoxZ);
	Selenomonas noxia ATCC 43541;	ZP_06602778 (hoxZ);
	Allochromatium vinosum DSM 180;	ADC63224 (hoxZ);
	Thiomonas intermedia K12;	ADG32404 (hoxZ);
	Aquifex aeolicus VF5;	AAC06857 (hoxZ);
71:	*Ralstonia eutropha* H16;	AAP85843 (hoxY), AAP85844
Soluble hydrogenase (SH)	*Ralstonia eutropha* H16;	(HoxH); NP_942730 (hoxH),
(NAD(P)-reducing)	*Ralstonia eutropha* H16;	NP_942729 (hoxY);
	Ralstonia eutropha H16;	NP_942727 (hoxF), NP_942728
	Ralstonia eutropha H16;	(hoxU); AAP85841 (hoxF),
	Ralstonia eutropha H16;	AAP85842 (hoxU); AAC06140
	Ralstonia eutropha H16;	(hoxF), AAC06141 (hoxU),
	Ralstonia eutropha H16;	AAC06142 (hoxY),
	Ralstonia eutropha H16;	AAC06143 (hoxH);
	Rhodobacter capsulatus;	AAD38065 (hoxH);
	Azotobacter vinelandii DJ;	YP_002797671 (hoxH);
	Microcystis aeruginosa NIES-843;	BAG01243 (hoxH);
	Acaryochloris marina MBIC11017;	ABW32682 (hoxH);
	Synechococcus sp. PCC 7002;	AAN03569 (hoxH);
	Synechococcus elongatus PCC 6301;	CAA66383 (hoxH);
	Synechococcus elongatus PCC 6301;	CAA66382 (hoxY);
	Allochromatium vinosum;	AAX89151 (hoxY);
	Microcystis aeruginosa PCC 7806;	CAO88137 (hoxY);
	Azotobacter vinelandii DJ;	YP_002797670 (hoxY);
	Synechococcus elongatus PCC 6301;	CAA66381 (hoxU);
	Allochromatium vinosum;	AAX89150 (hoxU);
	Arthrospira platensis FACHB341;	ABC26909 (hoxU);
	Microcystis aeruginosa PCC 7806;	CAO88140 (hoxU);
	Lyngbya majuscula CCAP 1446/4;	AAY57574 (hoxU);
	Synechococcus elongatus PCC 6301;	YP_172263 (hoxU);
	Cyanothece sp. ATCC 51142;	YP_001803733 (hoxU);
	Synechococcus elongatus PCC 6301;	CAA73873 (hoxF);
	Allochromatium vinosum;	AAX89149 (hoxF);
	Arthrospira platensis FACHB341;	ABC26907 (hoxF);
	Synechococcus sp. PCC 7002;	YP_001733465 (hoxF);
	Anaerolinea thermophila UNI-1;	BAJ63286 (hoxH);
	Caloramator australicus RC3;	CCC57856 (hoxF);
72:	*Ralstonia eutropha* H16;	NP_942649 (hoxO), AAP85763
Hydrogenase accessary	*Ralstonia eutropha* H16;	(hoxO), AAA16467 (hoxO);
proteins	*Cupriavidus metallidurans* CH34;	ABF08176 (hoxO); YP_583445
	Cupriavidus metallidurans CH34;	(hoxO);
	Ralstonia eutropha H16;	NP_942650 (hoxQ), AAP85764 (hoxQ), AAA16468 (hoxQ);
	Cupriavidus metallidurans CH34;	ABF08175 (hoxQ), YP_583444 (hoxQ);
	Azotobacter vinelandii;	AAA19504 (hoxQ);
	Salmonella enterica subsp.;	EHC91928 (hoxQ/hoxR), EFX49216 (hoxQ/hoxR),
	Escherichia coli B354;	ZP_06652932 (hoxQ);
	Methyloversatilis universalis FAM5;	ZP_08506135 (hoxQ);

TABLE 1-continued

lists examples of enzymes for construction of designer Calvin-cycle-linked pathways for production of butanol and related higher alcohols.

Enzyme/callout number	Source (Organism)	GenBank Accession Number, JGI Protein ID or Citation
	Shigella flexneri CDC 796-83;	EFW61888 (hoxQ);
	Ralstonia eutropha H16;	AAA16469 (hoxR), NP_942651(hoxR);
	Azotobacter vinelandii;	AAA19505 (hoxR);
	Ralstonia eutropha H16;	NP_942652 (hoxT), AAP85766 (hoxT), AAA16470 (hoxT);
	Cupriavidus metallidurans CH34;	ABF08173 (hoxT);
	Azotobacter vinelandii DJ;	YP_002802114 (hoxT), ACO1139 (hoxT);
	Ralstonia eutropha H16;	NP_942648 (hoxL), AAP85762 (hoxL), AAA16466 (hoxL);
	Azotobacter vinelandii;	AAA19502 (hoxL);
	Oligotropha carboxidovorans OM5;	YP_015634 (hoxL);
	Cupriavidus metallidurans CH34;	ABF08177 (hoxL), YP_583446 (hoxL);
	Salmonella enterica subsp. *enterica* serovar Weltevreden str. 2007-60-3289-1; *Oligotropha carboxidovorans* OM5;	CBY95754 (hoxL); YP_004638464 (hoxL);
	Oligotropha carboxidovorans OM4;	AEI04509 (hoxL);
	Azotobacter vinelandii DJ;	YP_002802118 (hoxL), ACO81143 (hoxL);
	Methyloversatilis universalis FAM5;	ZP_08506137 (hoxL), EGK70316 (hoxL);
	Ralstonia eutropha H16;	NP_942653 (hoxV), AAP85767 (hoxV), AAA16471 (hoxV);
	Azotobacter vinelandii;	AAA19507 (hoxV);
	Oligotropha carboxidovorans OM5;	YP_015636 (HoxV);
	Cupriavidus metallidurans CH34;	ABF08172 (hoxV);
	Azotobacter vinelandii DJ;	YP_002802113 (hoxV);
	Cupriavidus metallidurans CH34;	YP_583441 (hoxV);
	Methyloversatilis universalis FAM5;	ZP_08506132 (hoxV);
	Methyloversatilis universalis FAM5;	EGK70311 (hoxV);
	Ralstonia eutropha H16	NP_942647 (hoxM);
	Oligotropha carboxidovorans OM5,	YP_004638462 (hoxM);
	Oligotropha carboxidovorans OM4;	AEI04507 (hoxM);
	Azotobacter vinelandii;	AAA19501 (hoxM);
	Azotobacter vinelandii DJ;	YP_002802119 (hoxM);
	Cupriavidus metallidurans CH34;	YP_583447 (hoxM);
	Hydrogenobacter thermophilus TK-6;	BAF73673 (hoxM);
	Hydrogenobacter thermophilus TK-6;	YP_003432119 (hoxM);
	Thermoproteus tenax Kra 1;	CCC80713 (hoxM);
	Acidithiobacillus sp. GGI-221;	EGQ60729 (hoxM);
	Methyloversatilis universalis FAM5;	ZP_08506138 (hoxM);
	Burkholderiales bacterium 1_1_47;	ZP_07342912 (hoxM);
	Thiomonas intermedia K12;	YP_003644737 (hoxM);
	Thermococcus gammatolerans EJ3;	YP_002958602 (hybD/hycI/hoxM);
	Ralstonia eutropha H16;	NP_942661 (hoxA), AAP85775;
	Azorhizobium caulinodans ORS 571;	AAS91037 (hoxA);
	Bradyrhizobium japonicum;	CAA78991 (hoxA);
	Hyphomicrobium sp. MC1;	YP_004674255 (hoxA);
	Azoarcus sp. BH72;	YP_935307 (hoxA);
	Methyloversatilis universalis FAM5;	ZP_08506123 (hoxA);
	Grimontia hollisae CIP 101886;	ZP_06053565 (hoxA);
	Oxalobacteraceae bacterium;	ZP_08276168 (hoxA);
	Ralstonia eutropha H16;	NP_942662 (hoxB), AAP85776;
	Azoarcus sp. BH72;	YP_935309 (hoxB);
	Oligotropha carboxidovorans OM5;	YP_004638467 (hoxB);
	Ralstonia eutropha H16;	AAP85777 (hoxC), NP_942663;
	Azoarcus sp. BH72;	YP_935310 (hoxC);
	Oligotropha carboxidovorans OM4;	AEI04502 (hoxC);
	Oligotropha carboxidovorans OM5;	YP_004638457 (hoxC);
	Oxalobacteraceae bacterium IMCC9480;	ZP_08276171 (hoxJ), EGF30361 (hoxJ);
	Alcaligenes hydrogenophilus;	AAB49362 (hoxJ);
	Synechocystis sp. PCC 6803;	BAA18357 (hypA);
	Ralstonia eutropha H16;	NP_942654 (hypA1);
	Ralstonia eutropha H16;	NP_942733 (hypA2);
	Ralstonia eutropha H16;	NP_942716 (hypA3);
	Cupriavidus metallidurans CH34;	YP_583440 (hypA);
	Ralstonia eutropha H16;	NP_942655 (hypB1);

TABLE 1-continued

lists examples of enzymes for construction of designer Calvin-cycle-linked pathways for production of butanol and related higher alcohols.

Enzyme/callout number	Source (Organism)	GenBank Accession Number, JGI Protein ID or Citation
	Ralstonia eutropha H16;	AAP85769 (hypB1);
	Butyrivibrio proteoclasticus B316;	YP_003830670 (hypB1);
	Oligotropha carboxidovorans OM5;	YP_004638455 (hypB);
	Oligotropha carboxidovorans OM4;	AEI04500 (hypB);
	Desulfitobacterium metallireducens DSM 15288;	ZP_08976390 (hypB), EHC20145 (hypB);
	Synechocystis sp. PCC 6803;	BAA18180 (hypC);
	Cyanothece sp. CCY0110;	EAZ91066 (hypC);
	Cupriavidus metallidurans CH34,	ABF08421(hypC);
	Ralstonia eutropha H16;	NP_942657 (hypC1);
	Ralstonia eutropha H16;	AAP85826 (hypC2);
	Ralstonia eutropha H16;	CAA49734 (hypD);
	Cupriavidus metallidurans CH34;	YP_583436 (hypD);
	Cupriavidus metallidurans CH34;	ABF08422 (hypD);
	Escherichia coli BL21(DE3);	ACT44398 (hypD);
	Synechocystis sp. PCC 6803;	BAA17478 (hypE);
	Ralstonia eutropha H16;	CAA49735 (hypE);
	Ralstonia eutropha H16;	NP_942659 (hypE1);
	Ralstonia eutropha H16;	AAP85829 (hypE2);
	Rhizobium leguminosarum;	CAA37164 (hypE);
	Azotobacter vinelandii;	AAA19513 (hypE);
	Aeropyrum pernix K1;	NP_148343 (hypE);
	Sulfolobus solfataricus P2;	NP_341628 (hypE);
	Hydrogenobacter thermophilus TK-6;	YP_003432665 (hypE);
	Pelotomaculum thermopropionicum SI;	YP_001212249 (hypE);
	Syntrophothermus lipocalidus DSM 12680;	ADI01176 (hypE), YP_003701741 (hypE);
	Hydrogenobacter thermophilus TK-6;	YP_003432667 (hypF);
	Pelotomaculum thermopropionicum SI;	YP_001212246 (hypF);
	Syntrophothermus lipocalidus DSM 12680; *Caldicellulosiruptor bescii* DSM 6725;	ADI01173 (hypF), YP_003701738 (hypF); YP_002572964 (hypF);
	Ralstonia eutropha H16;	CAA49731 (hypF);
	Ralstonia eutropha H16;	NP_942660 (hypX);
	Ralstonia eutropha H16;	AAP85774 (hypX)
	Hydrogenobacter thermophilus TK-6;	YP_003433460 (hypX);
	Rhizobium leguminosarum;	CAA37165 (hypX);
	Methyloversatilis universalis FAM5;	ZP_08506124 (hoxX);
	Cupriavidus metallidurans CH34;	ABF08424 (hoxX);
	Ralstonia eutropha H16;	CAA52735 (hoxX);
73: NAD(P)-dependent hydrogenase	*Desulfobulbus propionicus* DSM 2032;	ADY56959, YP_004195043;
	Acetohalobium arabaticum DSM 5501;	YP_003826884;
	Ilyobacter polyt; ropus DSM 2926; beta *proteobacterium* KB13	ADO82414; EDZ65062, ZP_05082375;
	Acetohalobium arabaticum DSM 5501;	ADL11819
74: Formate dehydrogenase using NAD(P)H	*Moorella thermoacetica* ATCC 39073;	YP_429324, ABC18781;
	Moorella thermoacetica ATCC 39073;	YP_431142, ABC20599;
	Moorella thermoacetica;	AAB18330 (α), AAB18329 (β);
	Methanosaeta harundinacea 6Ac;	AET63712, AET63711,
	Methanoculleus marisnigri JR1;	YP_001047290;
	Methanocorpusculum labreanum Z;	YP_001029904, YP_001029903;
	Helicobacter bilis ATCC 43879;	ZP_04582064 (NADPH);
	Helicobacter bilis ATCC 43879;	EEO23341 (NADPH);
	Pelotomaculum thermopropionicum SI;	YP_001213196;
	Hydrogenobacter thermophilus TK-6;	YP_003432807;
	Hydrogenobacter thermophilus TK-6;	YP_003433330 (NDA dependent);
	Klebsiella variicola At-22;	ADC58081, YP_003439113;
	Azospirillum sp. B510;	YP_003451652, YP_003450092;
	Thermococcus gammatolerans EJ3;	YP_002958615;
	Yersinia pestis Antiqua;	ABG15899;
	Thermofilum pendens Hrk 5;	YP_919603;
	Ferrimonas balearica DSM 9799;	YP_003913071;
	Thermodesulfatator indicus DSM 15286; *Shewanella baltica* BA175;	AEH46025; AEG12633;
	Methanocella paludicola SANAE;	YP_003357462, YP_003357461;
	Methanosaeta harundinacea 6Ac;	AET64643, AET64987, AET65705;

TABLE 1-continued

lists examples of enzymes for construction of designer Calvin-cycle-linked pathways for production of butanol and related higher alcohols.

Enzyme/callout number	Source (Organism)	GenBank Accession Number, JGI Protein ID or Citation
75: 10-Formyl-H_4 folate synthetase (ADP forming, 10-Formyltetrahydrofolate Synthetase)	*Moorella thermoacetica* ATCC 39073;	YP_428991;
	Methanocorpusculum labreanum Z;	YP_001030445;
	Sphingomonas paucimobilis;	BAD61061;
	Desulfatibacillum alkenivorans AK-01;	ACL05327;
	Corynebacterium aurimucosum;	YP_002834788;
	Clostridium acidurici;	AAA53187;
	Sphingobium sp. SYK-6;	YP_004834408;
	Listeria monocytogenes serotype 4b str.	YP_002758587;
	CLIP 80459; Vibrio fischeri MJ11;	YP_002156619;
	Anoxybacillus flavithermus WK1;	YP_002315932;
	Thermotoga lettingae TMO;	YP_001471133;
	Fervidobacterium nodosum Rt17-B1;	YP_001410584;
	Thermosipho melanesiensis BI429;	YP_001305561;
	Thermotoga petrophila RKU-1	YP_001244647
	Pelotomaculum thermopropionicum SI;	YP_001210750;
76: 5,10-Methenyl-H_4 folate cyclohydrolase (Methenyltetrahydrofolate cyclohydrolase)	*Moorella thermoacetica* ATCC 39073;	YP_430368, ABC19825;
	Thermotoga lettingae TMO;	ABV34070;
	Caldicellulosiruptor bescii DSM 6725;	YP_002572856;
	Thermotoga petrophila RKU-1;	ABQ47072;
	Anoxybacillus flavithermus WK1;	YP_002315305;
	Geobacillus kaustophilus HTA426;	BAD76681;
	Geobacillus kaustophilus HTA426;	YP_148249;
	Synechococcus sp. JA-2-3B'a(2-13);	YP_476354;
	Synechococcus sp. JA-3-3Ab;	YP_475381;
	Exiguobacterium sp. AT1b;	YP_002884899;
	Thermotoga lettingae TMO;	YP_001471134;
77: 5,10-Methylene-H_4 folate dehydrogenase	*Moorella thermoacetica* ATCC 39073;	ABC19825, YP_430368;
	Geobacillus kaustophilus HTA426;	BAD76681;
	Syntrophothermus lipocalidus;	ADI01214;
	Caldicellulosiruptor kronotskyensis;	ADQ46551;
	Caldicellulosiruptor kristjanssonii;	ADQ40482;
	Caldicellulosiruptor hydrothermalis;	ADQ07463;
	Caldicellulosiruptor owensensis OL;	ADQ04336;
	Caldicellulosiruptor hydrothermalis;	YP_003992832;
	Kosmotoga olearia TBF 19.5.1;	ACR80790;
	Exiguobacterium sp. AT1b;	ACQ69454;
	Komagataella pastoris CBS 7435;	CCA37557;
	Homo sapiens;	AAH09806;
	Taeniopygia guttata;	XP_002200380;
	Syntrophobotulus glycolicus DSM 8271;	ADY56189;
	Olsenella uli DSM 7084;	ADK67906;
78: 5,10-Methylene-H_4 folate reductase (Methylenetetrahydrofolate reductase)	*Moorella thermoacetica* ATCC 39073;	YP_430048, ABC19505;
	Syntrophothermus lipocalidus;	ADI02156;
	Fervidobacterium nodosum Rt17-B1;	ABS61421;
	Thermotoga petrophila RKU-1;	ABQ46674;
	Fervidobacterium nodosum Rt17-B1;	ABS61126;
	Thermotoga lettingae TMO;	ABV33918;
	Thermosipho melanesiensis BI429;	YP_001305980;
	Synechococcus sp. JA-2-3B'a(2-13);	YP_477166;
	Hippea maritima DSM 10411;	YP_004340445;
	Spirochaeta thermophila DSM 6192;	YP_003875363;
	Deferribacter desulfuricans SSM1;	YP_003496368;
	Hydrogenobacter thermophilus TK-6;	YP_003432279;
	Pelotomaculum thermopropionicum SI;	BAF59187, YP_001211556;
79: Methyl-H_4 folate: corrinoid iron-sulfur protein Methyltransferase (Methyltetrahydrofolate:corrinoid/ iron-sulfur protein Methyltransferase)	*Moorella thermoacetica* ATCC 39073;	YP_430950, YP_430174;
	Pelotomaculum thermopropionicum SI;	YP_001211554;
	Clostridium carboxidivorans P7;	ADO12092;
	Desulfitobacterium hafniense DCB-2;	YP_002461301;
	Dinoroseobacter shibae DFL 12;	YP_001533020;
	Ammonifex degensii KC4;	YP_003238352;
	Desulfotomaculum acetoxidans;	YP_003190781;
	Rhodobacter sphaeroides KD131;	YP_002525435;
	Carboxydothermus hydrogenoformans;	YP_360065;
	Rhodobacter sphaeroides 2.4.1;	YP_352826;
	Heliobacterium modesticaldum Ice1;	YP_001680302;
	Sinorhizobium meliloti 1021; *Acetonema longum* DSM 6540	NP_386092; ZP_08625620;

TABLE 1-continued

lists examples of enzymes for construction of designer Calvin-cycle-linked pathways for production of butanol and related higher alcohols.

Enzyme/callout number	Source (Organism)	GenBank Accession Number, JGI Protein ID or Citation
80: Corrinoid iron-sulfur protein (CFeSP)	*Moorella thermoacetica*;	AAA23255;
	Carboxydothermus hydrogenoformans	2H9A_A, 2H9A_B;
	Clostridium ragsdalei;	AEI90763, AEI90762;
	Clostridium autoethanogenum;	AEI90746, AEI90745;
	Clostridium sticklandii DSM 519;	YP_003936194;
	Clostridium sticklandii;	CBH21289;
81: CO dehydrogenase/acetyl-CoA synthase (Fd^{2-})	*Moorella thermoacetica* ATCC 39073;	ABC19516, YP_430059;
	Moorella thermoacetica ATCC 39073;	YP_430813 (CODH);
	Moorella thermoacetica;	AAA23229, AAA23228;
	Caldicellulosiruptor kristjanssonii;	ADQ39747;
	Caldicellulosiruptor saccharolyticus;	YP_001179230;
	Clostridium ragsdalei;	AEI90761;
	Clostridium autoethanogenum;	AEI90744;
	Desulfosporosinus orientis DSM 765;	AET68776;
	Methanococcus aeolicus Nankai-3;	ABR56750;
	Desulfobacca acetoxidans DSM 11109;	YP_004370981;
	Thermodesulfatator indicus;	AEH46031;
	Acetohalobium arabaticum DSM 5501;	ADL12817;
	Desulfarculus baarsii DSM 2075;	YP_003806211;
	Archaeoglobus veneficus SNP6;	YP_004341848;
	Methanosalsum zhilinae DSM 4017;	AEH60991;
	Thermosediminibacter oceani;	ADL07576;
	Desulfotomaculum kuznetsovii;	YP_004517493, YP_004516875;
	Methanosalsum zhilinae DSM 4017;	AEH60989, AEH60993;
82: Pyruvate synthase (Fd^{2-})	*Thermodesulfobium narugense*;	YP_004437266;
	Desulfobacca acetoxidans;	YP_004370392;
	Archaeoglobus veneficus SNP6;	YP_004341929;
	Hippea maritima DSM 10411;	YP_004339618;
	Desulfurobacterium thermolithotrophum;	YP_004281767, YP_004281766, ADY73708;
	Archaeoglobus veneficus;	AEA47214;
	Thermodesulfobium narugense;	AEE14134;
	Archaeoglobus veneficus SNP6;	YP_004341930;
	Thermobacillus composti KWC4;	ZP_08918406;
	Desulfobacca acetoxidans;	AEB09210;
	Methanolinea tarda NOBI-1;	EHF09898;
	Methanobacterium sp. AL-21;	YP_004289712, ADZ08740;
	Methanocella paludicola SANAE;	YP_003356312, YP_003356313;
83: Formylmethanofuran dehydrogenase (Fmd) (Fd^{2-})	*Methanothermobacter marburgensis* str. Marburg;	ADL58895, ADL58894, ADL58283, ADL58893, ADL57751, ADL57749, ADL57750, ADL57748;
	Methanothermobacter thermautotrophicus;	CAA66401, CAA61212, CAA66400, CAA66402;
	Methanothermobacter thermautotrophicus;	CAA61213, CAA61214, CAA61210, CAA61211, CAA61209;
	Agrobacterium sp. H13-3;	YP_004444030;
	Agrobacterium vitis S4;	YP_002547540;
	Methylomonas methanica MC09;	YP_004511613;
	Desulfobacca acetoxidans DSM 11109;	YP_004370144, AEB08963;
	Methylovorus glucosetrophus SIP3-4;	YP_003051278;
	Methylotenera mobilis JLW8;	YP_003048298;
	Methylotenera versatilis 301;	ADI29297;
	Methanoculleus marisnigri JR1;	YP_001046285, YP_001046287, YP_001046533;
	Methanosaeta harundinacea 6Ac;	AET63761, AET64650, AET65189, AET64652;
	Methanosphaera stadtmanae;	ABC56660, ABC56659, YP_447302, ABC56661, ABC56658, ABC56657;
84: Formyl transferase	*Methanothermobacter marburgensis* str. Marburg;	ADL59225, YP_003850538;
	Methanosaeta harundinacea 6Ac;	AET65566;
	Methanosarcina barkeri;	CAA62582;
	Methanopyrus kandleri AV19;	NP_614099;
	Thermosipho melanesiensis BI429;	YP_001305762;
	Desulfobacca acetoxidans DSM 11109;	YP_004369335;
	Methylobacterium chloromethanicum;	YP_002421530;
	Methylomicrobium alcaliphilum;	YP_004917963;

TABLE 1-continued

lists examples of enzymes for construction of designer Calvin-cycle-linked pathways for production of butanol and related higher alcohols.

Enzyme/callout number	Source (Organism)	GenBank Accession Number, JGI Protein ID or Citation
	Methanopyrus kandleri AV19;	NP_613403;
	Methanoculleus marisnigri JR1;	YP_001046543;
	Methanocorpusculum labreanum Z;	YP_001029658, YP_001029834;
	Methanopyrus kandleri AV19;	AAM02029, AAM01333;
	Methanocella paludicola SANAE;	YP_003356088, BAI61105;
85:	*Methanosphaera stadtmanae*;	ABC57615, YP_448258;
5,10-Methenyl-	*Methanothermus fervidus* DSM 2088;	YP_004003819;
tetrahydromethanopterin (H4	*Methanosalsum zhilinae* DSM 4017;	AEH61193;
methanopterin)	*Methanohalophilus mahii* DSM 5219;	ADE36644;
cyclohydrolase	*Methanoplanus petrolearius*;	ADN34846;
	Archaeoglobus veneficus SNP6;	YP_004342719;
	Planctomyces brasiliensis DSM 5305;	YP_004269775;
	Methylobacillus flagellates;	AAD55893;
	Xanthobacter autotrophicus;	AAD55896;
	Methylosinus trichosporium OB3b;	AAD56174;
	Methylobacterium organophilum;	AAD55900;
	Methylococcus capsulatus;	AAD55899;
	Methylomicrobium kenyense;	AAS88982;
	Methylomonas sp. LW13;	AAS88987;
	Methylosinus sp. LW2;	AAS88975;
	Methylomicrobium kenyense;	AAS86344;
	Methanohalophilus mahii DSM 5219;	YP_003542289;
	Methanolinea tarda NOBI-1;	EHF09908;
	Methanothermococcus okinawensis IH1;	YP_004577331;
	Methanobacterium sp. SWAN-1;	YP_004519292;
	Methylomonas methanica MC09;	YP_004513168;
86:	*Methanothermobacter marburgensis*;	ADL57660, YP_003848973;
5,10-Methylene-H_4-	*Methanosphaera stadtmanae*;	YP_447224;
methanopterin	*Methanococcus maripaludis* X1;	AEK19019;
dehydrogenase ($F_{420}H_2$)	*Methanothermobacter thermautotrophicus*;	CAA63376;
	Methanopyrus kandleri;	CAA43127;
	Methylobacterium extorquens AM1;	AAC27020;
	Methylobacillus flagellatus KT;	ABE49928;
	Xanthobacter autotrophicus;	AAD55895;
	Methyloversatilis universalis FAM5;	ZP_08504846;
	Methylobacterium chloromethanicum;	ACK83011;
	Methylobacterium populi BJ001;	YP_001924478;
	Methylobacterium extorquens PA1;	YP_001639299;
	Burkholderia sp. CCGE1001;	YP_004230417;
	Methylovorus sp. MP688;	YP_004039958;
	Methanocaldococcus fervens AG86;	YP_003128308;
	Methanocaldococcus jannaschii;	NP_247770;
	Methanobrevibacter smithii;	YP_001273145;
87:	*Methanoplanus petrolearius*;	ADN36752;
5,10-Methylene-H_4-	*Methanocaldococcus* sp. FS406-22;	YP_003458803;
methanopterin reductase	*Methanocaldococcus infernus* ME;	ADG13507;
($F_{420}H_2$)	*Methanocaldococcus fervens AG*86;	ACV24808;
	anococcus maripaludis C6;	ABX01642;
	Stenotrophomonas sp. SKA14;	EED39154, ZP_05135093;
	Amycolatopsis mediterranei S699;	AEK43785;
	Corynebacterium glutamicum;	EHE83474;
	Acinetobacter sp. DR1;	ADI90167;
	Acinetobacter baumannii ABNIH4;	EGU03459;
	Acinetobacter sp. DR1;	YP_003731540;
	Paenibacillus terrae HPL-003;	AET61191;
	Acinetobacter baumannii ABNIH3;	EGT94264;
	Cupriavidus necator N-1;	AEI79563;
	Herbaspirillum seropedicae SmR1;	YP_003777169;
	Burkholderia cenocepacia HI2424;	YP_840196;
	Methanobrevibacter ruminantium M1;	YP_003423269, ADC46377;
	Methanococcus voltae A3;	ADI37005;
	Methanococcus aeolicus Nankai-3;	ABR56603;
	Methanocaldococcus vulcanius M7;	ACX71899;
88:	*Methanothermobacter marburgensis*;	MTBMA_c02920;
Methyl-H4-methanopterin:	*Methanothermobacter marburgensis* str.	ADL57900;
corrinoid iron-sulfur protein	Marburg;	
methyltransferase		

TABLE 1-continued

lists examples of enzymes for construction of designer Calvin-cycle-linked pathways for production of butanol and related higher alcohols.

Enzyme/callout number	Source (Organism)	GenBank Accession Number, JGI Protein ID or Citation
89: Corrinoid iron-sulfur protein (MTBMA_c02910)	*Methanothermobacter marburgensis*; *Methanothermobacter marburgensis* str. Marburg;	MTBMA_c02910; ADL57899;
90: CO dehydrogenase/acetyl-CoA synthase (Fd^{2-}_{red})	*Methanothermobacter marburgensis*;	αMTBMA_c02870/14220/14210/14200; ϵ MTBMA_c14190/02880; βMTBMA_c02890;
	Methanothermobacter marburgensis str. Marburg;	ADL57895; ADL59006; ADL57897;
91: Energy converting hydrogenase (Ech)	*Methanosphaera stadtmanae*;	ABC57827 (ehbA);
	Methanosphaera stadtmanae;	ABC57826 (ehbB);
	Methanosphaera stadtmanae;	ABC57825 (ehbC);
	Methanosphaera stadtmanae;	ABC57824 (ehbD);
	Methanosphaera stadtmanae;	ABC57823 (ehbE);
	Methanosphaera stadtmanae;	ABC57822 (ehbF);
	Methanosphaera stadtmanae;	ABC57821 (ehbG);
	Methanosphaera stadtmanae;	ABC57820 (ehbH);
	Methanosphaera stadtmanae;	ABC57819 (ehbI);
	Methanosphaera stadtmanae;	ABC57818 (ehbJ);
	Methanosphaera stadtmanae;	ABC57817 (ehbK);
	Methanosphaera stadtmanae;	ABC57816 (ehbL);
	Methanosphaera stadtmanae;	ABC57815 (ehbM);
	Methanosphaera stadtmanae;	ABC57814 (ehbN);
	Methanosphaera stadtmanae;	ABC57813 (ehbO);
	Methanosphaera stadtmanae;	ABC57812(ehbP);
	Methanosphaera stadtmanae;	ABC57807 (ehbQ);
	Methanothermobacter marburgensis;	ADL59203, YP_003850516;
	Methanobacterium sp. SWAN-1;	YP_004520980;
	Methanobrevibacter ruminantium M1;	YP_003424741, ADC47849;
92: Methyl-H4MPT: coenzyme M methyltransferase (MtrA-H)	*Methanosphaera stadtmanae*;	ABC56714 (mtrA);
	Methanosphaera stadtmanae;	ABC56713 (mtrB);
	Methanosphaera stadtmanae;	YP_447355 (mrtC);
	Methanosphaera stadtmanae;	YP_447354 (mtrD);
	Methanosaeta harundinacea 6Ac;	AET65445 (mtrE);
	Methanopyrus kandleri AV19;	AAM01871 (mtrE);
	Methanoculleus marisnigri JR1;	YP_001046527 (mtrE);
	Methanoculleus marisnigri JR1	YP_001046522 (mtrF);
	Methanopyrus kandleri AV19;	NP_614768 (mtrF);
	Methanosphaera stadtmanae;	YP_447359 (mtrG);
	Methanosphaera stadtmanae;	YP_447360 (mtrH);
	Archaeoglobus fulgidus DSM 4304;	NP_068850 (mtrH);
	Methanopyrus kandleri AV19;	AAM01874 (mtrB);
	Methanocella paludicola SANAE;	BAI60614 (mtrB);
	Methanosaeta harundinacea 6Ac;	AET65448 (mtrB);
	Methanoculleus marisnigri JR1;	YP_001046524 (mtrB);
	Methanocella paludicola SANAE;	YP_003355598 (mtrA);
	Methanocella paludicola SANAE;	YP_003355597 (mtrB);
	Methanocella paludicola SANAE;	YP_003355596 (mtrC);
	Methanocella paludicola SANAE;	YP_003355595 (mtrD);
	Methanocella paludicola SANAE;	YP_003355594 (mtrE);
	Methanocella paludicola SANAE;	BAI60616 (mtrF);
	Methanocella paludicola SANAE;	YP_003355600 (mtrG);
	Methanocella paludicola SANAE;	YP_003355601 (mtrH);
93: Methyl-coenzyme M reductase (Mcr)	*Methanobacterium aarhusense*;	AAR27839 (mcrA);
	Methanobacterium sp. MB4;	ABG78755 (mcrA);
	Methanosphaera stadtmanae;	CAE48306 (mcrA)
	Methanosphaera stadtmanae;	CAE48303 (mcrB)
	Methanosphaera stadtmanae;	ABC56709 (mcrC);
	Methanosphaera stadtmanae;	CAE48305 (McrG)
	Methanosphaera stadtmanae;	ABC56731, ABC56728;
	Methanosphaera stadtmanae;	YP_447371, ABC56730 (mrtG);
	Methanosphaera stadtmanae;	ABC56794;
94: Heterodisulfide reductases (HdrABC, HdrDE)	*Methanocella paludicola* SANAE;	YP_003357823 (hdrA);
	Methanocella paludicola SANAE;	YP_003357824 (hdrB);
	Methanocella paludicola SANAE;	YP_003357825 (hdrC)
	Methanosaeta harundinacea 6Ac;	AET63985 (hdrA);
	Methanosaeta harundinacea 6Ac;	AET63982 (hdrB);
	Methanosaeta harundinacea 6Ac;	AET63983 (C);
	Methanosaeta harundinacea 6Ac;	AET64166 (D);

TABLE 1-continued

lists examples of enzymes for construction of designer Calvin-cycle-linked pathways for production of butanol and related higher alcohols.

Enzyme/callout number	Source (Organism)	GenBank Accession Number, JGI Protein ID or Citation
	Methanosaeta harundinacea 6Ac;	AET64165 (E);
	Methanopyrus kandleri AV19;	NP_613552 (hdrA);
	Methanopyrus kandleri AV19;	NP_613857 (hdrB);
	Methanopyrus kandleri AV19;	NP_613858 (hdrC);
95:	*Methanosphaera stadtmanae*;	ABC56726 (mvhA);
[NiFe]-hydrogenase	*Cyanobium* sp. PCC 7001;	EDY38497 (mvhA);
MvhADG (non-F420	*Methanothermobacter marburgensis*;	ADL59096 (mvhA)
reducing hydrogenase;	*Methanobrevibacter ruminantium* M1	YP_003424648 (mvhA);
methyl viologen-reducing	*Desulfobacterium autotrophicum* HRM2	YP_002602450 (mvhA)
hydrogenase)	*Desulfatibacillum alkenivorans* AK-01	ACL06634 (mvhA);
	Methanothermobacter marburgensis;	ADL59095 (mvhB);
	Desulfatibacillum alkenivorans AK-01;	ACL06636 (mvhB);
	Methanobrevibacter smithii DSM 2374;	ZP_05975561 (mvhB);
	Methanothermobacter marburgensis;	ADL59098 (mvhD);
	Methanothermobacter marburgensis;	YP_003850411 (mvhD);
	Methanobrevibacter smithii;	YP_001273574 (mvhD);
	Methanobrevibacter smithii;	ABQ87206 (mvhD);
	Methanothermobacter thermautotrophicus;	AAB02349 (mvhD);
	Methanothermobacter marburgensis;	ADL59097 (mvhG);
	Desulfatibacillum alkenivorans AK-01;	ACL06635 (mvhG);
	Cyanobium sp. PCC 7001;	EDY38425 (mvhG);
	Methanosphaera stadtmanae;	ABC56725 (mvhG);
	Methanobrevibacter smithii DSM 2374;	EFC93226 (mvhG);
	Desulfatibacillum alkenivorans AK-01;	ACL06638;
	Desulfatibacillum alkenivorans AK-01;	ACL03322;
	Methanoculleus marisnigri JR1;	YP_001046332 (hypF);
96:	*Methanocella paludicola* SANAE;	YP_003357229 (frhB-1);
Coenzyme F420-reducing	*Methanocella paludicola* SANAE;	YP_003357467 (frhB-2);
hydrogenase (Frh)	*Methanocella paludicola* SANAE;	YP_003357509 (frhB-3);
	Synechococcus elongatus PCC 7942;	ABB57389 (frhB);
	Synechocystis sp. PCC 6803;	BAA18574, YP_001735870;
	Synechococcus sp. WH 7803;	YP_001225273;
	Synechococcus sp. RCC307;	YP_001227030;
	Cyanothece sp. PCC 8802;	ACV00312 (frhB);
	Cyanobium sp. PCC 7001;	EDY39891 (fehB);
	Synechococcus sp. RS9916;	EAU74116 (frhB);
	Synechococcus sp. JA-2-3B'a(2-13);	YP_477499;
	Pelotomaculum thermopropionicum SI;	YP_001212042, YP_001211959;
	Methanothermus fervidus DSM 2088;	YP_004004590;
	Methanococcus maripaludis S2;	CAF30376 (A), NP_988502 (A);
	Methanococcus maripaludis S2;	NP_988505 (B);
	Methanococcus maripaludis S2;	NP_988503 (D);
	Methanococcus maripaludis S2;	NP_988504 (G);
97:	*Methanobrevibacter ruminantium* M1;	YP_003423444 (ahaA);
A_1A_o-ATP synthase (AhaA-IK)	*Methanobrevibacter ruminantium* M1;	YP_003423445 (ahaB);
	Methanobrevibacter ruminantium M1;	YP_003423442 (ahaC);
	Methanobrevibacter ruminantium M1	ADC46554 (ahaD);
	Methanobrevibacter ruminantium M1;	ADC46549 (ahaE);
	Methanobrevibacter ruminantium M1;	YP_003423443 (ahaF);
	Methanobrevibacter ruminantium M1;	YP_003423438 (ahaH)
	Methanobrevibacter ruminantium M1;	ADC46547 (ahaI);
	Methanobrevibacter ruminantium M1;	YP_003423440 (ahaK);
	Ferroplasma acidarmanus fer1;	ZP_05570724;
	Thermococcus sibiricus MM 739;	YP_002995194;
	Thermoproteus tenax Kra 1;	CCC82573;
	Thermoproteus tenax Kra 1;	CCC82176;
	Methanosarcina mazei Go1;	AAC06375 (ahaA);
	Methanosarcina mazei Go1;	AAC06376 (ahaB);
	Methanosarcina mazei Go1;	AAC06373 (ahaC);
	Methanosarcina mazei Go1;	AAC06377 (ahaD)
	Methanosarcina mazei Go1;	AAC06372 (ahaE);
	Methanosarcina mazei Go1;	AAC06374 (ahaF);
	Methanosarcina mazei Go1;	AAC06378 (ahaG);
98:	*Methanosarcina mazei* Go1;	CAA58177 (mhtA);
Membrane bound	*Methanosarcina acetivorans* C2A;	NP_616088 (mhtA);
cytochrome-containing F420-	*Archaeoglobus fulgidus* DSM 4304;	NP_070209 (mhtA);
nonreducing hydrogenase	*Ferroglobus placidus* DSM 10642;	ADC65001 (mhtA);
(VhtGAC, VhtD)	*Methanosarcina acetivorans* C2A;	NP_616088 (mhtB);
	Archaeoglobus fulgidus DSM 4304;	NP_070209 (mhtB);

TABLE 1-continued

lists examples of enzymes for construction of designer Calvin-cycle-linked pathways for production of butanol and related higher alcohols.

Enzyme/callout number	Source (Organism)	GenBank Accession Number, JGI Protein ID or Citation
	Methanosarcina mazei Go1;	CAA58178 (mhtB);
	Methanocella paludicola SANAE;	YP_003357991 (mhtC);
	Methanosarcina acetivorans C2A;	NP_616084(mhtC);
	Methanosarcina mazei Go1;	CAA58178 (nhtC);
	Methanosarcina mazei Go1;	NP_634195 (mhtC);
	Methanosarcina acetivorans C2A;	AAM04564 (mhtC);
	Methanosarcina mazei Go1;	CAA62962 (nhtD);
	Methanocella paludicola SANAE;	YP_003355429 (mhtD);
	Methanosarcina acetivorans C2A;	NP_616085 (mhtD);
	Methanosarcina acetivorans C2A;	NP_616087 (mhtG);
	Methanosarcina mazei Go1;	CAA581769 (mhtG);
	Methanocella paludicola SANAE;	YP_003357989 (mhtG);
	Methanosarcina acetivorans C2A;	AAM04562 (mhtG);
	Archaeoglobus fulgidus DSM 4304;	AAB89863 (mhtG);
99a:	*Methanobrevibacter ruminantium* M1;	YP_003423415 (cofA);
CofA:Lactaldehyde	*Methanobrevibacter ruminantium* M1;	ADC46523 (cofA);
dehydrogenase (for F_{420}	*Methanothermococcus okinawensis* IH1;	YP_004576675;
synthesis)	*Methanotorris igneus* Kol 5;	YP_004484309;
	Methanolinea tarda NOBI-1;	EHF10591;
	Methanobacterium sp. SWAN-1;	YP_004520759;
	Methanobacterium sp. AL-21;	YP_004289639;
	Methanolinea tarda NOBI-1;	ZP_09042363;
99b:	*Methanothermobacter marburgensis*;	cofB;
CofB: L-Lactate kinase (for F_{420} synthesis)	*Methanothermobacter thermautotrophicus*	cofB;
99c:	*Methanothermobacter marburgensis*;	ADL58588;
CofC: 2-phospho-L-lactate	*Haloquadratum walsbyi* C23;	CCC41432;
guanylyltransferase (for F_{420}	*Methanobrevibacter ruminantium* M1;	YP_003423696;
synthesis)	*Archaeoglobus veneficus* SNP6;	YP_004342334;
	Natronobacterium gregoryi SP2;	ZP_08967286;
	Methanosalsum zhilinae DSM 4017;	AEH61444;
	Methanoplanus petrolearius;	ADN35493;
	Methanolinea tarda NOBI-1;	EHF10295;
99d:	*Methanococcus maripaludis* S2;	NP987524;
CofD: LPPG:Fo 2-phospho-	*Archaeoglobus veneficus* SNP6;	YP_004341066;
L-lactate transferase (for F_{420}	*Methanospirillum hungatei* JF-1;	YP_503864;
synthesis)	*Methanococcus maripaludis* XI;	YP_004742044;
	Methanocella paludicola SANAE;	YP_003356970;
	Methanosphaera stadtmanae;	YP_448417;
	Methanopyrus kandleri AV19;	NP_614772;
	Methanoculleus marisnigri JR1;	YP_001048050;
	Methanosaeta harundinacea 6Ac;	AET64321;
	Methanocorpusculum labreanum Z;	YP_001029596;
	Methanococcus maripaludis S2;	CAF29960;
99e:	*Methanothermobacter*	NP_276154;
CofE: F_{420}-0: gamma-	*thermautotrophicus*;	
glutamyl ligase	*Methanocorpusculum labreanum* Z;	YP_001030766;
(for F_{420} synthesis)	*Methanothermus fervidus* DSM 2088;	YP_004003885;
	Methanohalophilus mahii DSM 5219;	ADE37403;
	Mycobacterium sp. Spyr1;	YP_004078486;
	Halogeometricum borinquense;	YP_004035572;
	Methanococcus maripaludis C5;	ABO35054;
	Methanosarcina barkeri str. Fusaro;	YP_305815;
	Methanocorpusculum labreanum Z;	YP_001030766;
	Methanococcoides burtonii DSM 6242;	YP_566482;
	Methanoculleus marisnigri JR1;	ABN57125;
	Methanosaeta thermophila PT;	ABK13958;
	Acidothermus cellulolyticus 11B	ABK53734;
99f:	*Methanobrevibacter ruminantium* M1;	YP_003424716 (cofG);
CofGH: Fo synthase (for F_{420}	*Methanococcus maripaludis* S2;	CAF30432 (cofG);
synthesis)	*Methanosphaera stadtmanae*;	YP_447349 (cofG)
	Methanocella paludicola SANAE;	YP_003357513 (cofG);
	Methanopyrus kandleri AV19;	NP_614181 (cofG);
	Synechococcus sp. PCC 7002;	YP_001734664 (cofG);
	Cyanothece sp. PCC 7425;	YP_002481576 (cofG);
	Synechococcus elongatus PCC 7942;	ABB56922 (cofG);
	Synechocystis sp. PCC 6803	NP_440537 (cofG)
	Synechococcus elongatus PCC 7942;	YP_399705 (cofH);
	Synechocystis sp. PCC 6803;	NP_440146 (cofH);
	Thermosynechococcus elongatus BP-1;	NP_682387 (cofH);

TABLE 1-continued

lists examples of enzymes for construction of designer Calvin-cycle-linked pathways for production of butanol and related higher alcohols.

Enzyme/callout number	Source (Organism)	GenBank Accession Number, JGI Protein ID or Citation
	Cyanothece sp. ATCC 51472;	EHC24992 (cofH);
	Methanosphaera stadtmanae;	ABC56793 (cofH);
	Methanococcus maripaludis S2;	NP_987177 (cofH);
	Methanobrevibacter ruminantium M1,	YP_003424008 (cofH);
	Methanosarcina mazei Go1;	NP_634520 (cofH);
	Methanocella paludicola SANAE;	YP_003357511 (cofH);
100:	*Methanocella paludicola* SANAE;	YP_003355454;
Pyridoxal phosphate-dependent L-tyrosine decarboxylase (mfnA for methanofuran synthesis)	*Methanobrevibacter ruminantium* M1;	YP_003424638;
	Thermococcus gammatolerans EJ3;	YP_002960503;
	Halobacterium salinarum R1;	YP_001688512;
	Methanothermobacter marburgensis;	ADL59079;
	Thermococcus gammatolerans EJ3;	ACS34639;
	Haloferax vokanii DS2;	YP_003534871;
101a:	*Methanosphaera stadtmanae*;	YP_447347;
MptA: GTP cyclohydrolase (for Methanopterin synthesis)	*Methanobrevibacter ruminantium* M1;	YP_003424704;
	Methanococcus maripaludis S2;	NP_987154;
	Pyrococcus horikoshii OT3;	NP_143623;
	Thermococcus gammatolerans EJ3;	YP_002959796;
	Methanosarcina mazei Go1;	NP_633246;
	Methanospirillum hungatei JF-1;	YP_503757;
	Thermococcus kodakarensis KOD1;	YP_183206;
	Methanopyrus kandleri AV19;	NP_613770;
	Methanosarcina acetivorans C2A;	NP_619377;
	Methanocaldococcus fervens AG86;	YP_003128348;
	Methanoregula boonei 6A8;	YP_001403641;
	Methanothermobacter thermautotrophicus;	NP_276324;
	Methanosarcina barkeri str. Fusaro;	YP_304731;
	Methanocaldococcus jannaschii;	NP_247760;
101b:	*Methanococcus maripaludis* C5;	ABO35741;
MptB: Cyclic phosphodiesterase (for Methanopterin synthesis)	*Roseobacter denitrificans* OCh 114;	YP_683148;
	Arabidopsis thaliana;	AEE84108;
	Zea mays;	NP_001151923;
	Medicago truncatula;	XP_003629873;
101c:	*Methanothermus fervidus* DSM 2088;	YP_004003771;
RFAP: Ribofuranosylaminobenzene 5'-phosphate synthase (for Methanopterin synthesis)	*Methanocella paludicola* SANAE;	YP_003356610;
	Methanoplanus petrolearius;	ADN37264;
	Methanobrevibacter ruminantium M1;	YP_003424432;
	Archaeoglobus veneficus SNP6;	YP_004342012;
	Thermococcus sp. AM4;	YP_002582695;
	Methanococcus maripaludis S2;	NP_987399;
	Methanothermus fervidus DSM 2088;	ADP77009;
	Methanocella paludicola SANAE;	BAI61627;
102a:	*Methanothermobacter marburgensis*;	ADL57861;
ComA: Phosphosulfolactate synthase (for Coenzyme M synthesis)	*Methanococcus maripaludis* S2;	NP_987393;
	Methanosphaera stadtmanae;	ABC57647;
	Methanothermus fervidus DSM 2088;	YP_004004617;
	Methanothermococcus okinawensis IH1;	YP_004575938;
	Methanobacterium sp. SWAN-1;	YP_004519242;
	Methanocaldococcus fervens AG86;	YP_003127444;
	Methanococcus voltae A3;	ADI36986;
	Methanococcus maripaludis C6;	YP_001548728;
	Methanobacterium sp. AL-21;	YP_004291430;
	Methanococcus aeolicus Nankai-3;	YP_001324357;
	Methanotorris igneus Kol 5;	AEF96400;
	Methanobacterium sp. AL-21	ADZ10458;
	Methanococcus maripaludis X1;	AEK19167;
	Methanocaldococcus infernus ME;	ADG13665;
	Methanocaldococcus sp. FS406-22;	YP_003457919;
102b:	*Methanococcus maripaludis* S2;	NP_987281;
ComB: 2-Phosphosulfolactate phosphatase (for Coenzyme M synthesis)	*Methanopyrus kandleri* AV19;	AAM01355;
	Methanothermobacter marburgensis;	YP_003850451;
	Methanococcus maripaludis S2;	CAF29717;
	Methanocella paludicola SANAE;	YP_003357619
	Methanothermus fervidus DSM 2088;	YP_004004784;
	Methanothermus fervidus DSM 2088;	ADP78022;
	Methanobacterium sp. AL-21;	YP_004289567;
	Methanobrevibacter ruminantium M1;	YP_003424691;
	Synechocystis sp. PCC 6803;	BAK50080;
	Synechococcus sp. JA-2-3B'a(2-13);	YP_476548;

TABLE 1-continued

lists examples of enzymes for construction of designer Calvin-cycle-linked pathways for production of butanol and related higher alcohols.

Enzyme/callout number	Source (Organism)	GenBank Accession Number, JGI Protein ID or Citation
	Synechococcus sp. PCC 7002;	YP_001735079;
	Synechococcus sp. WH 7803;	YP_001224757;
	Cyanothece sp. ATCC 51472;	EHC21417;
	Synechococcus sp. WH 8016;	ZP_08955317;
102c:	*Methanothermobacter marburgensis*;	ADL59162;
ComC: Sulfolactate	*Methanosphaera stadtmanae*;	ABC56689;
	Methanothermobacter marburgensis;	YP_003850475;
dehydrogenase (for	*Methanothermus fervidus* DSM 2088;	YP_004003953;
Coenzyme M synthesis)	*Roseobacter litoralis* Och 149;	YP_004689622;
	Methanococcus maripaludis C5;	ABO34766;
	Methanothermus fervidus DSM 2088;	ADP77191;
102d:	*Methanosarcina acetivorans* C2A;	NP_618188;
ComDE: Sulfopyruvate	*Methanocella paludicola* SANAE;	YP_003357048;
decarboxylase (for	*Methanocorpusculum labreanum* Z;	YP_001029945;
Coenzyme M synthesis)	*Methanoculleus marisnigri* JR1;	ABN56047;
	Methanosarcina barkeri str. Fusaro;	YP_306991;
	Methanocella paludicola SANAE;	BAI62065;
	Methanosphaera stadtmanae;	ABC56687;
	Methanococcus maripaludis S2;	NP_988809;
102e:	*Methanothermobacter marburgensis*;	comF;
ComF: Sulfoacetaldehyde	*Methanothermobacter*	comF;
dehydrogenase (for	*thermautotrophicus*	
Coenzyme M synthesis)		
103a:	*Methanopyrus kandleri* AV19;	AAM01606;
LeuA homolog:	*Methanothermobacter*	AAB85956;
Isopropylmalate synthase	*thermautotrophicus*;	
(for Coenzyme B synthesis)	*Thermoproteus tenax*;	CAF18516;
	Thermoplasma volcanium GSS1;	NP_111428;
	Methanobrevibacter smithii;	ABQ87451;
	Methanosphaera stadtmanae;	YP_447259;
	Methanobrevibacter ruminantium M1;	YP_003424897;
	Methanococcus maripaludis S2;	NP_988183;
	Synechocystis sp. PCC 6803	NP_442009;
	Synechococcus elongatus PCC 7942;	ABB56460;
	Cyanothece sp. ATCC 51472;	EHC25498;
	Synechococcus sp. WH 8016;	ZP_08954784;
	Synechococcus sp. JA-2-3B'a(2-13)	YP_477672;
	Thermosynechococcus elongatus BP-1;	NP_682187;
103b:	*Methanopyrus kandleri* AV19;	NP_614498;
LeuB homolog:	*Methanothermobacter marburgensis*;	ADL58232;
Isopropylmalate	*Methanothermus fervidus* DSM 2088;	YP_004004146;
dehydrogenase (for	*Methanocella paludicola* SANAE;	YP_003358048;
Coenzyme B synthesis)	*Methanosphaera stadtmanae*;	YP_447715;
	Methanocella paludicola SANAE;	BAI63065;
	Methanococcus maripaludis S2;	CAF30095;
	Synechocystis sp. PCC 6803;	NP_441348;
	Synechococcus elongatus PCC 7942;	ABB57535;
	Cyanothece sp. ATCC 51472;	EHC23198;
	Synechococcus sp. JA-2-3B'a(2-13;	YP_477855;
	Thermosynechococcus elongatus BP-1;	NP_682390;
103c:	*Marinobacter adhaerens* HP15;	ADP98363, ADP98362;
LeuCD homolog:	*Halorhabdus tiamatea* SARL4B;	ZP_08559069;
Isopropylmalate isomerase	*Haloarcula marismortui* ATCC 43049;	YP_135090;
(for Coenzyme B synthesis)	*Halomicrobium mukohataei*;	YP_003178469;
	Haladaptatus paucihalophilus DX253;	ZP_08045715;
	Escherichia coli O103:H2 str. 12009;	YP_003220086, YP_003220085;
	Synechocystis sp. PCC 6803;	NP_442926, NP_441618;
	Cyanothece sp. PCC 8801;	YP_002370476, YP_002373868;
	Nostoc sp. PCC 7120;	NP_485460, NP_485459;
	Synechococcus sp. JA-2-3B'a(2-13);	YP_478232, YP_476588;
	Thermosynechococcus elongatus BP-1;	NP_681699, NP_682024;

Designer Calvin-Cycle-Channeled 1-Butanol Producing Pathways

[0173] According to one of the various embodiments, a designer Calvin-cycle-channeled pathway is created that takes the Calvin-cycle intermediate product, 3-phosphoglycerate, and converts it into 1-butanol by using, for example, a set of enzymes consisting of (as shown with the numerical labels 34, 35, 03-05, 36-43 in FIG. **4**): NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase 34, NAD-dependent glyceraldehyde-3-phosphate dehydrogenase 35, phosphoglycerate mutase 03, enolase 04, pyruvate kinase 05,

citramalate synthase 36, 2-methylmalate dehydratase 37, 3-isopropylmalate dehydratase 38, 3-isopropylmalate dehydrogenase 39, 2-isopropylmalate synthase 40, isopropylmalate isomerase 41, 2-keto acid decarboxylase 42, and alcohol dehydrogenase (NAD dependent) 43. In this pathway design, as mentioned above, the NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase 34 and NAD-dependent glyceraldehyde-3-phosphate dehydrogenase 35 serve as a NADPH/NADH conversion mechanism that can covert certain amount of photosynthetically generated NADPH to NADH which can be used by the NADH-requiring alcohol dehydrogenase 43 (examples of its encoding gene with the following GenBank accession numbers: BAB59540, CAA89136, NP_148480) for production of 1-butanol by reduction of butyraldehyde.

[0174] According to one of the various embodiments, it is a preferred practice to also use an NADPH-dependent alcohol dehydrogenase 44 that can use NADPH as the source of reductant so that it can help alleviate the requirement of NADH supply for enhanced photobiological production of butanol and other alcohols. As listed in Table 1, examples of NADPH-dependent alcohol dehydrogenase 44 include (but not limited to) the enzyme with any of the following GenBank accession numbers: YP_001211038, ZP_04573952, XP_002494014, CAY71835, NP_417484, EFC99049, and ZP_02948287.

[0175] Note, the 2-keto acid decarboxylase 42 (e.g., AAS49166, ADA65057, CAG34226, AAA35267, CAA59953, A0QBE6, A0PL16) and alcohol dehydrogenase 43 (and/or 44) have quite broad substrate specificity. Consequently, their use can result in production of not only 1-butanol but also other alcohols such as propanol depending on the genetic and metabolic background of the host photosynthetic organisms. This is because all 2-keto acids can be converted to alcohols by the 2-keto acid decarboxylase 42 and alcohol dehydrogenase 43 (and/or 44) owning to their broad substrate specificity. Therefore, according to another embodiment, it is a preferred practice to use a substrate-specific enzyme such as butanol dehydrogenase 12 when/if production of 1-butanol is desirable. As listed in Table 1, examples of butanol dehydrogenase 12 are NADH-dependent butanol dehydrogenase (e.g., GenBank: YP_148778, NP_561774, AAG23613, ZP_05082669, ADO12118) and/or NAD(P)H-dependent butanol dehydrogenase (e.g., NP_562172, AAA83520, EFB77036, EFF67629, ZP_06597730, EFE12215, EFC98086, ZP_05979561).

[0176] In one of the various embodiments, another designer Calvin-cycle-channeled 1-butanol production pathway is created that takes the Calvin-cycle intermediate product, 3-phosphoglycerate, and converts it into 1-butanol by using, for example, a set of enzymes consisting of (as shown with the numerical labels 34, 35, 03, 04, 45-52 and 40-43 (44/12) in FIG. **4**): NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase 34, NAD-dependent glyceraldehyde-3-phosphate dehydrogenase 35, phosphoglycerate mutase 03, enolase 04, phosphoenolpyruvate carboxylase 45, aspartate aminotransferase 46, aspartokinase 47, aspartate-semialdehyde dehydrogenase 48, homoserine dehydrogenase 49, homoserine kinase 50, threonine synthase 51, threonine ammonia-lyase 52, 2-isopropylmalate synthase 40, isopropylmalate isomerase 41, 3-isopropylmalate dehydrogenase 39, 2-keto acid decarboxylase 42, and NAD-dependent alcohol dehydrogenase 43 (and/or NADPH-dependent alcohol dehydrogenase 44, or butanol dehydrogenase 12).

[0177] According to another embodiment, the amino-acids-metabolism-related 1-butanol production pathways [numerical labels 03-05, 36-43; and/or 03, 04, 45-52 and 39-43 (44/12)] can operate in combination and/or in parallel with other photobiological butanol production pathways. For example, as shown also in FIG. **4**, the Frctose-6-photophate-branched 1-butanol production pathway (numerical labels 13-32 and 44/12) can operate with the parts of amino-acids-metabolism-related pathways [numerical labels 36-42, and/or 45-52 and 40-42) with pyruvate and/or phosphoenolpyruvate as their joining points.

[0178] Examples of designer Calvin-cycle-channeled 1-butanol production pathway genes (DNA constructs) are shown in the DNA sequence listings. SEQ ID NOS: 58-70 represent a set of designer genes for a designer nirA-promoter-controlled Calvin-cycle-channeled 1-butanol production pathway (as shown with numerical labels 34, 35, 03-05, and 36-43 in FIG. **4**) in a host oxyphotobacterium such as *Thermosynechococcus elongatus* BP1. Briefly, SEQ ID NO: 58 presents example 58 of a designer nirA-promoter-controlled NADPH-dependent Glyceraldehyde-3-Phosphate Dehydrogenase (34) DNA construct (1417 bp) that comprises: a PCR FD primer (sequence 1-20), a 231-bp nirA promoter from *Thermosynechococcus elongatus* BP1 (21-251), an enzyme-encoding sequence (252-1277) selected/modified from the sequences of a *Staphylococcus aureus* 04-02981 NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase (GenBank: ADC37857), a 120-bp rbcS terminator from BP1 (1278-1397), and a PCR RE primer (1398-1417) at the 3' end.

[0179] SEQ ID NO: 59 presents example 59 of a designer nirA-promoter-controlled NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (35) DNA construct (1387 bp) that comprises: a PCR FD primer (sequence 1-20), a 231-bp nirA promoter from *Thermosynechococcus elongatus* BP1 (21-251), an enzyme-encoding sequence (252-1247) selected/modified from the sequences of an *Edwardsiella tarda* FL6-60 NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (GenBank: ADM41489), a 120-bp rbcS terminator from BP1 (1248-1367), and a PCR RE primer (1368-1387) at the 3' end.

[0180] SEQ ID NO: 60 presents example 60 of a designer nirA-promoter-controlled Phosphoglycerate Mutase (03) DNA construct (1627 bp) that includes a PCR FD primer (sequence 1-20), a 231-bp nirA promoter from *Thermosynechococcus elongatus* BP1 (21-251), an enzyme-encoding sequence (252-1487) selected/modified from the sequences of a *Oceanithermus profundus* DSM 14977 phosphoglycerate mutase (GenBank: ADR35708), a 120-bp rbcS terminator from BP1 (1488-1607), and a PCR RE primer (1608-1627).

[0181] SEQ ID NO: 61 presents example 61 of a designer nirA-promoter-controlled Enolase (04) DNA construct (1678 bp) that includes a PCR FD primer (sequence 1-20), a 231-bp nirA promoter from *Thermosynechococcus elongatus* BP1 (21-251), an enzyme-encoding sequence (252-1538) selected from the sequences of a *Syntrophothermus* Enolase (GenBank: ADI02602), a 120-bp rbcS terminator from BP1 (1539-1658), and a PCR RE primer (1659-1678).

[0182] SEQ ID NO: 62 presents example 62 of a designer nirA-promoter-controlled Pyruvate Kinase (05) DNA construct (2137 bp) that includes a PCR FD primer (sequence 1-20), a 231-bp nirA promoter from *Thermosynechococcus elongatus* BP1 (21-251), an enzyme-encoding sequence (252-1997) selected from the sequences of a *Syntrophother-*

mus lipocalidus pyruvate kinase (GenBank: ADI02459), a 120-bp rbcS terminator from BP1 (1998-2117), and a PCR RE primer (2118-2137).

[0183] SEQ ID NO: 63 presents example 63 of a designer nirA-promoter-controlled Citramalate Synthase (36) DNA construct (2163 bp) that includes a PCR FD primer (sequence 1-20), a 305-bp nirA promoter (21-325), an enzyme-encoding sequence (326-1909) selected and modified from *Hydrogenobacter thermophilus* TK-6 citramalate synthase (YP_003433013), a 234-bp rbcS terminator from BP1 (1910-2143), and a PCR RE primer (2144-2163).

[0184] SEQ ID NO: 64 presents example 64 of a designer nirA-promoter-controlled 3-Isopropylmalate/(R)-2-Methylmalate Dehydratase (37) DNA construct (2878 bp) consisting of a PCR FD primer (sequence 1-20), a 231-bp nirA promoter from *Thermosynechococcus elongatus* BP1 (21-251), a 3-isopropylmalate/(R)-2-methylmalate dehydratase large subunit-encoding sequence (252-2012) selected/modified from the sequences of an *Eubacterium* 3-isopropylmalate/(R)-2-methylmalate dehydratase large subunit (YP_002930810), a 231-bp nirA promoter from *Thermosynechococcus* (2013-2243), a 3-isopropylmalate/(R)-2-methylmalate dehydratase small subunit-encoding sequence (2244-2738) selected/modified from the sequences of an *Eubacterium* 3-isopropylmalate/(R)-2-methylmalate dehydratase small subunit (YP_002930809), a 120-bp rbcS terminator from BP1 (2739-2858), and a PCR RE primer (2859-2878).

[0185] SEQ ID NO: 65 presents example 65 of a designer nirA-promoter-controlled 3-Isopropylmalate Dehydratase (38) DNA construct (2380 bp) comprises: a PCR FD primer (sequence 1-20), a 231-bp nirA promoter from *Thermosynechococcus elongatus* BP1 (21-251), a 3-isopropylmalate dehydratase large subunit-encoding sequence (252-1508) selected/modified from the sequences of a *Thermotoga petrophila* 3-isopropylmalate dehydratase large subunit (ABQ46641), a 231-bp nirA promoter from *Thermosynechococcus elongatus* BP1 (1509-1739), a 3-isopropylmalate dehydratase small subunit-encoding sequence (1740-2240) selected/modified from the sequences of a *Thermotoga* 3-isopropylmalate dehydratase small subunit (ABQ46640), a 120-bp rbcS terminator from BP1 (2241-2360), and a PCR RE primer (2361-2380).

[0186] SEQ ID NO: 66 presents example 66 of a designer nirA-promoter-controlled 3-Isopropylmalate Dehydrogenase (39) DNA construct (1456 bp) consisting of: a PCR FD primer (1-20), a 231-bp nirA promoter from *Thermosynechococcus elongatus* BP1 (21-251), a 3-isopropylmalate dehydrogenase-encoding sequence (252-1316) selected from the sequences of a *Thermotoga* 3-isopropylmalate dehydrogenase (GenBank: CP000702 Region 349983 . . . 351047), a 120-bp rbcS terminator from BP1 (1317-1436), and a PCR RE primer (1437-1456).

[0187] SEQ ID NO: 67 presents example 67 of a designer nirA-promoter-controlled 2-Isopropylmalate Synthase (40, EC 4.1.3.12) DNA construct (1933 bp) consisting of: a PCR FD primer (sequence 1-20), a 231-bp nirA promoter from *Thermosynechococcus elongatus* (21-251), an enzyme-encoding sequence (252-1793) selected/modified from the sequences of a *Thermotoga petrophila* 3-isopropylmalate dehydrogenase (CP000702 Region: 352811 . . . 354352), a 120-bp rbcS terminator from BP1 (1794-1913), and a PCR RE primer (1914-1933).

[0188] SEQ ID NO: 68 presents example 68 of a designer nirA-promoter-controlled Isopropylmalate Isomerase (41) DNA construct (2632 bp) comprises: a PCR FD primer (sequence 1-20), a 231-bp nirA promoter from *Thermosynechococcus elongatus* BP1 (21-251), a isopropylmalate isomerase large subunit-encoding sequence (252-1667) selected/modified from the sequences of a *Geobacillus kaustophilus* 3-isopropylmalate isomerase large subunit (YP_148509), a 231-bp nirA promoter from *Thermosynechococcus* (1668-1898), a isopropylmalate isomerase small subunit-encoding sequence (1899-2492) selected from the sequences of a *Geobacillus kaustophilus* isopropylmalate isomerase small subunit (YP_148508), a 120-bp rbcS terminator from BP1 (2493-2612), and a PCR RE primer (2613-2632).

[0189] SEQ ID NO: 69 presents example 69 of a designer nirA-promoter-controlled 2-Keto Acid Decarboxylase (42) DNA construct (2035 bp) consisting of: a PCR FD primer (sequence 1-20), a 231-bp nirA promoter from *Thermosynechococcus elongatus* BP1 (21-251), a 2-keto acid decarboxylase-encoding sequence (252-1895) selected/modified from the sequences of a *Lactococcus lactis* branched-chain alpha-ketoacid decarboxylase (AAS49166), a 120-bp rbcS terminator from BP1 (1896-2015), and a PCR RE primer (2016-2035) at the 3' end.

[0190] SEQ ID NO: 70 presents example 70 of a designer nirA-promoter-controlled NAD-dependent Alcohol Dehydrogenase (43) DNA construct (1426 bp) consisting of: a PCR FD primer (sequence 1-20), a 231-bp nirA promoter from *Thermosynechococcus elongatus* BP1 (21-251), an enzyme-encoding sequence (252-1286) selected/modified from the sequences of an *Aeropyrum pernix* K1 NAD-dependent alcohol dehydrogenase (NP_148480), a 120-bp rbcS terminator from BP1 (1287-1406), and a PCR RE primer (1407-1426).

[0191] As mentioned before, use of an NADPH-dependent alcohol dehydrogenase 44 that can use NADPH as the source of reductant can help alleviate the requirement of NADH supply for enhanced photobiological production of butanol and other alcohols. SEQ ID NO: 71 presents example 71 of a designer nirA-promoter-controlled NADPH-dependent Alcohol Dehydrogenase (44) DNA construct (1468 bp) that comprises: a PCR FD primer (sequence 1-20), a 231-bp nirA promoter from *Thermosynechococcus elongatus* BP1 (21-251), an enzyme-encoding sequence (252-1328) selected from the sequences of a *Pichia pastoris* NADPH-dependent medium chain alcohol dehydrogenase with broad substrate specificity (XP_002494014), a 120-bp rbcS terminator from BP1 (1329-1458), and a PCR RE primer (1459-1468) at the 3' end. In one of the examples, this type of NADPH-dependent alcohol dehydrogenase gene (SEQ ID NO: 71) is also used in construction of Calvin-cycle-channeled butanol production pathway.

[0192] However, because of the broad substrate specificity of the 2-keto acid decarboxylase (42, SEQ ID NO: 69) and the alcohol dehydrogenase (43, SEQ ID NO: 70; or 44, SEQ ID NO: 71), the pathway expressed with designer genes of SEQ ID NO: 69 and SEQ ID NO: 71 (and/or SEQ ID NO: 70) can result in the production of alcohol mixtures rather than single alcohols since all 2-keto acids can be converted to alcohols by the two broad substrate specificity enzymes. Therefore, to improve the specificity for 1-butanol production, it is a preferred practice to use a more substrate-specific butanol dehydrogenase 12. SEQ ID NO: 72 presents example 72 of a designer nirA-promoter-controlled NADH-dependent

Butanol Dehydrogenase (12a) DNA construct (1555 bp) that includes a PCR FD primer (sequence 1-20), a 231-bp nirA promoter from *Thermosynechococcus elongatus* BP1 (21-251), an enzyme-encoding sequence (252-1415) selected/modified from the sequences of a *Geobacillus kaustophilus* NADH-dependent butanol dehydrogenase (YP_148778), a 120-bp rbcS terminator from BP1 (1416-1535), and a PCR RE primer (1536-1555) at the 3' end.

[0193] SEQ ID NO: 73 presents example 73 of a designer nirA-promoter-controlled NADPH-dependent Butanol Dehydrogenase (12b) DNA construct (1558 bp) consisting of a PCR FD primer (sequence 1-20), a 231-bp nirA promoter from *Thermosynechococcus elongatus* BP1 (21-251), a NADPH-dependent butanol dehydrogenase-encoding sequence (252-1418) selected/modified from the sequences of a *Clostridium perfringens* NADPH-dependent butanol dehydrogenase (NP_562172), a 120-bp rbcS terminator from BP1 (1419-1528), and a PCR RE primer (1529-1558) at the 3' end.

[0194] Use of SEQ ID NOS: 72 and/or 73 (12a and/or 12b) along with SEQ ID NOS: 58-69 represents a specific Calvin-cycle-channeled 1-butanol production pathway numerically labeled as 34, 35, 03-05, 36-42 and 12 in FIG. **4**.

[0195] SEQ ID NOS: 74-81 represent an alternative (amino acids metabolism-related) pathway (45-52 in FIG. **4**) that branches from the point of phosphoenolpyruvate and merges at the point of 2-ketobutyrate in the Calvin-cycle-channeled 1-butanol production pathway. Briefly, SEQ ID NO: 74 presents example 74 of a designer nirA-promoter-controlled Phosphoenolpyruvate Carboxylase (45) DNA construct (3646 bp) consisting of: a PCR FD primer (sequence 1-20), a 231-bp nirA promoter from *Thermosynechococcus elongatus* BP1 (21-251), an enzyme-encoding sequence (252-3506) selected/modified from the sequences of a *Thermaerobacter subterraneus* DSM 13965 Phosphoenolpyruvate carboxylase (EFR61439), a 120-bp rbcS terminator from BP1 (3507-3626), and a PCR RE primer (3627-3646) at the 3' end.

[0196] SEQ ID NO: 75 presents example 75 of a designer nirA-promoter-controlled Aspartate Aminotransferase (46) DNA construct (1591 bp) that includes a PCR FD primer (sequence 1-20), a 231-bp nirA promoter from *Thermosynechococcus elongatus* BP1 (21-251), an enzyme-encoding sequence (252-1451) selected/modified from the sequences of a *Thermotoga lettingae* aspartate aminotransferase (YP_001470126), a 120-bp rbcS terminator from BP1 (1452-1471), and a PCR RE primer (1472-1591).

[0197] SEQ ID NO: 76 presents example 76 of a designer nirA-promoter-controlled Aspartate

[0198] Kinase (47) DNA construct (1588 bp) that includes a PCR FD primer (sequence 1-20), a 231-bp nirA promoter from *Thermosynechococcus elongatus* BP1 (21-251), an enzyme-encoding sequence (252-1448) selected/modified from the sequences of a *Thermotoga lettingae* TMO aspartate kinase (YP_001470361), a 120-bp rbcS terminator from BP1 (1449-1568), and a PCR RE primer (1569-1588).

[0199] SEQ ID NO: 77 presents example 77 of a designer nirA-promoter-controlled Aspartate-Semialdehyde Dehydrogenase (48) DNA construct (1411 bp) that includes a PCR FD primer (sequence 1-20), a 231-bp nirA promoter from *Thermosynechococcus elongatus* BP1 (21-251), an enzyme-encoding sequence (252-1271) selected/modified from the sequences of a *Thermotoga lettingae* TMO aspartate-semialdehyde dehydrogenase (YP_001470981), a 120-bp rbcS terminator from BP1 (1272-1391), and a PCR RE primer (1392-1411) at the 3' end.

[0200] SEQ ID NO: 78 presents example 78 of a designer nirA-promoter-controlled Homoserine Dehydrogenase (49) DNA construct (1684 bp) that includes a PCR FD primer (sequence 1-20), a 231-bp nirA promoter from *Thermosynechococcus elongatus* BP1 (21-251), an enzyme-encoding sequence (252-1544) selected/modified from the sequences of a *Syntrophothermus lipocalidus* DSM 12680 homoserine dehydrogenase (ADI02231), a 120-bp rbcS terminator from BP1 (1545-1664), and a PCR RE primer (1665-1684) at the 3' end.

[0201] SEQ ID NO: 79 presents example 79 of a designer nirA-promoter-controlled Homoserine Kinase (50) DNA construct (1237 bp) that includes a PCR FD primer (sequence 1-20), a 231-bp nirA promoter from *Thermosynechococcus elongatus* BP1 (21-251), an enzyme-encoding sequence (252-1097) selected/modified from the sequences of a *Thermotoga petrophila* RKU-1 Homoserine Kinase (YP_001243979), a 120-bp rbcS terminator from BP1 (1098-1217), and a PCR RE primer (1218-1237) at the 3' end.

[0202] SEQ ID NO: 80 presents example 80 of a designer nirA-promoter-controlled Threonine Synthase (51) DNA construct (1438 bp) that includes a PCR FD primer (sequence 1-20), a 231-bp nirA promoter from *Thermosynechococcus* (21-251), an enzyme-encoding sequence (252-1298) selected from the sequences of a *Thermotoga* Threonine Synthase (YP_001243978), a 120-bp rbcS terminator from BP1 (1299-1418), and a PCR RE primer (1419-1438).

[0203] SEQ ID NO: 81 presents example 81 of a designer nirA-promoter-controlled Threonine Ammonia-Lyase (52) DNA construct (1600 bp) consisting of a PCR FD primer (sequence 1-20), a 231-bp nirA promoter from *Thermosynechococcus elongatus* BP1 (21-251), an enzyme-encoding sequence (252-1460) selected/modified from the sequences of a *Geobacillus kaustophilus* threonine ammonia-lyase (BAD75876), a 120-bp rbcS terminator from BP1 (1461-1580), and a PCR RE primer (1581-1600) at the 3' end.

[0204] Note, SEQ ID NOS: 58-61, 74-81, 66-69, and 72 (and/or 73) represent a set of sample designer genes that can express a Calvin-cycle 3-phophoglycerate-branched photosynthetic NADPH-enhanced 1-butanol production pathway of 34, 35, 03, 04, 45-52 40, 41, 39, 42, and 12 while SEQ ID NOS: 58-69 and 72 (and/or 73) represent another set of sample designer genes that can express another Calvin-cycle 3-phophoglycerate-branched photosynthetic NADPH-enhanced 1-butanol production pathway as numerically labeled as 34, 35, 03-05, 36-42, and 12 in FIG. **4**. The net results of the designer photosynthetic NADPH-enhanced pathways in working with the Calvin cycle are photobiological production of 1-butanol ($CH_3CH_2CH_2CH_2OH$) from carbon dioxide (CO_2) and water (H_2O) using photosynthetically generated ATP (Adenosine triphosphate) and NADPH (reduced nicotinamide adenine dinucleotide phosphate) according to the following process reaction:

$$4CO_2+5H_2O \rightarrow CH_3CH_2CH_2CH_2OH+6O_2 \quad [5]$$

Designer Calvin-Cycle-Channeled 2-Methyl-1-Butanol Producing Pathways

[0205] According to one of the various embodiments, a designer Calvin-cycle-channeled 2-Methyl-1-Butanol production pathway is created that takes the Calvin-cycle inter-

mediate product, 3-phosphoglycerate, and converts it into 2-methyl-1-butanol by using, for example, a set of enzymes consisting of (as shown with the numerical labels 34, 35, 03-05, 36-39, 53-55, 42, 43 or 44/56 in FIG. **5**): NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase 34, NAD-dependent glyceraldehyde-3-phosphate dehydrogenase 35, phosphoglycerate mutase 03, enolase 04, pyruvate kinase 05, citramalate synthase 36, 2-methylmalate dehydratase 37, 3-isopropylmalate dehydratase 38, 3-isopropylmalate dehydrogenase 39, acetolactate synthase 53, ketol-acid reductoisomerase 54, dihydroxy-acid dehydratase 55, 2-keto acid decarboxylase 42, and NAD-dependent alcohol dehydrogenase 43 (or NADPH-dependent alcohol dehydrogenase 44; more preferably, 2-methylbutyraldehyde reductase 56).

[0206] In another embodiment, a designer Calvin-cycle-channeled 2-methyl-1-butanol production pathway is created that takes the intermediate product, 3-phosphoglycerate, and converts it into 2-methyl-1-butanol by using, for example, a set of enzymes consisting of (as shown with the numerical labels 34, 35, 03, 04, 45-55, 42, 43 or 44/56 in FIG. **5**): NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase 34, NAD-dependent glyceraldehyde-3-phosphate dehydrogenase 35, phosphoglycerate mutase 03, enolase 04, phosphoenolpyruvate carboxylase 45, aspartate aminotransferase 46, aspartokinase 47, aspartate-semialdehyde dehydrogenase 48, homoserine dehydrogenase 49, homoserine kinase 50, threonine synthase 51, threonine ammonia-lyase 52, acetolactate synthase 53, ketol-acid reductoisomerase 54, dihydroxy-acid dehydratase 55, 2-keto acid decarboxylase 42, and NAD dependent alcohol dehydrogenase 43 (or NADPH dependent alcohol dehydrogenase 44; more preferably, 2-methylbutyraldehyde reductase 56).

[0207] These pathways (FIG. **5**) are quite similar to those of FIG. **4**, except that acetolactate synthase 53, ketol-acid reductoisomerase 54, dihydroxy-acid dehydratase 55, and 2-methylbutyraldehyde reductase 56 are used to produce 2-Methyl-1-Butanol.

[0208] SEQ ID NO: 82 presents example 82 of a designer nirA-promoter-controlled Acetolactate Synthase (53) DNA construct (2107 bp) that includes a PCR FD primer (sequence 1-20), a 231-bp nirA promoter from *Thermosynechococcus elongatus* BP1 (21-251), an acetolactate synthase-encoding sequence (252-1967) selected/modified from the sequences of a *Bacillus subtilis* subsp. *subtilis* str. 168 acetolactate synthase (CAB07802), a 120-bp rbcS terminator from BP1 (1968-2087), and a PCR RE primer (2088-2107) at the 3' end.

[0209] SEQ ID NO: 83 presents example 83 of a designer nirA-promoter-controlled Ketol-Acid Reductoisomerase (54) DNA construct (1405 bp) that includes a PCR FD primer (sequence 1-20), a 231-bp nirA promoter from *Thermosynechococcus elongatus* BP1 (21-251), a ketol-acid reductoisomerase-encoding sequence (252-1265) selected/modified from the sequences of a *Syntrophothermus lipocalidus* DSM 12680 ketol-acid reductoisomerase (ADI02902), a 120-bp rbcS terminator from BP1 (1266-1385), and a PCR RE primer (1386-1405) at the 3' end.

[0210] SEQ ID NO: 84 presents example 84 of a designer nirA-promoter-controlled Dihydroxy-Acid Dehydratase (55) DNA construct (2056 bp) that includes a PCR FD primer (1-20), a 231-bp nirA promoter from *Thermosynechococcus elongatus* BP1 (21-251), an enzyme-encoding sequence (252-1916) selected from the sequences of a *Thermotoga* dihydroxy-acid dehydratase (YP_001243973), a 120-bp rbcS terminator from BP1 (1917-2036), and a PCR RE primer (2037-2056).

[0211] SEQ ID NO: 85 presents example 85 of a designer nirA-promoter-controlled 2-Methylbutyraldehyde Reductase (56) DNA construct (1360 bp) that includes a PCR FD primer (sequence 1-20), a 231-bp nirA promoter from *Thermosynechococcus elongatus* BP1 (21-251), an enzyme-encoding sequence (252-1220) selected/modified from the sequences of a *Schizosaccharomyces japonicus* 2-methylbutyraldehyde reductase (XP_002173231), a 120-bp rbcS terminator from BP1 (1221-1340), and a PCR RE primer (1341-1360) at the 3' end.

[0212] Note, SEQ ID NOS: 58-66, 82-84, 69 and 85 represent another set of sample designer genes that can express a Calvin-cycle 3-phophoglycerate-branched photosynthetic NADPH-enhanced 2-methyl-1-butanol production pathway numerically labeled as 34, 35, 03-05, 36-39, 53-55, 42 and 56; while SEQ ID NOS: 58-61, 74-84, 69 and 85 represent a set of sample designer genes that can express another Calvin-cycle 3-phophoglycerate-branched photosynthetic NADPH-enhanced 2-methyl-1-butanol production pathway of 34, 35, 03, 04, 45-55, 42 and 56 in FIG. **5**. These designer genes can be used in combination with other pathway gene(s) to express certain other pathways such as a Calvin-cycle Fructose-6-phosphate branched 2-methyl-1-butanol production pathway numerically labeled as 13-26, 36-39, 53-55, 42 and 56 (and/or, as 13-25, 45-55, 42 and 56) in FIG. **5** as well. The net results of the designer photosynthetic NADPH-enhanced pathways in working with the Calvin cycle are production of 2-methyl-1-butanol [$CH_3CH_2CH(CH_3)CH_2OH$] from carbon dioxide (CO_2) and water (H_2O) using photosynthetically generated ATP and NADPH according to the following process reaction:

$$10CO_2+12H_2O\rightarrow 2CH_3CH_2CH(CH_3)CH_2OH+15O_2 \quad [6]$$

Calvin-Cycle-Channeled Pathways for Production of Isobutanol and 3-Methyl-1-Butanol

[0213] According to one of the various embodiments, a designer Calvin-cycle-channeled pathway is created that takes the Calvin-cycle intermediate product, 3-phosphoglycerate, and converts it into isobutanol by using, for example, a set of enzymes consisting of (as shown with numerical labels 34, 35, 03-05, 53-55, 42, 43 (or 44) in FIG. **6**): NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase 34, NAD-dependent glyceraldehyde-3-phosphate dehydrogenase 35, phosphoglycerate mutase 03, enolase 04, pyruvate kinase 05, acetolactate synthase 53, ketol-acid reductoisomerase 54, dihydroxy-acid dehydratase 55, 2-keto acid decarboxylase 42, and NAD-dependent alcohol dehydrogenase 43 (or NADPH-dependent alcohol dehydrogenase 44). The net result of this pathway in working with the Calvin cycle is photobiological production of isobutanol ($(CH_3)_2CHCH_2OH$) from carbon dioxide (CO_2) and water (H_2O) using photosynthetically generated ATP and NADPH according to the following process reaction:

$$4CO_2+5H_2O\rightarrow (CH_3)_2CHCH_2OH+6I_2 \quad [7]$$

[0214] According to another embodiment, a designer Calvin-cycle-channeled pathway is created that takes the intermediate product, 3-phosphoglycerate, and converts it into 3-methyl-1-butanol by using, for example, a set of enzymes consisting of (as shown with the numerical labels

34, 35, 03-05, 53-55, 40, 38, 39, 42, 43 (or 44/57) in FIG. **6**): NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase 34, NAD-dependent glyceraldehyde-3-phosphate dehydrogenase 35, phosphoglycerate mutase 03, enolase 04, pyruvate kinase 05, acetolactate synthase 53, ketol-acid reductoisomerase 54, dihydroxy-acid dehydratase 55, 2-isopropylmalate synthase 40, 3-isopropylmalate dehydratase 38, 3-isopropylmalate dehydrogenase 39, 2-keto acid decarboxylase 42, and NAD-dependent alcohol dehydrogenase 43 (or NADPH-dependent alcohol dehydrogenase 44; or more preferably, 3-methylbutanal reductase 57). The net result of this pathway in working with the Calvin cycle is photobiological production of 3-methyl-1-butanol($CH_3CH(CH_3)CH_2CH_2OH$) from carbon dioxide (CO_2) and water (H_2O) using photosynthetically generated ATP and NADPH according to the following process reaction:

$$10CO_2+12H_2O\rightarrow 4CH_3CH(CH_3)CH_2CH_2OH+15O_2 \quad [8]$$

[0215] These designer pathways (FIG. **6**) share a number of designer pathway enzymes with those of FIGS. **4** and **5**, except that a 3-methylbutanal reductase 57 is preferably used for production of 3-methyl-1-butanol; they all have a common feature of using an NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase 34 and an NAD-dependent glyceraldehyde-3-phosphate dehydrogenase 35 as an NADPH/NADH conversion mechanism to covert certain amount of photosynthetically generated NADPH to NADH which can be used by NADH-requiring pathway enzymes such as an NADH-requiring alcohol dehydrogenase 43.

[0216] SEQ ID NO: 86 presents example 86 of a designer nirA-promoter-controlled 3-Methylbutanal Reductase (57) DNA construct (1420 bp) that includes a PCR FD primer (sequence 1-20), a 231-bp nirA promoter from *Thermosynechococcus elongatus* BP1 (21-251), an enzyme-encoding sequence (252-1280) selected/modified from the sequences of a *Saccharomyces cerevisiae* S288c 3-Methylbutanal reductase (DAA10635), a 120-bp rbcS terminator from BP1 (1281-1400), and a PCR RE primer (1401-1420) at the 3' end.

[0217] SEQ ID NOS: 58-62, 82-84, 69, 70 (or 71) represent a set of sample designer genes that can express a Calvin-cycle 3-phosphoglycerate-branched photosynthetic NADPH-enhanced isobutanol production pathway (34, 35, 03-05, 53-55, 42, 43 or 44); while SEQ ID NOS: 58-62, 82-84, 65-67, 69 and 86 represent another set of sample designer genes that can express a Calvin-cycle 3-phosphoglycerate-branched photosynthetic NADPH-enhanced 3-methyl-1-butanol production pathway (34, 35, 03-05, 53-55, 40, 38, 39, 42, and 57 in FIG. **6**).

[0218] These designer genes can be used with certain other designer genes to express certain other pathways such as a Calvin-cycle Fructose-6-phosphate-branched 3-methyl-1-butanol production pathway shown as 13-26, 53-54, 39-40, 42 and 57 (or 43/44) in FIG. **6** as well. The net results of the designer photosynthetic NADPH-enhanced pathways in working with the Calvin cycle are also production of isobutanol ($(CH_3)_2CHCH_2OH$) and/or 3-methyl-1-butanol ($CH_3CH(CH_3)CH_2CH_2OH$) from carbon dioxide (CO_2) and water (H_2O) using photosynthetically generated ATP and NADPH.

Designer Calvin-Cycle-Channeled Pathways for Production of 1-Hexanol and 1-Octanol

[0219] According to one of the various embodiments, a designer Calvin-cycle-channeled pathway is created that takes the Calvin-cycle intermediate product, 3-phosphoglycerate, and converts it into 1-hexanol by using, for example, a set of enzymes consisting of (as shown with the numerical labels 34, 35, 03-10, 07'-12' in FIG. **7**): NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase 34, NAD-dependent glyceraldehyde-3-phosphate dehydrogenase 35, phosphoglycerate mutase 03, enolase 04, pyruvate kinase 05, pyruvate-ferredoxin oxidoreductase 06, thiolase 07, 3-hydroxybutyryl-CoA dehydrogenase 08, crotonase 09, butyryl-CoA dehydrogenase 10, designer 3-ketothiolase 07', designer 3-hydroxyacyl-CoA dehydrogenase 08', designer enoyl-CoA dehydratase 09', designer 2-enoyl-CoA reductase 10', designer acyl-CoA reductase 11', and hexanol dehydrogenase 12'. The net result of this designer pathway in working with the Calvin cycle is photobiological production of 1-hexanol ($CH_3CH_2CH_2CH_2CH_2CH_2OH$) from carbon dioxide ($CO_2$) and water ($H_2O$) using photosynthetically generated ATP and NADPH according to the following process reaction:

$$6CO_2+7H_2O\rightarrow CH_3CH_2CH_2CH_2CH_2CH_2OH+9O_2 \quad [9]$$

[0220] According to another embodiment, a designer Calvin-cycle-channeled pathway is created that takes the intermediate product, 3-phosphoglycerate, and converts it into 1-octanol by using, for example, a set of enzymes consisting of (as shown with the numerical labels 34, 35, 03-10, 07'-10', and 07"-12" in FIG. **7**): NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase 34, NAD-dependent glyceraldehyde-3-phosphate dehydrogenase 35, phosphoglycerate mutase 03, enolase 04, pyruvate kinase 05, pyruvate-ferredoxin oxidoreductase 06, thiolase 07, 3-hydroxybutyryl-CoA dehydrogenase 08, crotonase 09, butyryl-CoA dehydrogenase 10, designer 3-ketothiolase 07', designer 3-hydroxyacyl-CoA dehydrogenase 08', designer enoyl-CoA dehydratase 09', designer 2-enoyl-CoA reductase 10', designer 3-ketothiolase 07", designer 3-hydroxyacyl-CoA dehydrogenase 08", designer enoyl-CoA dehydratase 09", designer 2-enoyl-CoA reductase 10", designer acyl-CoA reductase 11", and octanol dehydrogenase 12".

[0221] These pathways represent a significant upgrade in the pathway designs with part of a previously disclosed 1-butanol production pathway (03-10). The key feature is the utilization of an NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase 34 and an NAD-dependent glyceraldehyde-3-phosphate dehydrogenase 35 as a mechanism for NADPH/NADH conversion to drive an NADH-requiring designer hydrocarbon chain elongation pathway (07'-10') for 1-hexanol production (07'-12' as shown in FIG. **7**).

[0222] SEQ ID NOS: 87-92 represent a set of designer genes that can express the designer hydrocarbon chain elongation pathway for 1-hexanol production (07'-12' as shown in FIG. **7**). Briefly, SEQ ID NO: 87 presents example 87 of a designer nirA-promoter-controlled 3-Ketothiolase (07') DNA construct (1540 bp) that includes a PCR FD primer (sequence 1-20), a 231-bp nirA promoter from *Thermosynechococcus elongatus* BP1 (21-251), an enzyme-encoding sequence (252-1400) selected/modified from the sequences of a *Geobacillus kaustophilus* 3-Ketothiolase (YP_147173), a 120-bp rbcS terminator from BP1 (1401-1520), and a PCR RE primer (1521-1540).

[0223] SEQ ID NO: 88 presents example 88 of a designer nirA-promoter-controlled 3-Hydroxyacyl-CoA Dehydrogenase (08') DNA construct (1231 bp) that includes a PCR FD primer (sequence 1-20), a 231-bp nirA promoter from *Thermosynechococcus elongatus* BP1 (21-251), an enzyme-en-

coding sequence (252-1091) selected/modified from the sequences of a *Syntrophothermus lipocalidus* 3-Hydroxyacyl-CoA dehydrogenase (YP_003702743), a 120-bp rbcS terminator from BP1 (1092-1211), and a PCR RE primer (1212-1231).

[0224] SEQ ID NO: 89 presents example 89 of a designer nirA-promoter-controlled Enoyl-CoA Dehydratase (09') DNA construct (1162 bp) that includes a PCR FD primer (sequence 1-20), a 231-bp nirA promoter from *Thermosynechococcus elongatus* BP1 (21-251), an enzyme-encoding sequence (252-1022) selected/modified from the sequences of a *Bordetella petrii* Enoyl-CoA dehydratase (CAP41574), a 120-bp rbcS terminator from BP1 (1023-1442), and a PCR RE primer (1443-1162) at the 3' end.

[0225] SEQ ID NO: 90 presents example 90 of a designer nirA-promoter-controlled 2-Enoyl-CoA Reductase (10') DNA construct (1561 bp) that includes a PCR FD primer (sequence 1-20), a 231-bp nirA promoter from *Thermosynechococcus elongatus* BP1 (21-251), an enzyme-encoding sequence (252-1421) selected/modified from the sequences of a *Xanthomonas campestris* 2-Enoyl-CoA Reductase (CAP53709), a 120-bp rbcS terminator from BP1 (1422-1541), and a PCR RE primer (1542-1561).

[0226] SEQ ID NO: 91 presents example 91 of a designer nirA-promoter-controlled Acyl-CoA Reductase (11') DNA construct (1747 bp) that includes a PCR FD primer (sequence 1-20), a 231-bp nirA promoter from *Thermosynechococcus elongatus* BP1 (21-251), an enzyme-encoding sequence (252-1607) selected/modified from the sequences of a *Clostridium cellulovorans* Acyl-CoA reductase (YP_003845606), a 120-bp rbcS terminator from BP1 (1608-1727), and a PCR RE primer (1728-1747).

[0227] SEQ ID NO: 92 presents example 92 of a designer nirA-promoter-controlled Hexanol Dehydrogenase (12') DNA construct (1450 bp) that includes a PCR FD primer (sequence 1-20), a 231-bp nirA promoter from *Thermosynechococcus elongatus* BP1 (21-251), an enzyme-encoding sequence (252-1310) selected/modified from the sequences of a *Mycobacterium chubuense* hexanol dehydrogenase (ACZ56328), a 120-bp rbcS terminator from BP1 (1311-1430), and a PCR RE primer (1431-1450).

[0228] SEQ ID NO: 93 presents example 93 of a designer nirA-promoter-controlled Octanol Dehydrogenase (12") DNA construct (1074 bp) that includes a PCR FD primer (sequence 1-20), a 231-bp nirA promoter from *Thermosynechococcus elongatus* BP1 (21-251), an enzyme-encoding sequence (252-934) selected/modified from the sequences of a *Drosophila subobscura* octanol dehydrogenase (ABO65263), a 120-bp rbcS terminator from BP1 (935-1054), and a PCR RE primer (1055-1074) at the 3' end.

[0229] Note, the designer enzymes of SEQ ID NOS: 87-91 have certain broad substrate specificity. Consequently, they can also be used as designer 3-ketothiolase 07", designer 3-hydroxyacyl-CoA dehydrogenase 08", designer enoyl-CoA dehydratase 09", designer 2-enoyl-CoA reductase 10", and designer acyl-CoA reductase 11". Therefore, SEQ ID NOS: 87-91 and 93 represent a set of designer genes that can express another designer hydrocarbon chain elongation pathway for 1-octanol production (07'40' and 07"-12" as shown in FIG. **7**). SEQ ID NO: 93 (encoding for octanol dehydrogenase 12") is one of the key designer genes that enable production of 1-octanol production in this pathway. The net result of this pathway in working with the Calvin cycle are photobiological production of 1-octanol ($CH_3CH_2CH_2CH_2CH_2CH_2CH_2CH_2OH$) from carbon dioxide ($CO_2$) and water ($H_2O$) using photosynthetically generated ATP and NADPH according to the following process reaction:

$$8CO_2+9H_2O\rightarrow CH_3CH_2CH_2CH_2CH_2CH_2CH_2CH_2OH+12O_2 \quad [10]$$

Calvin-Cycle-Channeled Pathways for Production of 1-Pentanol, 1-Hexanol and 1-Heptanol

[0230] According to one of the various embodiments, a designer Calvin-cycle-channeled pathway is created that takes the Calvin-cycle intermediate product, 3-phosphoglycerate, and converts it into 1-pentanol, 1-hexanol, and/or 1-heptanol by using, for example, a set of enzymes consisting of (as shown with the numerical labels 34, 35, 03-05, 36-41, 39, 39'-43', 39'-43', 12', and 39"-43" in FIG. **8**): NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase 34, NAD-dependent glyceraldehyde-3-phosphate dehydrogenase 35, phosphoglycerate mutase 03, enolase 04, pyruvate kinase 05, citramalate synthase 36, 2-methylmalate dehydratase 37, 3-isopropylmalate dehydratase 38, 3-isopropylmalate dehydrogenase 39, 2-isopropylmalate synthase 40, isopropylmalate isomerase 41, 3-isopropylmalate dehydrogenase 39, designer isopropylmalate synthase 40', designer isopropylmalate isomerase 41', designer 3-isopropylmalate dehydrogenase 39', designer 2-keto acid decarboxylase 42', short-chain alcohol dehydrogenase 43', hexanol dehydrogenase 12', designer isopropylmalate synthase 40", designer isopropylmalate isomerase 41", designer 3-isopropylmalate dehydrogenase 39", designer 2-keto acid decarboxylase 42", and designer short-chain alcohol dehydrogenase 43". This designer pathway works with the Calvin cycle using photosynthetically generated ATP and NADPH for photobiological production of 1-pentanol ($CH_3CH_2CH_2CH_2CH_2OH$), 1-hexanol ($CH_3CH_2CH_2CH_2CH_2CH_2OH$), and/or 1-heptanol ($CH_3CH_2CH_2CH_2CH_2CH_2CH_2OH$) from carbon dioxide ($CO_2$) and water ($H_2O$) according to the following process reactions:

$$10CO_2+12H_2O\rightarrow 2CH_3CH_2CH_2CH_2CH_2OH+15O_2 \quad [11]$$

$$6CO_2+7H_2O\rightarrow CH_3CH_2CH_2CH_2CH_2CH_2OH+9O_2 \quad [12]$$

$$14CO_2+16H_2O\rightarrow 2CH_3CH_2CH_2CH_2CH_2CH_2CH_2OH+21O_2 \quad [13]$$

[0231] According to another embodiment, a designer Calvin-cycle-channeled pathway is created that takes the intermediate product, 3-phosphoglycerate, and converts it into 1-pentanol, 1-hexanol, and/or 1-heptanol by using, for example, a set of enzymes consisting of (as shown with the numerical labels 34, 35, 03, 04, 45-52, 40, 41, 39, 39'-43', 39'-43', 12', and 39"-43" in FIG. **8**): NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase 34, NAD-dependent glyceraldehyde-3-phosphate dehydrogenase 35, phosphoglycerate mutase 03, enolase 04, phosphoenolpyruvate carboxylase 45, aspartate aminotransferase 46, aspartokinase 47, aspartate-semialdehyde dehydrogenase 48, homoserine dehydrogenase 49, homoserine kinase 50, threonine synthase 51, threonine ammonia-lyase 52, 2-isopropylmalate synthase 40, isopropylmalate isomerase 41, 3-isopropylmalate dehydrogenase 39, designer isopropylmalate synthase 40', designer isopropylmalate isomerase 41', designer 3-isopro-

pylmalate dehydrogenase 39', designer 2-keto acid decarboxylase 42', short-chain alcohol dehydrogenase 43', hexanol dehydrogenase 12', designer isopropylmalate synthase 40", designer isopropylmalate isomerase 41", designer 3-isopropylmalate dehydrogenase 39", designer 2-keto acid decarboxylase 42", and designer short-chain alcohol dehydrogenase 43".

[0232] These pathways (FIG. **8**) share a common feature of using an NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase 34 and an NAD-dependent glyceraldehyde-3-phosphate dehydrogenase 35 as a mechanism for NADPH/NADH conversion to drive production of 1-pentanol, 1-hexanol, and/or 1-heptanol through a designer Calvin-cycle-channeled pathway in combination with a designer hydrocarbon chain elongation pathway (40', 41', 39'). This embodiment also takes the advantage of the broad substrate specificity (promiscuity) of 2-isopropylmalate synthase 40, isopropylmalate isomerase 41, 3-isopropylmalate dehydrogenase 39, 2-keto acid decarboxylase 42, and short-chain alcohol dehydrogenase 43 so that they can be used also as: designer isopropylmalate synthase 40', designer isopropylmalate isomerase 41', designer 3-isopropylmalate dehydrogenase 39', designer 2-keto acid decarboxylase 42', and short-chain alcohol dehydrogenase 43'; isopropylmalate synthase 40", designer isopropylmalate isomerase 41", designer 3-isopropylmalate dehydrogenase 39", designer 2-keto acid decarboxylase 42", and designer short-chain alcohol dehydrogenase 43".

[0233] In this case, proper selection of a short-chain alcohol dehydrogenase with certain promiscuity is also essential. SEQ ID NO: 94 presents example 94 of a designer nirA-promoter-controlled Short Chain Alcohol Dehydrogenase DNA construct (1096 bp) that includes a PCR FD primer (sequence 1-20), a 231-bp nirA promoter from *Thermosynechococcus elongatus* BP1 (21-251), an enzyme-encoding sequence (252-956) selected/modified from the sequences of a *Pyrococcus furiosus* DSM 3638 Short chain alcohol dehydrogenase (AAC25556), a 120-bp rbcS terminator from BP1 (957-1076), and a PCR RE primer (1077-1096) at the 3' end.

[0234] Therefore, SEQ ID NOS: 58-69 and 94 represent a set of designer genes that can express a designer Calvin-cycle 3-phosphoglycerate-braned photosynthetic NADPH-enhanced pathway for production of 1-pentanol, 1-hexanol, and/or 1-heptanol as shown with numerical labels 34, 35, 03-05, 36-41, 39, 39'-43', 39'-43', 39"-43" in FIG. **8**. Similarly, SEQ ID NOS: 58-61, 74-81, 66-69, and 94 represent another set of sample designer genes that can express another Calvin-cycle 3-phophoglycerate-branched NADPH-enhanced pathway for production of 1-pentanol, 1-hexanol, and/or 1-heptanol as numerically labeled as 34, 35, 03, 04, 45-52, 40, 41, 39, 39'-43', 39'-43', 39"-43" in FIG. **8**. Note, both of these two pathways produce alcohol mixtures with different chain lengths rather than single alcohols since all 2-keto acids (such as 2-ketohexanoate, 2-ketaheptanoate, and 2-ketooctanoate) can be converted to alcohol because of the use of the promiscuity of designer 2-keto acid decarboxylase 42' and designer short-chain alcohol dehydrogenase 43'.

[0235] To improve product specificity, it is a preferred practice to use substrate specific designer enzymes. For example, use of substrate specific designer 1-hexanol dehydrogenase 12' (SEQ ID NO: 92) instead of short-chain alcohol dehydrogenase with promiscuity (43') can improve product specificity more toward 1-hexanol. Consequently, SEQ ID NOS: 58-69 and 92 represent a set of designer genes that can express a designer Calvin-cycle 3-phosphoglycerate-braned photosynthetic NADPH-enhanced pathway for production of 1-hexanol as shown with numerical labels 34, 35, 03-05, 36-41, 39, 39'-40', 39'-42' and 12' in FIG. **8**.

Designer Calvin-Cycle-Channeled Pathways for Production of 3-Methyl-1-Pentanol, 4-Methyl-1-Hexanol, and 5-Methyl-1-Heptanol

[0236] According to one of the various embodiments, a designer Calvin-cycle-channeled pathway is created that takes the Calvin-cycle intermediate product, 3-phosphoglycerate, and converts it into 3-methyl-1-pentanol, 4-methyl-1-hexanol, and/or 5-methyl-1-heptanol by using, for example, a set of enzymes consisting of (as shown with the numerical labels 34, 35, 03-05, 36-39, 53-55, 39'-43', 39'-43', and 39"-43" in FIG. **9**): NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase 34, NAD-dependent glyceraldehyde-3-phosphate dehydrogenase 35, phosphoglycerate mutase 03, enolase 04, pyruvate kinase 05, citramalate synthase 36, 2-methylmalate dehydratase 37, 3-isopropylmalate dehydratase 38, 3-isopropylmalate dehydrogenase 39, acetolactate synthase 53, ketol-acid reductoisomerase 54, dihydroxy-acid dehydratase 55, designer isopropylmalate synthase 40', designer isopropylmalate isomerase 41', designer 3-isopropylmalate dehydrogenase 39', designer 2-keto acid decarboxylase 42', short-chain alcohol dehydrogenase 43', designer isopropylmalate synthase 40", designer isopropylmalate isomerase 41", designer 3-isopropylmalate dehydrogenase 39", designer 2-keto acid decarboxylase 42", and designer short-chain alcohol dehydrogenase 43".

[0237] According to another embodiment, a designer Calvin-cycle-channeled pathway is created that takes the intermediate product, 3-phosphoglycerate, and converts it into 3-methyl-1-pentanol, 4-methyl-1-hexanol, and/or 5-methyl-1-heptanol by using, for example, a set of enzymes consisting of (as shown with the numerical labels 34, 35, 03, 04, 45-55, 39'-43', 39'-43', and 39"-43" in FIG. **9**): NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase 34, NAD-dependent glyceraldehyde-3-phosphate dehydrogenase 35, phosphoglycerate mutase 03, enolase 04, phosphoenolpyruvate carboxylase 45, aspartate aminotransferase 46, aspartokinase 47, aspartate-semialdehyde dehydrogenase 48, homoserine dehydrogenase 49, homoserine kinase 50, threonine synthase 51, threonine ammonia-lyase 52, acetolactate synthase 53, ketol-acid reductoisomerase 54, dihydroxy-acid dehydratase 55, designer isopropylmalate synthase 40', designer isopropylmalate isomerase 41', designer 3-isopropylmalate dehydrogenase 39', designer 2-keto acid decarboxylase 42', short-chain alcohol dehydrogenase 43', designer isopropylmalate synthase 40", designer isopropylmalate isomerase 41", designer 3-isopropylmalate dehydrogenase 39", designer 2-keto acid decarboxylase 42", and designer short-chain alcohol dehydrogenase 43".

[0238] These pathways (FIG. **9**) are similar to those of FIG. **8**, except they use acetolactate synthase 53, ketol-acid reductoisomerase 54, dihydroxy-acid dehydratase 55 as part of the pathways for production of 3-methyl-1-pentanol, 4-methyl-1-hexanol, and/or 5-methyl-1-heptanol. They all share a common feature of using an NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase 34 and an NAD-dependent glyceraldehyde-3-phosphate dehydrogenase 35 as a mechanism for NADPH/NADH conversion to drive production of 3-methyl-1-pentanol, 4-methyl-1-hexanol, and/or 5-methyl-1-heptanol through a designer Calvin-cycle-channeled path-

way in combination with a hydrocarbon chain elongation pathway (40', 41', 39'). This embodiment also takes the advantage of the broad substrate specificity (promiscuity) of 2-isopropylmalate synthase 40, isopropylmalate isomerase 41, 3-isopropylmalate dehydrogenase 39, 2-keto acid decarboxylase 42, and short-chain alcohol dehydrogenase 43 so that they can also serve as: designer isopropylmalate synthase 40', designer isopropylmalate isomerase 41', designer 3-isopropylmalate dehydrogenase 39', designer 2-keto acid decarboxylase 42', and short-chain alcohol dehydrogenase 43'; designer isopropylmalate synthase 40", designer isopropylmalate isomerase 41", designer 3-isopropylmalate dehydrogenase 39", designer 2-keto acid decarboxylase 42", and designer short-chain alcohol dehydrogenase 43".

[0239] Therefore, SEQ ID NOS: 58-69, 82-84, and 94 represent a set of designer genes that can express a designer Calvin-cycle 3-phosphoglycerate-braned photosynthetic NADPH-enhanced pathway for production of 3-methyl-1-pentanol, 4-methyl-1-hexanol, and 5-methyl-1-heptanol as shown with numerical labels 34, 35, 03-05, 36-39, 53-55, 39'-43', 39'-43', and 39"-43" in FIG. **9**. Similarly, SEQ ID NOS: 58-61, 74-81, 82-84, 66-69, and 94 represent another set of sample designer genes that can express another Calvin-cycle 3-phophoglycerate-branched NADPH-enhanced pathway for production of 3-methyl-1-pentanol, 4-methyl-1-hexanol, and/or 5-methyl-1-heptanol as numerically labeled as 34, 35, 03, 04, 45-55, 39'-43', 39'-43', 39"-43" in FIG. **9**. The net results of the designer photosynthetic NADPH-enhanced pathways in working with the Calvin cycle are production of 3-methyl-1-pentanol ($CH_3CH_2CH(CH_3)CH_2CH_2OH$), 4-methyl-1-hexanol ($CH_3CH_2CH(CH_3)CH_2CH_2CH_2OH$), and 5-methyl-1-heptanol($CH_3CH_2CH(CH_3)CH_2CH_2CH_2CH_2OH$) from carbon dioxide ($CO_2$) and water ($H_2O$) using photosynthetically generated ATP and NADPH according to the following process reactions:

$$6CO_2+7H_2O\rightarrow CH_3CH_2CH(CH_3)CH_2CH_2OH+9O_2 \quad [14]$$

$$14CO_2+16H_2O\rightarrow 2CH_3CH_2CH(CH_3)CH_2CH_2CH_2OH+21O_2 \quad [15]$$

$$8CO_2+9H_2O\rightarrow CH_3CH_2CH(CH_3)CH_2CH_2CH_2CH_2OH+12O_2 \quad [16]$$

Designer Calvin-Cycle-Channeled Pathways for Production of 4-Methyl-1-Pentanol, 5-Methyl-1-Hexanol, and 6-Methyl-1-Heptanol

[0240] According to one of the various embodiments, a designer Calvin-cycle-channeled pathway is created that takes the Calvin-cycle intermediate product, 3-phosphoglycerate, and converts it into 4-methyl-1-pentanol, 5-methyl-1-hexanol, and 6-methyl-1-heptanol by using, for example, a set of enzymes consisting of (as shown with the numerical labels 34, 35, 03-05, 53-55, 40, 38, 39, 39'-43', 39'-43', and 39"-43" in FIG. **10**): NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase 34, NAD-dependent glyceraldehyde-3-phosphate dehydrogenase 35, phosphoglycerate mutase 03, enolase 04, pyruvate kinase 05, acetolactate synthase 53, ketol-acid reductoisomerase 54, dihydroxy-acid dehydratase 55, isopropylmalate synthase 40, dehydratase 38, 3-isopropylmalate dehydrogenase 39, designer isopropylmalate synthase 40', designer isopropylmalate isomerase 41', designer 3-isopropylmalate dehydrogenase 39', designer 2-keto acid decarboxylase 42', short-chain alcohol dehydrogenase 43', designer isopropylmalate synthase 40", designer isopropylmalate isomerase 41", designer 3-isopropylmalate dehydrogenase 39", designer 2-keto acid decarboxylase 42", and designer short-chain alcohol dehydrogenase 43".

[0241] This pathway (FIG. **10**) is similar to those of FIG. **8**, except that it does not use citramalate synthase 36 and 2-methylmalate dehydratase 37, but uses acetolactate synthase 53, ketol-acid reductoisomerase 54, dihydroxy-acid dehydratase 55 as part of the pathways for production of 4-methyl-1-pentano-1,5-methyl-1-hexanol, and/or 6-methyl-1-heptanol. They all share a common feature of using an NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase 34 and an NAD-dependent glyceraldehyde-3-phosphate dehydrogenase 35 as a mechanism for NADPH/NADH conversion to drive production of 3-methyl-1-butanol, 4-methyl-1-butanol, and 5-methyl-1-butanol through a Calvin-cycle-channeled pathway in combination with a designer hydrocarbon chain elongation pathway (40', 41', 39'). This embodiment also takes the advantage of the broad substrate specificity (promiscuity) of 2-isopropylmalate synthase 40, isopropylmalate isomerase 41, 3-isopropylmalate dehydrogenase 39, 2-keto acid decarboxylase 42, and short-chain alcohol dehydrogenase 43 so that they may also serve as: designer isopropylmalate synthase 40', designer isopropylmalate isomerase 41', designer 3-isopropylmalate dehydrogenase 39', designer 2-keto acid decarboxylase 42', and short-chain alcohol dehydrogenase 43', designer isopropylmalate synthase 40", designer isopropylmalate isomerase 41", designer 3-isopropylmalate dehydrogenase 39", designer 2-keto acid decarboxylase 42", and designer short-chain alcohol dehydrogenase 43".

[0242] Therefore, SEQ ID NOS: 58-62, 82-84, 65-69 and 94 represent a set of sample designer genes that can be used to express a designer Calvin-cycle 3-phosphoglycerate-braned photosynthetic NADPH-enhanced pathway for production of 4-methyl-1-pentanol, 5-methyl-1-hexanol, and/or 6-methyl-1-heptanol as shown with numerical labels 34, 35, 03-05, 53-55, 40, 38, 39, 39'-43', 39'-43', and 39"-43" in FIG. **10**. The net results of the designer photosynthetic NADPH-enhanced pathway in working with the Calvin cycle are production of 4-methyl-1-pentanol ($CH_3CH(CH_3)CH_2CH_2CH_2OH$), 5-methyl-1-hexanol ($CH_3CH(CH_3)CH_2CH_2CH_2CH_2OH$), and 6-methyl-1-heptanol ($CH_3CH(CH_3)CH_2CH_2CH_2CH_2CH_2OH$) from carbon dioxide ($CO_2$) and water ($H_2O$) using photosynthetically generated ATP and NADPH according to the following process reactions:

$$6CO_2+7H_2O\rightarrow CH_3CH(CH_3)CH_2CH_2CH_2OH+9O_2 \quad [17]$$

$$14CO_2+16H_2O\rightarrow 2CH_3CH(CH_3)CH_2CH_2CH_2CH_2OH+21O_2 \quad [18]$$

$$8CO_2+9H_2O\rightarrow CH_3CH(CH_3)CH_2CH_2CH_2CH_2CH_2OH+12O_2 \quad [19]$$

Designer Oxyphotobacteria with Calvin-Cycle-Channeled Pathways for Production of Butanol and Related Higher Alcohols

[0243] According to one of the various embodiments, use of designer DNA constructs in genetic transform of certain oxyphotobacteria hosts can create various designer transgenic oxyphotobacteria with Calvin-cycle-channeled pathways for photobiological production of butanol and related higher alcohols from carbon dioxide and water. To ensure biosafety for use of the designer transgenic photosynthetic organism-based biofuels production technology, it is a preferred practice to incorporate biosafety-guarded features into

the designer transgenic photosynthetic organisms as well. Therefore, in accordance with the present invention, various designer photosynthetic organisms including designer transgenic oxyphotobacteria are created with a biosafety-guarded photobiological biofuel-production technology based on cell-division-controllable designer transgenic photosynthetic organisms. The cell-division-controllable designer photosynthetic organisms contain two key functions: a designer biosafety mechanism(s) and a designer biofuel-production pathway(s). The designer biosafety feature(s) is conferred by a number of mechanisms including: a) the inducible insertion of designer proton-channels into cytoplasm membrane to permanently disable any cell division and/or mating capability, b) the selective application of designer cell-division-cycle regulatory protein or interference RNA (iRNA) to permanently inhibit the cell division cycle and preferably keep the cell at the G_1 phase or G_0 state, and c) the innovative use of a high-CO_2-requiring host photosynthetic organism for expression of the designer biofuel-production pathway(s). The designer cell-division-control technology can help ensure biosafety in using the designer organisms for biofuel production.

[0244] Oxyphotobacteria (including cyanobacteria and oxychlorobacteria) that can be selected for use as host organisms to create designer transgenic oxyphotobacteria for photobiological production of butanol and related higher alcohols include (but not limited to): *Thermosynechococcus elongatus* BP-1, *Nostoc* sp. PCC 7120, *Synechococcus elongatus* PCC 6301, *Syncechococcus* sp. strain PCC 7942, *Syncechococcus* sp. strain PCC 7002, *Syncechocystis* sp. strain PCC 6803, *Prochlorococcus marinus* MED4, *Prochlorococcus marinus* MIT 9313, *Prochlorococcus marinus* NATL1A, *Prochlorococcus* SS120, *Spirulina platensis* (*Arthrospira platensis*), *Spirulina pacifica, Lyngbya majuscule, Anabaena* sp., *Synechocystis* sp., *Synechococcus elongates, Synechococcus* (MC-A), *Trichodesmium* sp., *Richelia intracellularis, Synechococcus* WH7803, *Synechococcus* WH8102, *Nostoc punctiforme, Syncechococcus* sp. strain PCC 7943, Synechocyitis PCC 6714 phycocyanin-deficient mutant PD-1, *Cyanothece* strain 51142, *Cyanothece* sp. CCY0110, *Oscillatoria limosa, Lyngbya majuscula, Symploca muscorum, Gloeobacter violaceus, Prochloron didemni, Prochlorothrix hollandica, Prochlorococcus marinus, Prochlorococcus* SS120, *Synechococcus* WH8102, *Lyngbya majuscula, Symploca muscorum, Synechococcus bigranulatus*, cryophilic *Oscillatoria* sp., *Phormidium* sp., *Nostoc* sp.-1, *Calothrix parietina*, thermophilic *Synechococcus bigranulatus, Synechococcus lividus*, thermophilic *Mastigocladus laminosus, Chlorogloeopsis fritschii* PCC 6912, *Synechococcus vulcanus, Synechococcus* sp. strain MA4, *Synechococcus* sp. strain MA19, and *Thermosynechococcus elongatus*.

[0245] According to one of the examples, use of designer DNA constructs such as SEQ ID NOS: 58-94 in genetic transform of certain oxyphotobacteria hosts such as *Thermosynechococcus elongatus* BP1 can create a series of designer transgenic oxyphotobacteria with Calvin-cycle-channeled pathways for production of butanol and related higher alcohols. Consequently, SEQ ID NOS: 58-61, 74-81, 66-69, and 72 (and/or 73) represent a designer transgenic oxyphotobacterium such as a designer transgenic *Thermosynechococcus* that comprises the designer genes of a Calvin-cycle 3-phophoglycerate-branched photosynthetic NADPH-enhanced pathway (numerically labeled as 34, 35, 03, 04, 45-52, 39-42, and 12 in FIG. **4**) for photobiological production of 1-butanol from carbon dioxide and water. SEQ ID NOS: 58-69 and 72 (and/or 73) represent another designer transgenic oxyphotobacterium such as designer transgenic *Thermosynechococcus* that comprises the designer genes of a Calvin-cycle 3-phophoglycerate-branched photosynthetic NADPH-enhanced pathway (numerically labeled as 34, 35, 03-05, 36-42, and 12 in FIG. **4**) for photobiological production of 1-butanol from carbon dioxide and water as well.

[0246] Similarly, SEQ ID NOS: 58-66, 82-84, 69 and 85 represent another designer transgenic oxyphotobacterium such as designer transgenic *Thermosynechococcus* with a Calvin-cycle 3-phophoglycerate-branched photosynthetic NADPH-enhanced pathway (numerically labeled as 34, 35, 03-05, 36-39, 53-55, 42 and 56 in FIG. **5**) for photobiological production of 2-methyl-1-butanol production from carbon dioxide and water; while SEQ ID NOS: 58-61, 74-84, 69 and 85 represent another designer transgenic *Thermosynechococcus* with a Calvin-cycle 3-phophoglycerate-branched photosynthetic NADPH-enhanced 2-methyl-1-butanol production pathway (34, 35, 03, 04, 45-55, 42 and 56 in FIG. **5**) for photobiological production of 2-methyl-1-butanol production from carbon dioxide and water.

[0247] SEQ ID NOS: 58-63, 82-84, 69, 70 (or 71) represent another designer transgenic oxyphotobacterium such as designer transgenic *Thermosynechococcus* with a Calvin-cycle 3-phosphoglycerate-branched photosynthetic NADPH-enhanced isobutanol production pathway (34, 35, 03-05, 53-5, 42, 43 or 44); while SEQ ID NOS: 58-62, 81-83, 65-67, 69 and 86 represent another designer transgenic *Thermosynechococcus* with a Calvin-cycle 3-phosphoglycerate-branched photosynthetic NADPH-enhanced 3-methyl-1-butanol production pathway (numerical labels 34, 35, 03-05, 53-55, 40, 38, 39, 42, and 57 in FIG. **6**).

[0248] SEQ ID NOS: 87-92 represent another designer transgenic *Thermosynechococcus* with a designer hydrocarbon chain elongation pathway (07'-12' as shown in FIG. **7**) for photobiological production of 1-hexanol. SEQ ID NOS: 87-91 and 93 represent another designer transgenic *Thermosynechococcus* with a designer hydrocarbon chain elongation pathway (07'-10' and 07"-12" as shown in FIG. **7**) for photobiological production of 1-octanol.

[0249] SEQ ID NOS: 58-69 and 92 represent another designer transgenic *Thermosynechococcus* with a designer Calvin-cycle 3-phosphoglycerate-braned photosynthetic NADPH-enhanced pathway (34, 35, 03-05, 36-41, 39, 39'-40', 39'-42' and 12' in FIG. **8**) for photobiological production of 1-hexanol from carbon dioxide and water.

[0250] SEQ ID NOS: 58-69, 82-84, and 94 represent a designer transgenic *Thermosynechococcus* with a designer Calvin-cycle 3-phosphoglycerate-braned photosynthetic NADPH-enhanced pathway (34, 35, 03-05, 36-39, 53-55, 39'-43', 39'-43', 39"-43" in FIG. **9**) for production of 3-methyl-1-pentanol, 4-methyl-1-hexanol, and 5-methyl-1-heptanol from carbon dioxide and water. Similarly, SEQ ID NOS: 58-61, 74-81, 82-84, 66-69, and 94 represent another designer transgenic *Thermosynechococcus* with a Calvin-cycle 3-phophoglycerate-branched NADPH-enhanced pathway (34, 35, 03, 04, 45-55, 39'-43', 39'-43', 39"-43" in FIG. **9**) for photobiological production of 3-methyl-1-pentanol, 4-methyl-1-hexanol, and 5-methyl-1-heptanol from carbon dioxide and water as well.

[0251] SEQ ID NOS: 58-62, 82-84, 65-69 and 94 represent a designer transgenic *Thermosynechococcus* with a designer Calvin-cycle 3-phosphoglycerate-braned photosynthetic

NADPH-enhanced pathway labels (34, 35, 03-05, 53-55, 40, 38, 39, 39'-43', 39'-43', and 39"-43" in FIG. **10**) for photobiological production of 4-methyl-1-pentanol, 5-methyl-1-hexanol, and/or 6-methyl-1-heptanol from carbon dioxide and water.

[0252] Use of other host oxyphotobacteria such as *Synechococcus* sp. strain PCC 7942, *Synechocystis* sp. strain PCC 6803, *Prochlorococcus marinus, Cyanothece* sp. ATCC 51142, for genetic transformation with proper designer DNA constructs (genes) can create other designer oxyphotobacteria for photobiological production of butanol and higher alcohols as well. For example, use of *Synechococcus* sp. strain PCC 7942 as a host organism in genetic transformation with SEQ ID NOS: 95-98 (and/or 99) can create a designer transgenic *Synechococcus* for photobiological production of 1-butanol. Briefly, SEQ ID NO: 95 presents example 95 of a detailed DNA construct (1438 base pairs (bp)) of a designer NADPH-dependent Glyceraldehyde-3-Phosphate-Dehydrogenase (34) gene that includes a PCR FD primer (sequence by 1-20), a 88-bp nirA promoter (21-108) selected from the *Synechococcus* sp. strain PCC 7942 (freshwater cyanobacterium) nitrite-reductase-gene promoter sequence, an enzyme-encoding sequence (109-1110) selected and modified from a *Staphylococcus* NADPH-dependent glyceraldehyde-3-phosphate-dehydrogenase sequence (GenBank accession number: YP_003471459), a 308-bp *Synechococcus* rbcS terminator (1111-1418), and a PCR RE primer (1419-1438).

[0253] SEQ ID NO: 96 presents example 96 of a detailed DNA construct (1447 bp) of a designer NAD-dependent Glyceraldehyde-3-Phosphate-Dehydrogenase (35) gene that includes a PCR FD primer (sequence by 1-20), a 88-bp nirA promoter (21-108) selected from the *Synechococcus* nitrite-reductase-gene promoter sequence, an enzyme-encoding sequence (109-1119) selected from a *Staphylococcus aureus* NAD-dependent glyceraldehyde-3-phosphate-dehydrogenase sequence (GenBank accession number: ADC36961), a 308-bp *Synechococcus* rbcS terminator (1120-1427), and a PCR RE primer (1428-1447).

[0254] SEQ ID NO: 97 presents example 97 of a detailed DNA construct (2080 bp) of a designer 2-Keto Acid Decarboxylase (42) gene that includes a PCR FD primer (sequence by 1-20), a 88-bp nirA promoter (21-108) selected from the *Synechococcus* nitrite-reductase-gene promoter sequence, an enzyme-encoding sequence (109-1752) selected from a *Lactococcus lactis* branched-chain alpha-ketoacid decarboxylase (GenBank accession number: AAS49166), a 308-bp *Synechococcus* rbcS terminator (1753-2060), and a PCR RE primer (2061-2080).

[0255] SEQ ID NO: 98 presents a detailed DNA construct (1603 bp) of a designer NADH-dependent butanol dehydrogenase (12a) gene that include a PCR FD primer (sequence by 1-20), a 88-bp nirA promoter (21-108) selected from the *Synechococcus* nitrite-reductase-gene promoter sequence, an enzyme-encoding sequence (109-1275) selected from a *Clostridium* NADH-dependent butanol dehydrogenase (GenBank accession number: ADO12118), a 308-bp *Synechococcus* rbcS terminator (1276-1583), and a PCR RE primer (1584-1603).

[0256] SEQ ID NO: 99 presents example 99 of a detailed DNA construct (1654 bp) of a designer NADPH-dependent Butanol Dehydrogenase (12b) gene including: a PCR FD primer (sequence by 1-20), a 88-bp nirA promoter (21-108) selected from the *Synechococcus* nitrite-reductase-gene promoter sequence, an enzyme-encoding sequence (109-1326) selected from a *Butyrivibrio* NADPH-dependent butanol dehydrogenase (GenBank: EFF67629), a 308-bp *Synechococcus* rbcS terminator (1327-1634), and a PCR RE primer (1635-1654).

[0257] Note, in the designer transgenic *Synechococcus* that is represented by SEQ ID NOS: 95-98 (and/or 99), *Synechococcus*'s native enzymes of 03-05, 36-41 and 45-52 are used in combination with the designer nirA-promoter-controlled enzymes of 34, 35, 42 and 12 [encoded by SEQ ID NOS: 95-98 (and/or 99)] to confer the Calvin-cycle 3-phophoglycerate-branched photosynthetic NADPH-enhanced pathways for photobiological production of 1-butanol from carbon dioxide and water (FIG. **4**).

[0258] Similarly, use of *Synechocystis* sp. strain PCC 6803 as a host organism in genetic transformation with SEQ ID NOS: 100-102 (and/or 103) creates a designer transgenic *Synechocystis* for photobiological production of 1-butanol. Briefly, SEQ ID NO: 100 presents example 100 of a designer nirA-promoter-controlled NAD-dependent Glyceraldehyde-3-Phosphate Dehydrogenase (35) DNA construct (1440 bp) that includes a PCR FD primer (sequence 1-20), a 89-bp *Synechocystis* sp. strain PCC 6803 nitrite-reductase nirA promoter (21-109), an enzyme-encoding sequence (110-1011) selected from a *Streptococcus pyogenes* NAD-dependent Glyceraldehyde-3-phosphate dehydrogenase (GenBank: YP_002285269), a 409-bp *Synechocystis* sp. PCC 6803 rbcS terminator (1012-1420), and a PCR RE primer (1421-1440).

[0259] SEQ ID NO: 101 presents example 101 of a designer nirA-promoter-controlled 2-Keto Acid Decarboxylase (42) DNA construct (2182 bp) that includes a PCR FD primer (sequence 1-20), a 89-bp *Synechocystis* sp. strain PCC 6803 nitrite-reductase nirA promoter (21-109), an enzyme-encoding sequence (110-1753) selected from a *Lactococcus lactis* branched-chain alpha-ketoacid decarboxylase (GenBank: AAS49166), a 409-bp *Synechocystis* sp. PCC 6803 rbcS terminator (1754-2162), and a PCR RE primer (2163-2182).

[0260] SEQ ID NO: 102 presents example 102 of a designer nirA-promoter-controlled NADH-dependent Butanol Dehydrogenase (12a) DNA construct (1705 bp) that includes a PCR FD primer (sequence 1-20), a 89-bp *Synechocystis* sp. strain PCC 6803 nitrite-reductase nirA promoter (21-109), an enzyme-encoding sequence (110-1276) selected from a *Clostridium carboxidivorans* P7 NADH-dependent butanol dehydrogenase (GenBank: ADO12118), a 409-bp *Synechocystis* sp. PCC 6803 rbcS terminator (1277-1685), and a PCR RE primer (1686-1705).

[0261] SEQ ID NO: 103 presents example 103 of a designer nirA-promoter-controlled NADPH-dependent butanol dehydrogenase (12b) DNA construct (1756 bp) that includes a PCR FD primer (sequence 1-20), a 89-bp *Synechocystis* sp. strain PCC 6803 nitrite-reductase nirA promoter (21-109), an enzyme-encoding sequence (110-1327) selected from a *Butyrivibrio crossotus* NADPH-dependent butanol dehydrogenase (GenBank: EFF67629), a 409-bp *Synechocystis* sp. PCC 6803 rbcS terminator (1328-1736), and a PCR RE primer (1737-1756).

[0262] Note, in the designer transgenic *Synechocystis* that contains the designer genes of SEQ ID NOS: 100-102 (and/or 103), *Synechocystis*'s native enzymes of 34, 03-05, 36-41 and 45-52 are used in conjunction with the designer nirA-promoter-controlled enzymes of 35, 42 and 12 [encoded by SEQ ID NOS: 100-102 (and/or 103)] to confer the Calvin-cycle 3-phophoglycerate-branched photosynthetic NADPH-en-

hanced pathways for photobiological production of 1-butanol from carbon dioxide and water (FIG. **4**).

[0263] Use of *Nostoc* sp. strain PCC 7120 as a host organism in genetic transformation with SEQ ID NOS: 104-109 can create a designer transgenic *Nostoc* for photobiological production of 2-methyl-1-butanol (FIG. **5**). Briefly, SEQ ID NO: 104 presents example 104 of a designer hox-promoter-controlled NAD-dependent Glyceraldehyde-3-Phosphate Dehydrogenase (35) DNA construct (1655 bp) that includes a PCR FD primer (sequence 1-20), a 172-bp *Nostoc* sp. strain PCC 7120 (*Anabaena* PCC 7120) hox promoter (21-192), an enzyme-encoding sequence (193-1203) selected/modified from the sequence of a *Streptococcus pyogenes* NZ131 NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (GenBank: YP_002285269), a 432-bp *Nostoc* sp. strain PCC 7120 gor terminator (1204-1635), and a PCR RE primer (1636-1655).

[0264] SEQ ID NO: 105 presents example 105 of a designer hox-promoter-controlled Acetolactate Synthase (53) DNA construct (2303 bp) that includes a PCR FD primer (sequence 1-20), a 172-bp *Nostoc* sp. strain PCC 7120 (*Anabaena* PCC 7120) hox promoter (21-192), an enzyme-encoding sequence (193-1851) selected/modified from the sequence of a *Thermosynechococcus elongatus* BP-1 acetolactate synthase (GenBank: NP_682614), a 432-bp *Nostoc* sp. strain PCC 7120 gor terminator (1852-2283), and a PCR RE primer (2284-2303).

[0265] SEQ ID NO: 106 presents example 106 of a designer hox-promoter-controlled Ketol-Acid Reductoisomerase (54) DNA construct (1661 bp) that includes a PCR FD primer (sequence 1-20), a 172-bp *Nostoc* sp. strain PCC 7120 (*Anabaena* PCC 7120) hox promoter (21-192), an enzyme-encoding sequence (193-1209) selected/modified from the sequence of a *Calditerrivibrio nitroreducens* ketol-acid reductoisomerase (GenBank: YP_004050904), a 432-bp *Nostoc* sp. gor terminator (1210-1641), and a PCR RE primer (1642-1661).

[0266] SEQ ID NO: 107 presents example 107 of a designer hox-promoter-controlled Dihydroxy-Acid Dehydratase (55) DNA construct (2324 bp) that includes a PCR FD primer (sequence 1-20), a 172-bp *Nostoc* sp. strain PCC 7120 (*Anabaena* PCC 7120) hox promoter (21-192), an enzyme-encoding sequence (193-1872) selected/modified from the sequence of a *Marivirga tractuosa* DSM 4126 dihydroxy-acid dehydratase (GenBank: YP_004053736), a 432-bp *Nostoc* sp. gor terminator (1873-2304), and a PCR RE primer (2305-2324).

[0267] SEQ ID NO: 108 presents example 108 of a designer hox-promoter-controlled branched-chain alpha-Ketoacid Decarboxylase (42) DNA construct (2288 bp) that includes a PCR FD primer (sequence 1-20), a 172-bp *Nostoc* sp. (*Anabaena* PCC 7120) hox promoter (21-192), an enzyme-encoding sequence (193-1836) selected/modified from the sequence of a *Lactococcus lactis* branched-chain alpha-ketoacid decarboxylase (GenBank: AAS49166), a 432-bp *Nostoc* sp. gor terminator (1837-2268), and a PCR RE primer (2269-2288).

[0268] SEQ ID NO: 109 presents example 109 of a designer hox-promoter-controlled 2-Methylbutyraldehyde Reductase (56) DNA construct (1613 bp) that includes a PCR FD primer (sequence 1-20), a 172-bp *Nostoc* sp. (*Anabaena* PCC 7120) hox promoter (21-192), an enzyme-encoding sequence (193-1461) selected/modified from the sequence of a *Schizosaccharomyces japonicus* y 2-methylbutyraldehyde reductase (GenBank: XP_002173231), a 432-bp *Nostoc* sp. strain PCC 7120 gor terminator (1462-1893), and a PCR RE primer (1894-1613).

[0269] Note, in the designer transgenic *Nostoc* that contains designer hox-promoter-controlled genes of SEQ ID NOS: 104-109, *Nostoc*'s native enzymes (genes) of 34, 03-05, 36-39 and 45-52 are used in combination with the designer hox-promoter-controlled enzymes of 35, 53-55, 42 and 56 (encoded by DNA constructs of SEQ ID NOS: 104-109) to confer the Calvin-cycle 3-phophoglycerate-branched photosynthetic NADPH-enhanced pathways for photobiological production of 2-methyl-1-butanol from carbon dioxide and water (FIG. **5**).

[0270] Use of *Prochlorococcus marinus* MIT 9313 as a host organism in genetic transformation with SEQ ID NOS: 110-122 can create a designer transgenic *Prochlorococcus marinus* for photobiological production of isobutanol and/or 3-methyl-1-butanol (FIG. **6**). Briefly, SEQ ID NO:110 presents example 110 for a designer groE-promoter-controlled NAD-dependent Glyceraldehyde-3-Phosphate Dehydrogenase (35) DNA construct (1300 bp) that includes a PCR FD primer (sequence 1-20), a 137-bp *Prochlorococcus marinus* MIT 9313 heat- and light-responsive groE promoter (21-157), an enzyme-encoding sequence (158-1159) selected from a *Vibrio cholerae* MJ-1236 NAD-dependent Glyceraldehyde-3-phosphate dehydrogenase (GenBank: ACQ61431), a 121-bp *Prochlorococcus marinus* MIT9313 rbcS terminator (1160-1280), and a PCR RE primer (1281-1300).

[0271] SEQ ID NO:111 presents example 111 for a designer groE-promoter-controlled Phosphoglycerate Mutase (03) DNA construct (1498 bp) that includes a PCR FD primer (sequence 1-20), a 137-bp *Prochlorococcus marinus* MIT9313 heat- and light-responsive groE promoter (21-157), an enzyme-encoding sequence (158-1357) selected from a *Pelotomaculum thermopropionicum* SI phosphoglycerate mutase (GenBank: YP_001212148), a 121-bp *Prochlorococcus marinus* rbcS terminator (1358-1478), and a PCR RE primer (1479-1498).

[0272] SEQ ID NO:112 presents example 112 for a designer groE-promoter-controlled Enolase (04) DNA construct (1588 bp) that includes a PCR FD primer (sequence 1-20), a 137-bp *Prochlorococcus* heat- and light-responsive groE promoter (21-157), an enzyme-encoding sequence (158-1447) selected from a *Thermotoga* enolase (GenBank: ABQ46079), a 121-bp *Prochlorococcus marinus* rbcS terminator (1448-1568), and a PCR RE primer (1569-1588).

[0273] SEQ ID NO:113 presents example 113 for a designer groE-promoter-controlled Pyruvate Kinase (05) DNA construct (1717 bp) that includes a PCR FD primer (sequence 1-20), a 137-bp *Prochlorococcus marinus* MIT9313 heat- and light-responsive groE promoter (21-157), an enzyme-encoding sequence (158-1576) selected from a *Thermotoga lettingae* TMO pyruvate kinase (GenBank: YP_001471580), a 121-bp *Prochlorococcus marinus* MIT9313 rbcS terminator (1577-1697), and a PCR RE primer (1698-1717).

[0274] SEQ ID NO:114 presents example 114 for a designer groE-promoter-controlled Acetolactate Synthase (53) DNA construct (2017 bp) that includes a PCR FD primer (sequence 1-20), a 137-bp *Prochlorococcus marinus* MIT 9313 heat- and light-responsive groE promoter (21-157), an enzyme-encoding sequence (158-1876) selected from a *Bacillus licheniformis* ATCC 14580 acetolactate synthase

(GenBank: AAU42663), a 121-bp *Prochlorococcus marinus* MIT 9313 rbcS terminator (1877-1997), and a PCR RE primer (1998-2017).

[0275] SEQ ID NO:115 presents example 115 for a designer groE-promoter-controlled Ketol-Acid Reductoisomerase (54) DNA construct (1588 bp) that includes a PCR FD primer (sequence 1-20), a 137-bp *Prochlorococcus marinus* MIT9313 heat- and light-responsive groE promoter (21-157), an enzyme-encoding sequence (158-1168) selected from a *Thermotoga petrophila* RKU-1 ketol-acid reductoisomerase (GenBank: ABQ46398), a 400-bp *Prochlorococcus marinus* MIT9313 rbcS terminator (1169-1568), and a PCR RE primer (1569-1588).

[0276] SEQ ID NO:116 presents example 116 for a designer groE-promoter-controlled Dihydroxy-Acid Dehydratase (55) DNA construct (1960 bp) that includes a PCR FD primer (sequence 1-20), a 137-bp *Prochlorococcus marinus* heat- and light-responsive groE promoter (21-157), an enzyme-encoding sequence (158-1819) selected from a *Syntrophothermus lipocalidus* DSM 12680 dihydroxy-acid dehydratase (GenBank: ADI02905), a 121-bp *Prochlorococcus marinus* rbcS terminator (1820-1940), and a PCR RE primer (1941-1960).

[0277] SEQ ID NO:117 presents example 117 for a designer groE-promoter-controlled 2-Keto Acid Decarboxylase (42) DNA construct (1945 bp) that includes a PCR FD primer (sequence 1-20), a 137-bp *Prochlorococcus* heat- and light-responsive groE promoter (21-157), an enzyme-encoding sequence (158-1804) selected from a *Lactococcus lactis* Alpha-ketoisovalerate decarboxylase (GenBank: ADA65057), a 121-bp *Prochlorococcus* rbcS terminator (1805-1925), and a PCR RE primer (1926-1945).

[0278] SEQ ID NO:118 presents example 118 for a designer nirA-promoter-controlled Alcohol Dehydrogenase (43/44) DNA construct (1138 bp) that includes a PCR FD primer (sequence 1-20), a 251-bp *Prochlorococcus* nirA promoter (21-271), an enzyme-encoding sequence (272-997) selected from a *Geobacillus* short chain alcohol dehydrogenase (GenBank: YP_146837), a 121-bp *Prochlorococcus* rbcS terminator (998-1118), and a PCR RE primer (1119-1138).

[0279] Note, in the designer transgenic *Prochlorococcus* that contains the designer genes of SEQ ID NOS: 110-118, *Prochlorococcus*'s native gene (enzyme) of 34 is used in combination with the designer groE and nirA-promoters-controlled genes (enzymes) of 35, 03-05, 53-55, 42 and 43/44 (encoded by DNA constructs of SEQ ID NOS: 110-118) to confer the Calvin-cycle 3-phophoglycerate-branched photosynthetic NADPH-enhanced pathways for photobiological production of isobutanol from carbon dioxide and water (FIG. **6**). Addition of the following four designer groE promoter-controlled genes (SEQ ID NO:119-122) results in another designer transgenic *Prochlorococcus* that can produce both isobutanol and 3-methyl-1-butanol from carbon dioxide and water (35, 03-05, 53-55, 42, 43/44, plus 38-40 and 57 as shown in FIG. **6**).

[0280] Briefly, SEQ ID NO:119 presents example 119 for a designer groE-promoter-controlled 2-Isopropylmalate Synthase (40) DNA construct (1816 bp) that includes a PCR FD primer (sequence 1-20), a 137-bp *Prochlorococcus marinus* MIT9313 heat- and light-responsive groE promoter (21-157), an enzyme-encoding sequence (158-1675) selected from a *Pelotomaculum thermopropionicum* S12-isopropylmalate synthase (GenBank: YP_001211081), a 121-bp *Prochlorococcus marinus* rbcS terminator (1676-1796), and a PCR RE primer (1797-1816).

[0281] SEQ ID NO:120 presents example 120 for a designer groE-promoter-controlled 3-Isopropylmalate Dehydratase (38) DNA construct (2199 bp) that includes a PCR FD primer (sequence 1-20), a 137-bp *Prochlorococcus marinus* MIT9313 heat- and light-responsive groE promoter (21-157), a 3-isopropylmalate dehydratase large subunit-encoding sequence (158-1420) selected from a *Pelotomaculum thermopropionicum* S13-isopropylmalate dehydratase large subunit (GenBank: YP_001211082), a 137-bp *Prochlorococcus marinus* MIT9313 heat- and light-responsive groE promoter (1421-1557), a 3-isopropylmalate dehydratase small subunit-encoding sequence (1558-2058) selected from a *Pelotomaculum thermopropionicum* SI 3-isopropylmalate dehydratase small subunit (GenBank: YP_001211083), a 121-bp *Prochlorococcus marinus* rbcS terminator (2059-2179), and a PCR RE primer (2180-2199).

[0282] SEQ ID NO:121 presents example 121 for a designer groE-promoter-controlled 3-Isopropylmalate Dehydrogenase (39) DNA construct (1378 bp) that includes a PCR FD primer (sequence 1-20), a 137-bp *Prochlorococcus marinus* MIT9313 heat- and light-responsive groE promoter (21-157), an enzyme-encoding sequence (158-1237) selected from a *Syntrophothermus lipocalidus* DSM 12680 3-isopropylmalate dehydrogenase (GenBank: ADI02898), a 121-bp *Prochlorococcus marinus* rbcS terminator (1238-1358), and a PCR RE primer (1359-1378).

[0283] SEQ ID NO:122 presents example 122 for a designer groE-promoter-controlled 3-Methylbutanal Reductase (57) DNA construct (1327 bp) that includes a PCR FD primer (sequence 1-20), a 137-bp *Prochlorococcus marinus* MIT9313 heat- and light-responsive groE promoter (21-157), an enzyme-encoding sequence (158-1186) selected from a *Saccharomyces cerevisiae* S288c 3-Methylbutanal reductase (GenBank: DAA10635), a 121-bp *Prochlorococcus marinus* MIT9313 rbcS terminator (1187-1307), and a PCR RE primer (1308-1327).

[0284] Note, the use of SEQ ID NOS: 110-117 and 119-122 in genetic transformation of *Prochlorococcus marinus* MIT 9313 creates another designer transgenic *Prochlorococcus marinus* with a groE promoter-controlled designer Calvin-cycle-channeled pathway (identified as 34 (native), 35, 03-05, 53-55, 38-40, 42 and 57 in FIG. **6**) for photobiological production of 3-methyl-1-butanol from carbon dioxide and water.

[0285] Use of *Cyanothece* sp. ATCC 51142 as a host organism in genetic transformation with SEQ ID NOS: 123-128 can create a designer transgenic *Cyanothece* for photobiological production of 1-pentanol, 1-hexanol, and/or 1-heptanol (FIG. **8**). Briefly, SEQ ID NO:123 presents example 123 for a designer nirA-promoter-controlled 2-Isopropylmalate Synthase (40) DNA construct (2004 bp) that includes a PCR FD primer (sequence 1-20), a 203-bp *Cyanothece* sp. nirA promoter (21-223), an enzyme-encoding sequence (224-1783) selected from a *Hydrogenobacter thermophilus* 2-isopropylmalate synthase sequence (GenBank: BAI69273), a 201-bp *Cyanothece* sp. rbcS terminator (1784-1984), and a PCR RE primer (1985-2004).

[0286] SEQ ID NO:124 presents example 124 for a designer nirA-promoter-controlled Isopropylmalate Isomerase (41) large/small subunits DNA construct (2648 bp) that includes a PCR FD primer (sequence 1-20), a 203-bp

Cyanothece sp. ATCC 51142 nirA promoter (21-223), an enzyme-large-subunit-encoding sequence (224-1639) selected from a *Anoxybacillus flavithermus* WK1 isopropylmalate isomerase large subunit sequence (GenBank: YP_002314962), a 203-bp *Cyanothece* sp. ATCC 51142 nirA promoter (1640-1842), an enzyme-small-subunit-encoding sequence (1843-2427) selected from a *Anoxybacillus flavithermus* WK1 isopropylmalate isomerase small subunit sequence (GenBank: YP_002314963), a 201-bp *Cyanothece* sp. ATCC 51142 rbcS terminator (2428-1628), and a PCR RE primer (2629-2648).

[0287] SEQ ID NO:125 presents example 125 for a designer g nirA-promoter-controlled 3-Isopropylmalate Dehydrogenase (39) DNA construct (1530 bp) that includes a PCR FD primer (sequence 1-20), a 203-bp *Cyanothece* sp. ATCC 51142 nirA promoter (21-223), an enzyme-encoding sequence (224-1309) selected from a *Thermosynechococcus elongatus* BP-1 3-isopropylmalate dehydrogenase sequence (GenBank: BAC09152), a 201-bp *Cyanothece* sp. ATCC 51142 rbcS terminator (1310-1310), and a PCR RE primer (1311-1530).

[0288] SEQ ID NO:126 presents example 126 for a designer nirA-promoter-controlled 2-Keto Acid Decarboxylase (42') DNA construct (2088 bp) that includes a PCR FD primer (sequence 1-20), a 203-bp *Cyanothece* nirA promoter (21-223), an enzyme-encoding sequence (224-1867) selected from a *Lactococcus lactis* 2-keto acid decarboxylase (GenBank: AAS49166), a 201-bp *Cyanothece* rbcS terminator (1868-2068), and a PCR RE primer (2069-2088).

[0289] SEQ ID NO:127 presents example 127 for a designer nirA-promoter-controlled Hexanol Dehydrogenase (12') DNA construct (1503 bp) that includes a PCR FD primer (sequence 1-20), a 203-bp *Cyanothece* nirA promoter (21-223), an enzyme-encoding sequence (224-1282) selected from a *Mycobacterium chubuense* hexanol dehydrogenase (GenBank: ACZ56328), a 201-bp *Cyanothece* rbcS terminator (1283-1483), and a PCR RE primer (1484-1503).

[0290] SEQ ID NO:128 presents example 128 for a designer nirA-promoter-controlled short-chain Alcohol Dehydrogenase (43', 43") DNA construct (1149 bp) that includes a PCR FD primer (sequence 1-20), a 203-bp *Cyanothece* sp. ATCC 51142 nirA promoter (21-223), an enzyme-encoding sequence (224-928) selected from a *Pyrococcus furiosus* DSM 3638 Short chain alcohol dehydrogenase (GenBank: AAC25556), a 201-bp *Cyanothece* sp. ATCC 51142 rbcS terminator (929-1129), and a PCR RE primer (1130-1149).

[0291] Note, in the designer transgenic *Cyanothece* that contains designer nirA promoter-controlled genes of SEQ ID NOS: 123-127, *Cyanothece*'s native enzymes of 34,03-05, 36-38, and 45-52 are used in combination with the designer nirA-promoters-controlled enzymes of 35, 39-41 (39'-41', 39'-41'), 42' and 12' (encoded by DNA constructs of SEQ ID NOS: 123-127) to confer the Calvin-cycle 3-phophoglycerate-branched photosynthetic NADPH-enhanced pathways for photobiological production of 1-hexanol from carbon dioxide and water (FIG. **8**). Addition of a designer nirA-promoters-controlled gene (SEQ ID NO: 128) of a short chain alcohol dehydrogenase 43' (43") with promiscuity results in another designer transgenic *Cyanothece* containing a Calvin-cycle-channeled pathway (35, 39-41, 39'-43', 39'-43', and 39"-43" as shown in FIG. **8**) that can produce 1-pentanol, 1-hexanol, and 1-hexanol from carbon dioxide and water.

Designer Advanced Photosynthetic Organisms with Calvin-Cycle-Channeled Pathways for Production of Butanol and Related Higher Alcohols

[0292] According to one of the various embodiments, use of certain designer DNA constructs in genetic transformation of eukaryotic photosynthetic organisms such as plant cells, eukaryotic aquatic plants (including, for example, eukaryotic algae, submersed aquatic herbs, duckweeds, water cabbage, water lily, water hyacinth, *Bolbitis heudelotii, Cabomba* sp., and seagrasses) can create designer transgenic eukaryotic photosynthetic organisms for production of butanol and related higher alcohols from carbon dioxide and water. Eukaryotic algae that can be selected for use as host organisms to create designer algae for photobiological production of butanol and related higher alcohols include (but not limited to): *Dunaliella salina, Dunaliella viridis, Dunaliella bardowil, Crypthecodinium cohnii, Schizochytrium* sp., *Chlamydomonas reinhardtii, Platymonas subcordiformis, Chlorella fusca, Chlorella sorokiniana, Chlorella vulgaris, 'Chlorella' ellipsoidea, Chlorella* spp., *Haematococcus pluvialis; Parachlorella kessleri, Betaphycus gelatinum, Chondrus crispus, Cyanidioschyzon merolae, Cyanidium caldarium, Galdieria sulphuraria, Gelidiella acerosa, Gracilaria changii, Kappaphycus alvarezii, Porphyra miniata, Ostreococcus tauri, Porphyra yezoensis, Porphyridium* sp., *Palmaria palmata, Gracilaria* spp., *Isochrysis galbana, Kappaphycus* spp., *Laminaria japonica, Laminaria* spp., *Monostroma* spp., *Nannochloropsis oculata, Porphyra* spp., *Porphyridium* spp., *Undaria pinnatifida, Ulva lactuca, Ulva* spp., *Undaria* spp., *Phaeodactylum Tricornutum, Navicula saprophila, Cylindrotheca fusiformis, Cyclotella cryptica, Euglena gracilis, Amphidinium* sp., *Symbiodinium microadriaticum, Macrocystis pyrifera, Ankistrodesmus braunii, Scenedesmus obliquus, Stichococcus* sp., *Platymonas* sp., *Dunalielki sauna*, and *Stephanoptera gracilis.*

[0293] According to another embodiment, the transgenic photosynthetic organism comprises a designer transgenic plant or plant cells selected from the group consisting of aquatic plants, plant cells, green algae, red algae, brown algae, blue-green algae (oxyphotobacteria including cyanobacteria and oxychlorobacteria), diatoms, marine algae, freshwater algae, salt-tolerant algal strains, cold-tolerant algal strains, heat-tolerant algal strains, antenna-pigment-deficient mutants, butanol-tolerant algal strains, higher-alcohols-tolerant algal strains, butanol-tolerant oxyphotobacteria, higher-alcohols-tolerant oxyphotobacteria, and combinations thereof.

[0294] According to another embodiment, said transgenic photosynthetic organism comprises a biosafety-guarded feature selected from the group consisting of: a designer proton-channel gene inducible under pre-determined inducing conditions, a designer cell-division-cycle iRNA gene inducible under pre-determined inducing conditions, a high-CO_2-requiring mutant as a host organism for transformation with designer biofuel-production-pathway genes in creating designer cell-division-controllable photosynthetic organisms, and combinations thereof.

[0295] The greater complexity and compartmentalization of eukaryotic plant cells allow for creation of a wider range of photobiologically active designer organisms and novel metabolic pathways compartmentally segregated for production of butanol and/or higher alcohols from water and carbon dioxide. In a eukaryotic algal cell, for example, the translation of designer nuclear genes occurs in cytosol whereas the pho-

tosynthesis/Calvin cycle is located inside an algal chloroplast. This clear separation of algal chloroplast photosynthesis from other subcellular functions such as the functions of cytoplasm membrane, cytosol and mitochondria can be used as an advantage in creation of a biosafety-guarded designer algae through an inducible insertion of designer proton-channels into cytoplasm membrane to permanently disable any cell division and/or mating capability while keeping the algal chloroplast functional work with the designer biofuel production, pathways to produce butanol and related higher alcohols. However, it is essential to genetically deliver designer enzyme(s) into the chloroplast to tame the Calvin cycle and funnel metabolism toward butanol directly from CO_2 and H_2O. This requires more complicated gene design to achieve desirable results.

[0296] According to one of various embodiments, designer Calvin-cycle-channeled pathway enzymes encoded with designer unclear genes are targetedly expressed into algal chloroplast through use of a transit signal peptide sequence. The said signal peptide is selected from the group consisting of the hydrogenase transit-peptide sequences (HydA1 and HydA2), ferredoxin transit-peptide sequence (Frx1), thioredoxin-m transit-peptide sequence (Trx2), glutamine synthase transit-peptide sequence (Gs2), LhcII transit-peptide sequences, PSII-T transit-peptide sequence (PsbT), PSII-S transit-peptide sequence (PsbS), PSII-W transit-peptide sequence (PsbW), CF_0CF_1 subunit-γ transit-peptide sequence (AtpC), CF_0CF_1 subunit-δ transit-peptide sequence (AtpD), $CFoCF_1$ subunit-II transit-peptide sequence (AtpG), photosystem I (PSI) transit-peptide sequences, Rubisco SSU transit-peptide sequences, and combinations thereof. Preferred transit peptide sequences include the Hyd1 transit peptide, the Frx1 transit peptide, and the Rubisco SSU transit peptides (such as RbcS2).

[0297] SEQ ID NOS. 129-165 present examples for designer DNA constructs of designer chloroplast-targeted enzymes for creation of designer eukaryotic photosynthetic organisms such as designer algae with Calvin-cycle-channeled photosynthetic NADPH-enhanced pathways for photobiological production of butanol and related higher alcohols. Briefly, SEQ ID NO. 129 presents example 129 for a designer Nia1-promoter-controlled chloroplast-targeted Phosphoglycerate Mutase (03) DNA construct (1910 bp) that includes a PCR FD primer (sequence 1-20), a 2×84-bp *Chlamydomonas* Nia1 (nitrate reductase) promoter (21-188), a 135-bp *Chlamydomonas* RbcS2 transit peptide (189-323), a Phosphoglycerate Mutase-encoding sequence (324-1667) selected from *Nostoc azollae* Phosphoglycerate Mutase (ADI65627), a 223-bp *Chlamydomonas* RbcS2 terminator (1668-1890), and a PCR RE primer (1891-1910).

[0298] SEQ ID NO. 130 presents example 130 for a designer Nia1-promoter-controlled chloroplast-targeted Enolase (04) DNA construct (1856 bp) that includes a PCR FD primer (sequence 1-20), a 2×84-bp *Chlamydomonas reinhardtii* Nia1 promoter (21-188), a 135-bp *Chlamydomonas reinhardtii* RbcS2 transit peptide (189-323), an Enolase-encoding sequence (324-1613) selected/modified from *Nostoc azollae* Enolase (ADI63801), a 223-bp *Chlamydomonas* RbcS2 terminator (1614-1836), and a PCR RE primer (18837-1856).

[0299] SEQ ID NO. 131 presents example 131 for a designer Nia1-promoter-controlled chloroplast-targeted Pyruvate-Kinase (05) DNA construct (1985 bp) that includes a PCR FD primer (sequence 1-20), a 2×84-bp *Chlamydomonas reinhardtii* Nia1 promoter (21-188), a 135-bp *Chlamydomonas reinhardtii* RbcS2 transit peptide (189-323), an enzyme-encoding sequence (324-1742) selected/modified from *Cyanothece* sp. PCC 8802 pyruvate-kinase (YP_003138017), a 223-bp *Chlamydomonas* RbcS2 terminator (1743-1965), and a PCR RE primer (1966-1985).

[0300] SEQ ID NO. 132 presents example 132 for a designer Nia1-promoter-controlled chloroplast-targeted NADPH-dependent Glyceraldehyde-3-Phosphate Dehydrogenase (34) DNA construct (1568 bp) that includes a PCR FD primer (sequence 1-20), a 2×84-bp *Chlamydomonas reinhardtii* Nia1 promoter (21-188), a 135-bp *Chlamydomonas* RbcS2 transit peptide (189-323), a NADPH-dependent Glyceraldehyde-3-phosphate dehydrogenase-encoding sequence (324-1325) selected/modified from *Staphylococcus lugdunensis* NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase (ADC87332), a 223-bp *Chlamydomonas* RbcS2 terminator (1326-1548), and a PCR RE primer (1549-1568).

[0301] SEQ ID NO. 133 presents example 133 for a designer Nia1-promoter-controlled chloroplast-targeted NAD-dependent Glyceraldehyde-3-phosphate dehydrogenase (35) DNA construct (1571 bp) that includes a PCR FD primer (sequence 1-20), a 2×84-bp *Chlamydomonas* Nia1 (nitrate reductase) promoter (21-188), a 135-bp *Chlamydomonas* RbcS2 transit peptide (189-323), a NAD-dependent Glyceraldehyde-3-phosphate dehydrogenase-encoding sequence (324-1328) selected/modified from *Flavobacteriaceae bacterium* NAD-dependent Glyceraldehyde-3-phosphate dehydrogenase (YP_003095198), a 223-bp *Chlamydomonas* RbcS2 terminator (1329-1551), and a PCR RE primer (1552-1571).

[0302] SEQ ID NO. 134 presents example 134 for a designer Nia1-promoter-controlled chloroplast-targeted Citramalate Synthase (36) DNA construct (2150 bp) that includes a PCR FD primer (sequence 1-20), a 2×84-bp *Chlamydomonas* Nia1 (nitrate reductase) promoter (21-188), a 135-bp *Chlamydomonas* RbcS2 transit peptide (189-323), a Citramalate Synthase-encoding sequence (324-1907) selected from Hydrogenobacter Citramalate Synthase (ADO45737), a 223-bp *Chlamydomonas* RbcS2 terminator (1908-2130), and a PCR RE primer (2131-2150).

[0303] SEQ ID NO. 135 presents example 135 for a designer Nia1-promoter-controlled chloroplast-targeted 3-Isopropylmalate/(R)-2-Methylmalate Dehydratase (37) large/small subunits DNA construct (3125 bp) that includes a PCR FD primer (sequence 1-20), a 2×84-bp *Chlamydomonas reinhardtii* Nia1 promoter (21-188), a 135-bp *Chlamydomonas* RbcS2 transit peptide (189-323), a 3-isopropylmalate/(R)-2-methylmalate dehydratase large subunit-encoding sequence (324-2084) selected/modified from *Eubacterium eligens* 3-isopropylmalate/(R)-2-methylmalate dehydratase large subunit (YP_002930810), a 2×84-bp *Chlamydomonas* Nia1 promoter (2085-2252), a 135-bp *Chlamydomonas* RbcS2 transit peptide (2253-2387), a 3-isopropylmalate/(R)-2-methylmalate dehydratase small subunit-encoding sequence (2388-2882) selected/modified from *Eubacterium eligens* 3-isopropylmalate/(R)-2-methylmalate dehydratase small subunit (YP_002930809), a 223-bp *Chlamydomonas* RbcS2 terminator (2883-3105), and a PCR RE primer (3106-3125).

[0304] SEQ ID NO. 136 presents example 136 for a designer Nia1-promoter-controlled chloroplast-targeted 3-Isopropylmalate Dehydratase (38) large/small subunits DNA construct (2879 bp) that includes a PCR FD primer

(sequence 1-20), a 2×84-bp *Chlamydomonas* Nia1 promoter (21-188), a 135-bp *Chlamydomonas* RbcS2 transit peptide (189-323), a 3-isopropylmalate dehydratase large subunit-encoding sequence (324-1727) selected/modified from *Cyanothece* 3-isopropylmalate dehydratase large subunit (YP_003886427), a 2×84-bp *Chlamydomonas* Nia1 promoter (1727-1894), a 135-bp *Chlamydomonas* RbcS2 transit peptide (1895-2029), a 3-isopropylmalate dehydratase small subunit-encoding sequence (2030-2636) selected from *Cyanothece* 3-isopropylmalate dehydratase small subunit (YP_003889452), a 223-bp *Chlamydomonas* r RbcS2 terminator (2637-2859), and a PCR RE primer (2860-2879).

[0305] SEQ ID NO. 137 presents example 137 for a designer Nia1-promoter-controlled chloroplast-targeted 3-Isopropylmalate Dehydrogenase (39) DNA construct (1661 bp) that includes a PCR FD primer (sequence 1-20), a 2×84-bp *Chlamydomonas* Nia1 (nitrate reductase) promoter (21-188), a 135-bp *Chlamydomonas* RbcS2 transit peptide (189-323), a 3-isopropylmalate dehydrogenase-encoding sequence (324-1418) selected/modified from *Cyanothece* 3-isopropylmalate dehydrogenase (YP_003888480), a 223-bp *Chlamydomonas* RbcS2 terminator (1419-1641), and a PCR RE primer (1642-1661).

[0306] SEQ ID NO. 138 presents example 138 for a designer Nia1-promoter-controlled chloroplast-targeted 2-Isopropylmalate Synthase (40) DNA construct (2174 bp) that includes a PCR FD primer (sequence 1-20), a 2×84-bp *Chlamydomonas* Nia1 promoter (21-188), a 135-bp *Chlamydomonas* RbcS2 transit peptide (189-323), a 2-isopropylmalate synthase-encoding sequence (324-1931) selected/modified from *Cyanothece* 2-isopropylmalate synthase (YP_003890122), a 223-bp *Chlamydomonas* RbcS2 terminator (1932-2154), and a PCR RE primer (2155-2174).

[0307] SEQ ID NO. 139 presents example 139 for a designer Nia1-promoter-controlled chloroplast-targeted Isopropylmalate Isomerase (41) large/small subunit DNA construct (2882 bp) that includes a PCR FD primer (sequence 1-20), a 2×84-bp *Chlamydomonas* Nia1 promoter (21-188), a 135-bp *Chlamydomonas* RbcS2 transit peptide (189-323), an isopropylmalate isomerase large subunit-encoding sequence (324-1727) selected/modified from *Anabaena variabilis* isopropylmalate isomerase large subunit (YP_324467), a 2×84-bp *Chlamydomonas* reinhardtii Nia1 promoter (1728-1895), a 135-bp *Chlamydomonas* RbcS2 transit peptide (1896-2030), an isopropylmalate isomerase small subunit-encoding sequence (2031-2639) selected/modified from *Anabaena* isopropylmalate isomerase small subunit (YP_324466), a 223-bp *Chlamydomonas* RbcS2 terminator (2640-2862), and a PCR RE primer (2863-2882).

[0308] SEQ ID NO. 140 presents example 140 for a designer Nia1-promoter-controlled chloroplast-targeted 2-Keto Acid Decarboxylase (42) DNA construct (2210 bp) that includes a PCR FD primer (1-20), a 2×84-bp *Chlamydomonas* Nia1 promoter (21-188), a 135-bp *Chlamydomonas* RbcS2 transit peptide (189-323), a 2-keto acid decarboxylase-encoding sequence (324-1967) selected from *Lactococcus* 2-keto acid decarboxylase (AAS49166), a 223-bp *Chlamydomonas* RbcS2 terminator (1968-2190), and a PCR RE primer (2191-2210).

[0309] SEQ ID NO. 141 presents example 141 for a designer Nia1-promoter-controlled chloroplast-targeted NADH-dependent Alcohol Dehydrogenase (43) DNA construct (1724 bp) that includes a PCR FD primer (sequence 1-20), a 2×84-bp *Chlamydomonas* Nia1 promoter (21-188), a 135-bp *Chlamydomonas* RbcS2 transit peptide (189-323), a NADH-dependent alcohol dehydrogenase-encoding sequence (324-1481) selected/modified from *Gluconacetobacter hansenii* NADH-dependent alcohol dehydrogenase (ZP_06834544), a 223-bp *Chlamydomonas* RbcS2 terminator (1482-1704), and a PCR RE primer (1705-1724).

[0310] SEQ ID NO. 142 presents example 142 for a designer Nia1-promoter-controlled chloroplast-targeted NADPH-dependent Alcohol Dehydrogenase (44) DNA construct (1676 bp) that includes a PCR FD primer (sequence 1-20), a 2×84-bp *Chlamydomonas reinhardtii* Nia1 promoter (21-188), a 135-bp *Chlamydomonas reinhardtii* RbcS2 transit peptide (189-323), a NADPH-dependent alcohol dehydrogenase-encoding sequence (324-1433) selected/modified from *Fusobacterium* NADPH-dependent alcohol dehydrogenase (ZP_04573952), a 223-bp *Chlamydomonas reinhardtii* RbcS2 terminator (1434-1656), and a PCR RE primer (1657-1676).

[0311] Note, use of SEQ ID NOS. 129-141 (and/or 142) in genetic transformation of an eukaryotic photosynthetic organism such as *Chlamydomonas* can create a designer eukaryotic photosynthetic organism such as designer *Chlamydomonas* with a Calvin-cycle 3-phosphoglycerate-branched NADPH-enhanced pathway (03-05, 34-43/44 in FIG. **4**) for photobiological production of 1-butanol from carbon dioxide and water.

[0312] SEQ ID NO. 143 presents example 143 for a designer Nia1-promoter-controlled chloroplast-targeted Phosphoenolpyruvate Carboxylase (45) DNA construct (3629 bp) that includes a PCR FD primer (sequence 1-20), a 2×84-bp *Chlamydomonas reinhardtii* Nia1 promoter (21-188), a 135-bp *Chlamydomonas reinhardtii* RbcS2 transit peptide (189-323), a Phosphoenolpyruvate Carboxylase-encoding sequence (324-3386) selected/modified from *Cyanothece* sp. PCC 7822 Phosphoenolpyruvate Carboxylase (YP_003887888), a 223-bp *Chlamydomonas reinhardtii* RbcS2 terminator (3387-3609), and a PCR RE primer (3610-3629).

[0313] SEQ ID NO. 144 presents example 144 for a designer Nia1-promoter-controlled chloroplast-targeted Aspartate Aminotransferase (46) DNA construct (1745 bp) that includes a PCR FD primer (sequence 1-20), a 2×84-bp *Chlamydomonas reinhardtii* Nia1 promoter (21-188), a 135-bp *Chlamydomonas reinhardtii* RbcS2 transit peptide (189-323), a Aspartate Aminotransferase-encoding sequence (324-1502) selected/modified from *Synechococcus elongatus* PCC 6301 Aspartate Aminotransferase (YP_172275), a 223-bp *Chlamydomonas reinhardtii* RbcS2 terminator (1503-1525), and a PCR RE primer (1526-1745).

[0314] SEQ ID NO. 145 presents example 145 for a designer Nia1-promoter-controlled chloroplast-targeted Aspartokinase (47) DNA construct (2366 bp) that includes a PCR FD primer (sequence 1-20), a 2×84-bp *Chlamydomonas reinhardtii* Nia1 promoter (21-188), a 135-bp *Chlamydomonas reinhardtii* RbcS2 transit peptide (189-323), an Aspartokinase-encoding sequence (324-2123) selected/modified from *Cyanothece* Aspartokinase (YP_003136939), a 223-bp *Chlamydomonas* RbcS2 terminator (2124-2346), and a PCR RE primer (2347-2366).

[0315] SEQ ID NO. 146 presents example 146 for a designer Nia1-promoter-controlled chloroplast-targeted Aspartate-Semialdehyde Dehydrogenase (48) DNA construct (1604 bp) that includes a PCR FD primer (sequence 1-20), a 2×84-bp *Chlamydomonas reinhardtii* Nia1 promoter

(21-188), a 135-bp *Chlamydomonas reinhardtii* RbcS2 transit peptide (189-323), an Aspartate-semialdehyde dehydrogenase-encoding sequence (324-1361) selected/modified from *Trichodesmium erythraeum* IMS101 Aspartate-semialdehyde dehydrogenase (ABG50031), a 223-bp *Chlamydomonas* RbcS2 terminator (1362-1584), and a PCR RE primer (1585-1604).

[0316] SEQ ID NO. 147 presents example 147 for a designer Nia1-promoter-controlled chloroplast-targeted Homoserine Dehydrogenase (49) DNA construct (1868 bp) that includes a PCR FD primer (sequence 1-20), a 2×84-bp *Chlamydomonas* Nia1 promoter (21-188), a 135-bp *Chlamydomonas* RbcS2 transit peptide (189-323), a homoserine dehydrogenase-encoding sequence (324-1625) selected from *Cyanothece* homoserine dehydrogenase (YP_003887242), a 223-bp *Chlamydomonas* RbcS2 terminator (1626-1848), and a PCR RE primer (1849-1868).

[0317] SEQ ID NO. 148 presents example 148 for a designer Nia1-promoter-controlled chloroplast-targeted Homoserine Kinase (50) DNA construct (1472 bp) that includes a PCR FD primer (sequence 1-20), a 2×84-bp *Chlamydomonas* Nia1 promoter (21-188), a 135-bp *Chlamydomonas* RbcS2 transit peptide (189-323), a Homoserine kinase-encoding sequence (324-1229) selected/modified from *Cyanothece* Homoserine kinase (YP_003886645), a 223-bp *Chlamydomonas* RbcS2 terminator (1230-1452), and a PCR RE primer (1453-1472).

[0318] SEQ ID NO. 149 presents example 149 for a designer Nia1-promoter-controlled chloroplast-targeted Threonine Synthase (51) DNA construct (1655 bp) that includes a PCR FD primer (sequence 1-20), a 2×84-bp *Chlamydomonas* Nia1 promoter (21-188), a 135-bp *Chlamydomonas* RbcS2 transit peptide (189-323), a Threonine synthase-encoding sequence (324-1412) selected/modified from *Cyanothece* Threonine synthase (YP_002485009), a 223-bp *Chlamydomonas* RbcS2 terminator (1413-1635), and a PCR RE primer (1636-1655).

[0319] SEQ ID NO. 150 presents example 150 for a designer Nia1-promoter-controlled chloroplast-targeted Threonine Ammonia-Lyase (52) DNA construct (2078 bp) that includes a PCR FD primer (sequence 1-20), a 2×84-bp *Chlamydomonas* Nia1 promoter (21-188), a 135-bp *Chlamydomonas* RbcS2 transit peptide (189-323), a threonine ammonia-lyase-encoding sequence (324-1835) selected/modified from *Synechococcus* threonine ammonia-lyase (ZP_05035047), a 223-bp *Chlamydomonas* RbcS2 terminator (1836-2058), and a PCR RE primer (2059-2078).

[0320] Note, use of SEQ ID NOS. 129, 130, 132, 133, 143-150, 137-141 (and/or 141) through genetic transformation of an eukaryotic photosynthetic organism such as *Chlamydomonas* can create a designer eukaryotic photosynthetic organism such as designer *Chlamydomonas* with a Calvin-cycle 3-phosphogylcerate-branched NADPH-enhanced pathway (03, 04, 34, 35, 45-52, 39-43/44 in FIG. **4**) for photobiological production of 1-butanol from carbon dioxide and water.

[0321] SEQ ID NO. 151 presents example 151 for a designer Nia1-promoter-controlled chloroplast-targeted Acetolactate Synthase (53) DNA construct (2282 bp) that includes a PCR FD primer (sequence 1-20), a 2×84-bp *Chlamydomonas reinhardtii* Nia1 promoter (21-188), a 135-bp *Chlamydomonas* RbcS2 transit peptide (189-323), an acetolactate synthase-encoding sequence (324-2039) selected from *Bacillus subtilis* acetolactate synthase (CAB07802), a 223-bp *Chlamydomonas* RbcS2 terminator (2040-2262), and a PCR RE primer (2263-2282).

[0322] SEQ ID NO. 152 presents example 152 for a designer Nia1-promoter-controlled chloroplast-targeted Ketol-Acid Reductoisomerase (54) DNA construct (1562 bp) that includes a PCR FD primer (sequence 1-20), a 2×84-bp *Chlamydomonas* Nia1 promoter (21-188), a 135-bp *Chlamydomonas* RbcS2 transit peptide (189-323), an enzyme-encoding sequence (324-1319) selected/modified from *Cyanothece* ketol-acid reductoisomerase (YP_003885458), a 223-bp *Chlamydomonas* RbcS2 terminator (1320-1542), and a PCR RE primer (1543-1562).

[0323] SEQ ID NO. 153 presents example 153 for a designer Nia1-promoter-controlled chloroplast-targeted Dihydroxy-Acid Dehydratase (55) DNA construct (2252 bp) that includes a PCR FD primer (sequence 1-20), a 2×84-bp *Chlamydomonas* Nia1 promoter (21-188), a 135-bp *Chlamydomonas* RbcS2 transit peptide (189-323), a dihydroxy-acid dehydratase-encoding sequence (324-2009) selected from *Cyanothece* dihydroxy-acid dehydratase (YP_003887466), a 223-bp *Chlamydomonas* RbcS2 terminator (2010-2232), and a PCR RE primer (2233-2252).

[0324] SEQ ID NO. 154 presents example 154 for a designer Nia1-promoter-controlled chloroplast-targeted 2-Methylbutyraldehyde Reductase (56) DNA construct (1496 bp) that includes a PCR FD primer (sequence 1-20), a 2×84-bp *Chlamydomonas reinhardtii* Nia1 promoter (21-188), a 135-bp *Chlamydomonas reinhardtii* RbcS2 transit peptide (189-323), an enzyme-encoding sequence (324-1253) selected/modified from *Pichia pastoris* GS115 2-methylbutyraldehyde reductase (XP_002490018), a 223-bp *Chlamydomonas reinhardtii* RbcS2 terminator (1254-1476), and a PCR RE primer (1477-1496).

[0325] Note, use of SEQ ID NOS. 129-137, 140, and 151-154 in genetic transformation of an eukaryotic photosynthetic organism such as *Chlamydomonas* can create a designer eukaryotic photosynthetic organism such as designer *Chlamydomonas* with a Calvin-cycle 3-phosphogylcerate-branched NADPH-enhanced pathway (03-05, 34-39, 53-55, 42, and 56 in FIG. **5**) for photobiological production of 2-methyl-1-butanol from carbon dioxide and water.

[0326] SEQ ID NO. 155 presents example 155 for a designer Nia1-promoter-controlled chloroplast-targeted 3-Methylbutanal Reductase (57) DNA construct (1595 bp) that includes a PCR FD primer (sequence 1-20), a 2×84-bp *Chlamydomonas reinhardtii* Nia1 promoter (21-188), a 135-bp *Chlamydomonas reinhardtii* RbcS2 transit peptide (189-323), a 3-methylbutanal reductase-encoding sequence (324-1352) selected/modified from *Saccharomyces cerevisiae* S288c 3-methylbutanal reductase (DAA10635), a 223-bp *Chlamydomonas reinhardtii* RbcS2 terminator (1353-1575), and a PCR RE primer (1576-1595).

[0327] Note, use of SEQ ID NOS. 129-133, 151-153, 140 and 141 (or 142) in genetic transformation of an eukaryotic photosynthetic organism such as *Chlamydomonas* can create a designer eukaryotic photosynthetic organism such as designer *Chlamydomonas* with a Calvin-cycle 3-phosphogylcerate-branched NADPH-enhanced pathway (03-05, 34, 35, 53-55, 42, and 43 (44) in FIG. **6**) for photobiological production of isobutanol from carbon dioxide and water. Whereas, SEQ ID NOS. 129-133, 151-153, 136-138, 140 and 155 represent a designer eukaryotic photosynthetic organism such as designer *Chlamydomonas* with a Calvin-cycle 3-phosphogylcerate-branched NADPH-enhanced pathway

(03-05, 34, 35, 53-55, 40, 38, 39, 42, and 57 in FIG. **6**) that can photobiologically produce 3-methyl-1-butanol from carbon dioxide and water.

[0328] SEQ ID NO. 156 presents example 156 for a designer Nia1-promoter-controlled chloroplast-targeted NADH-dependent Butanol Dehydrogenase (12a) DNA construct (1739 bp) that includes a PCR FD primer (sequence 1-20), a 2×84-bp *Chlamydomonas reinhardtii* Nia1 (nitrate reductase) promoter (21-188), a 135-bp *Chlamydomonas reinhardtii* RbcS2 transit peptide (189-323), an enzyme-encoding sequence (324-1496) selected/modified from *Clostridium perfringens* NADH-dependent butanol dehydrogenase (NP_561774), a 223-bp *Chlamydomonas* RbcS2 terminator (1497-1719), and a PCR RE primer (1720-1739).

[0329] SEQ ID NO. 157 presents example 157 for a designer Nia1-promoter-controlled chloroplast-targeted NADPH-dependent Butanol Dehydrogenase (12b) DNA construct (1733 bp) that includes a PCR FD primer (sequence 1-20), a 2×84-bp *Chlamydomonas reinhardtii* Nia1 promoter (21-188), a 135-bp *Chlamydomonas reinhardtii* RbcS2 transit peptide (189-323), an enzyme-encoding sequence (324-1490) selected/modified from *Clostridium saccharobutylicum* NADPH-dependent butanol dehydrogenase (AAA83520), a 223-bp *Chlamydomonas reinhardtii* RbcS2 terminator (1491-1713), and a PCR RE primer (1714-1733).

[0330] Note, use of SEQ ID NOS. 129-140 and 156 (and/or 157) in genetic transformation of an eukaryotic photosynthetic organism such as *Chlamydomonas* can create a designer eukaryotic photosynthetic organism such as designer *Chlamydomonas* with a Calvin-cycle 3-phosphoglycerate-branched NADPH-enhanced butanol production pathway (03-05, 34-42 and 12 in FIG. **4**) for more specific photobiological production of 1-butanol from carbon dioxide and water. Similarly, SEQ ID NOS. 129, 130, 132, 133, 143-150, 137-140, and 156 (and/or 157) represent another designer eukaryotic photosynthetic organism such as designer *Chlamydomonas* with a Calvin-cycle 3-phosphoglycerate-branched NADPH-enhanced butanol-production pathway (03, 04, 34, 35, 45-52, 39-42 and 12 in FIG. **4**) for photobiological production of 1-butanol from carbon dioxide and water.

[0331] SEQ ID NO. 158 presents example 158 for a designer Nia1-promoter-controlled chloroplast-targeted 3-Ketothiolase (07') DNA construct (1745 bp) that includes a PCR FD primer (sequence 1-20), a 2×84-bp *Chlamydomonas* Nia1 (nitrate reductase) promoter (21-188), a 135-bp *Chlamydomonas* RbcS2 transit peptide (189-323), a 3-Ketothiolase-encoding sequence (324-1502) selected/modified from *Azohydromonas lata* 3-Ketothiolase (AAD10275), a 223-bp *Chlamydomonas* RbcS2 terminator (1503-1725), and a PCR RE primer (1726-1745).

[0332] SEQ ID NO. 159 presents a designer Nia1-promoter-controlled chloroplast-targeted 3-Hydroxyacyl-CoA dehydrogenase (08') DNA construct (1439 bp) that includes a PCR FD primer (sequence 1-20), a 2×84-bp *Chlamydomonas* Nia1 promoter (21-188), a 135-bp *Chlamydomonas* RbcS2 transit peptide (189-323), an enzyme-encoding sequence (324-1196) selected/modified from *Oceanithermus* 3-Hydroxyacyl-CoA dehydrogenase (ADR36325), a 223-bp *Chlamydomonas* RbcS2 terminator (1197-1419), and a PCR RE primer (1420-1439).

[0333] SEQ ID NO. 160 presents example 160 for a designer Nia1-promoter-controlled chloroplast-targeted Enoyl-CoA dehydratase (09') DNA construct (1337 bp) that includes a PCR FD primer (sequence 1-20), a 2×84-bp *Chlamydomonas* Nia1 promoter (21-188), a 135-bp *Chlamydomonas* RbcS2 transit peptide (189-323), an enzyme-encoding sequence (324-1094) selected/modified from *Bordetella petrii* Enoyl-CoA dehydratase (YP_001629844), a 223-bp *Chlamydomonas* RbcS2 terminator (1095-1317), and a PCR RE primer (1318-1337).

[0334] SEQ ID NO. 161 presents example 161 for a designer Nia1-promoter-controlled 2-Enoyl-CoA reductase (10') DNA construct (1736 bp) that includes a PCR FD primer (sequence 1-20), a 2×84-bp *Chlamydomonas* Nia1 promoter (21-188), a 135-bp *Chlamydomonas* RbcS2 transit peptide (189-323), an enzyme-encoding sequence (324-1493) selected/modified from *Xanthomonas campestris* 2-Enoyl-CoA reductase (YP_001905744), a 223-bp *Chlamydomonas* RbcS2 terminator (1494-1716), and a PCR RE primer (1717-1736).

[0335] SEQ ID NO. 162 presents example 162 for a designer Nia1-promoter-controlled chloroplast-targeted Acyl-CoA reductase (11') DNA construct (2036 bp) that includes a PCR FD primer (sequence 1-20), a 2×84-bp *Chlamydomonas reinhardtii* Nia1 promoter (21-188), a 135-bp *Chlamydomonas* RbcS2 transit peptide (189-323), an enzyme-encoding sequence (324-1793) selected/modified from *Thermosphaera aggregans* Acyl-CoA reductase (YP_003649571), a 223-bp *Chlamydomonas* RbcS2 terminator (1794-2016), and a PCR RE primer (2017-2036).

[0336] SEQ ID NO. 163 presents example 163 for a designer Nia1-promoter-controlled chloroplast-targeted Hexanol Dehydrogenase (12') DNA construct (1625 bp) that includes a PCR FD primer (sequence 1-20), a 2×84-bp *Chlamydomonas* Nia1 promoter (21-188), a 135-bp *Chlamydomonas* RbcS2 transit peptide (189-323), an enzyme-encoding sequence (324-1382) selected/modified from *Mycobacterium chubuense* hexanol dehydrogenase (ACZ56328), a 223-bp *Chlamydomonas* RbcS2 terminator (1383-1605), and a PCR RE primer (1606-1625).

[0337] Note, use of SEQ ID NOS. 158-163 with other proper DNA constructs such as SEQ ID NOS. 132 and 133 in genetic transformation of an eukaryotic photosynthetic organism such as *Chlamydomonas* can create a designer eukaryotic photosynthetic organism such as designer *Chlamydomonas* with a Calvin-cycle 3-phosphoglycerate-branched NADPH-enhanced hexanol production pathway (34, 35, 03-10, and 07'-12' in FIG. **7**) for photobiological production of 1-hexanol from carbon dioxide and water.

[0338] SEQ ID NO. 164 presents example 164 for a designer Nia1-promoter-controlled chloroplast-targeted Octanol Dehydrogenase (12") DNA construct (1249 bp) that includes a PCR FD primer (sequence 1-20), a 2×84-bp *Chlamydomonas* Nia1 promoter (21-188), a 135-bp *Chlamydomonas* RbcS2 transit peptide (189-323), an enzyme-encoding sequence (324-1006) selected/modified from *Drosophila subobscura* Octanol dehydrogenase (ABO65263), a 223-bp *Chlamydomonas* RbcS2 terminator (1007-1229), and a PCR RE primer (1230-1249).

[0339] Note, SEQ ID NOS. 132, 133, and 158-163 represent a designer eukaryotic photosynthetic organism such as a designer *Chlamydomonas* with a designer hydrocarbon chain elongation pathway (34, 35, 07'-12' as shown in FIG. **7**) for photobiological production of 1-hexanol. SEQ ID NOS: 132, 133, 158-162 and 164 represent another designer eukaryotic photosynthetic organism such as a designer *Chlamydomonas*

with a designer hydrocarbon chain elongation pathway (34, 35, 07'-10' and 07"-12" as shown in FIG. **7**) for photobiological production of 1-octanol.

[0340] SEQ ID NO. 165: a designer Nia1-promoter-controlled chloroplast-targeted Short Chain Alcohol Dehydrogenase (43') DNA construct (1769 bp) that includes a PCR FD primer (sequence 1-20), a 2×84-bp *Chlamydomonas* Nia1 promoter (21-188), a 135-bp *Chlamydomonas* RbcS2 transit peptide (189-323), an enzyme-encoding sequence (324-1526) selected/modified from *Burkholderia* Short chain alcohol dehydrogenase (AB056626), a 223-bp *Chlamydomonas* RbcS2 terminator (1527-1749), and a PCR RE primer (1750-1769).

[0341] Note, use of SEQ ID NOS. 129-140 and 165 in genetic transformation of an eukaryotic photosynthetic organism such as *Chlamydomonas* can create a designer eukaryotic photosynthetic organism such as designer *Chlamydomonas* with a Calvin-cycle 3-phosphogylcerate-branched NADPH-enhanced pathway (03-05, 34-41, 39'-43', 39'-43' and 39"-43" in FIG. **8**) for photobiological production of 1-pentanol, 1-hexanol, and 1-heptanol from carbon dioxide and water. Similarly, SEQ ID NOS. 129-140 and 163 represent another designer eukaryotic photosynthetic organism such as designer *Chlamydomonas* with a Calvin-cycle 3-phosphogylcerate-branched NADPH-enhanced pathway (03-05, 34-41, 39'-41', 39'-42' and 12' in FIG. **8**) for photobiological production of 1-hexanol from carbon dioxide and water.

[0342] Likewise, use of SEQ ID NOS. 129-137, 151-153, 138-140 and 165 through genetic transformation of an eukaryotic photosynthetic organism such as *Chlamydomonas* can create a designer eukaryotic photosynthetic organism such as designer *Chlamydomonas* with a Calvin-cycle 3-phosphogylcerate-branched NADPH-enhanced pathway (03-05, 34-39, 53-55, 39'-43', 39'-43', and 39"-43" in FIG. **9**) for photobiological production of 3-methyl-1-pentanol, 4-methyl-1-hexanol, and 5-methyl-1-heptanol from carbon dioxide and water; The expression of SEQ ID NOS. 129, 130, 132, 133, 143-150, 151-153, 137-140 and 165 in an eukaryotic photosynthetic organism such as a host *Chlamydomonas* represent another designer eukaryotic photosynthetic organism with a Calvin-cycle 3-phosphogylcerate-branched NADPH-enhanced pathway (03, 05, 34, 35, 42-55, 39'-43', 39'-43', and 39"-43" in FIG. **9**) for photobiological production of 3-methyl-1-pentanol, 4-methyl-1-hexanol, and 5-methyl-1-heptanol from carbon dioxide and water; The expression of SEQ ID NOS. 129-133, 151-153, 136-140 and 165 in a host eukaryotic photosynthetic organism such as *Chlamydomonas* represent yet another designer eukaryotic photosynthetic organism with a Calvin-cycle 3-phosphogylcerate-branched NADPH-enhanced pathway (03-05, 34, 35, 53-55, 40, 38, 39, 39'-43', 39'-43', and 39"-43" in FIG. **10**) for photobiological production of 4-methyl-1-pentanol, 5-methyl-1-hexanol, and 6-methyl-1-heptanol from carbon dioxide and water.

Use of Designer Photosynthetic Organisms with Photobioreactor for Production and Harvesting of Butanol and Related Higher Alcohols

[0343] The designer photosynthetic organisms with designer Calvin-cycle channeled photosynthetic NADPH-enhanced pathways (FIGS. **1**, and **4-10**) can be used with photobioreactors for production and harvesting of butanol and/or related higher alcohols. The said butanol and/or related higher alcohols are selected from the group consisting of: 1-butanol, 2-methyl-1-butanol, isobutanol, 3-methyl-1-butanol, 1-hexanol, 1-octanol, 1-pentanol, 1-heptanol, 3-methyl-1-pentanol, 4-methyl-1-hexanol, 5-methyl-1-heptanol, 4-methyl-1-pentanol, 5-methyl-1-hexanol, 6-methyl-1-heptanol, and combinations thereof.

[0344] The said designer photosynthetic organisms such as designer transgenic oxyphotobacteria and algae comprise designer Calvin-cycle-channeled and photosynthetic NADPH-enhanced pathway gene(s) and biosafety-guarding technology for enhanced photobiological production of butanol and related higher alcohols from carbon dioxide and water. According to one of the various embodiments, it is a preferred practice to grow designer photosynthetic organisms photoautotrophically using carbon dioxide (CO_2) and water (H_2O) as the sources of carbon and electrons with a culture medium containing inorganic nutrients. The nutrient elements that are commonly required for oxygenic photosynthetic organism growth are: N, P, and K at the concentrations of about 1-10 mM, and Mg, Ca, S, and Cl at the concentrations of about 0.5 to 1.0 mM, plus some trace elements Mn, Fe, Cu, Zn, B, Co, Mo among others at μM concentration levels. All of the mineral nutrients can be supplied in an aqueous minimal medium that can be made with well-established recipes of oxygenic photosynthetic organism (such as algal) culture media using water (freshwater for the designer freshwater algae; seawater for the salt-tolerant designer marine algae) and relatively small of inexpensive fertilizers and mineral salts such as ammonium bicarbonate (NH_4HCO_3) (or ammonium nitrate, urea, ammonium chloride), potassium phosphates (K_2HPO_4 and KH_2PO_4), magnesium sulfate heptahydrate ($MgSO_4.7H_2O$), calcium chloride ($CaCl_2$), zinc sulfate heptahydrate ($ZnSO_4.7H_2O$), iron (II) sulfate heptahydrate ($FeSO_4.7H_2O$), and boric acid (H_3BO_3), among others. That is, large amounts of designer algae (or oxyphotobacteria) cells can be inexpensively grown in a short period of time because, under aerobic conditions such as in an open pond, the designer algae can photoautotrophically grow by themselves using air CO_2 as rapidly as their wild-type parental strains. This is a significant feature (benefit) of the invention that could provide a cost-effective solution in generation of photoactive biocatalysts (the designer photosynthetic biofuel-producing organisms such as designer algae or oxyphotobacteria) for renewable solar energy production.

[0345] According to one of the various embodiments, when designer photosynthetic organism culture is grown and ready for photobiological production of butanol and/or related higher alcohols, the designer photosynthetic organism cells are then induced to express the designer Calvin-cycle channeled photosynthetic NADPH-enhanced pathway(s) to photobiologically produce butanol and/or related higher alcohols from carbon dioxide and water. The method of induction is designer pathway gene(s) specific. For example, if/when a nirA promoter is used to control the designer Calvin-cycle channeled pathway gene(s) such as those of SEQ ID NOS: 58-69 and 72 (and/or 73) which represent a designer transgenic *Thermosynechococcus* that comprises the designer genes of a Calvin-cycle 3-phophoglycerate-branched photosynthetic NADPH-enhanced pathway (numerically labeled as 34, 35, 03-05, 36-42, and 12 in FIG. **4**) for photobiological production of 1-butanol from carbon dioxide and water, the designer transgenic *Thermosynechococcus* is grown in a minimal liquid culture medium containing ammonium (but no nitrate) and other inorganic nutrients. When the designer transgenic *Thermosynechococcus* culture is grown and ready for photobiological production of biofuel 1-butanol, nitrate

fertilizer will then be added into the culture medium to induce the expression of the designer nirA-controlled Calvin-cycle-channeled pathway to photobiologically produce 1-butanol from carbon dioxide and water in this example.

[0346] For the designer photosynthetic organism(s) with anaerobic promoter-controlled pathway(s) such as the designer transgenic *Nostoc* that contains designer hox-promoter-controlled Calvin-cycle 3-phophoglycerate-branched pathway genes of SEQ ID NOS. 104-109, anaerobic conditions can be used to induce the expression of the designer pathway gene(s) for photobiological production of 2-methyl-1-butanol from carbon dioxide and water (FIG. **5**). That is, when the designer transgenic *Nostoc* culture is grown and ready for photobiological biofuel production, its cells will then be placed (or sealed) into certain anaerobic conditions to induce the expression of the designer hox-controlled pathway gene(s) to photobiologically produce 2-methyl-1-butanol from carbon dioxide and water.

[0347] For those designer photosynthetic organism(s) that contains a heat- and light-responsive promoter-controlled and nirA-promoter-controlled pathway(s) such as the designer transgenic *Prochlorococcus* that contains a set of designer groE-promoter-controlled and nirA-promoter-controlled Calvin-cycle 3-phophoglycerate-branched pathway genes of SEQ ID NOS. 110-118, light and heat are used in conjunction of nitrate addition to induce the expression of the designer pathway genes for photobiological production of isobutanol from carbon dioxide and water (FIG. **6**).

[0348] According to another embodiment, use of designer marine algae or marine oxyphotobacteria enables the use of seawater and/or groundwater for photobiological production of biofuels without requiring freshwater or agricultural soil. For example, designer *Prochlorococcus marinus* that contains the designer genes of SEQ ID NOS: 110-117 and 119-122 can use seawater and/or certain groundwater for photoautotrophic growth and synthesis of 3-methyl-1-butanol from carbon dioxide and water with its groE promoter-controlled designer Calvin-cycle-channeled pathway (identified as 34 (native), 35, 03-05, 53-55, 38-40, 42 and 57 in FIG. **6**). The designer photosynthetic organisms can be used also in a sealed photobioreactor that is operated on a desert for production of isobutanol with highly efficient use of water since there will be little or no water loss by evaporation and/or transpiration that a common crop system would suffer. That is, this embodiment may represent a new generation of renewable energy (butanol and related higher alcohols) production technology without requiring arable land or freshwater resources.

[0349] According to another embodiment, use of nitrogen-fixing designer oxyphotobacteria enables photobiological production of biofuels without requiring nitrogen fertilizer. For example, the designer transgenic *Nostoc* that contains designer hox-promoter-controlled genes of SEQ ID NOS. 104-109 is capable of both fixing nitrogen (N_2) and photobiologically producing 2-methyl-1-butanol from carbon dioxide and water (FIG. **6**). Therefore, use of the designer transgenic *Nostoc* enables photoautotrophic growth and 2-methyl-1-butanol synthesis from carbon dioxide and water.

[0350] Certain designer oxyphotobacteria are designed to perform multiple functions. For example, the designer transgenic *Cyanothece* that contains designer nirA promoter-controlled genes of SEQ ID NOS. 123-127 is capable of (1) using seawater, (2) N_2 fixing nitrogen, and photobiological producing 1-hexanol from carbon dioxide and water (FIG. **8**). Use of this type of designer oxyphotobacteria enables photobiological production of advanced biofuels such as 1-hexanol using seawater without requiring nitrogen fertilizer

[0351] According to one of various embodiments, a method for photobiological production and harvesting of butanol and related higher alcohols comprises: a) introducing a transgenic photosynthetic organism into a photobiological reactor system, the transgenic photosynthetic organism comprising transgenes coding for a set of enzymes configured to act on an intermediate product of a Calvin cycle and to convert the intermediate product into butanol and related higher alcohols; b) using reducing power and energy associated with the transgenic photosynthetic organism acquired from photosynthetic water splitting and proton gradient coupled electron transport process in the photobioreactor to synthesize butanol and related higher alcohols from carbon dioxide and water; and c) using a product separation process to harvest the synthesized butanol and/or related higher alcohols from the photobioreactor.

[0352] In summary, there are a number of embodiments on how the designer organisms may be used for photobiological butanol (and/or related higher alcohols) production. One of the preferred embodiments is to use the designer organisms for direct photosynthetic butanol production from CO_2 and H_2O with a photobiological reactor and butanol-harvesting (filtration and distillation/evaporation) system, which includes a specific operational process described as a series of the following steps: a) Growing a designer transgenic organism photoautotrophically in minimal culture medium using air CO_2 as the carbon source under aerobic (normal) conditions before inducing the expression of the designer butanol-production-pathway genes; b) When the designer organism culture is grown and ready for butanol production, sealing or placing the culture into a specific condition to induce the expression of designer Calvin-cycle-channeled pathway genes; c) When the designer pathway enzymes are expressed, supplying visible light energy such as sunlight for the designer-genes-expressed cells to work as the catalysts for photosynthetic production of butanol and/or related higher alcohols from CO_2 and H_2O; d) Harvesting the product butanol and/or related higher alcohols by any method known to those skilled in the art. For example, harvesting the butanol and/or related higher alcohols from the photobiological reactor can be achieved by a combination of membrane filtration and distillation/evaporation butanol-harvesting techniques.

[0353] The above process to use the designer organisms for photosynthetic production and harvesting of butanol and related higher alcohols can be repeated for a plurality of operational cycles to achieve more desirable results. Any of the steps a) through d) of this process described above can also be adjusted in accordance of the invention to suit for certain specific conditions. In practice, any of the steps a) through d) of the process can be applied in full or in part, and/or in any adjusted combination as well for enhanced photobiological production of butanol and higher alcohol in accordance of this invention.

[0354] In addition to butanol and/or related higher alcohols production, it is also possible to use a designer organism or part of its designer butanol-production pathway(s) to produce certain intermediate products of the designer Calvin-cycle-channeled pathways (FIGS. **1** and **4-10**) including (but not limited to): butyraldehyde, butyryl-CoA, crotonyl-CoA, 3-hydroxybutyryl-CoA, acetoacetyl-CoA, acetyl-CoA, pyruvate, phosphoenolpyruvate, 2-phosphoglycerate, 1,3-diphos-

phoglycerate, glyceraldehye-3-phosphate, dihydroxyacetone phosphate, fructose-1,6-diphosphate, fructose-6-phosphate, glucose-6-phosphate, glucose, glucose-1-phosphate, citramalate, citraconate, methyl-D-malate, 2-ketobutyrate, 2-ketovalerate, oxaloacetate, aspartate, homoserine, threonine, 2-keto-3-methylvalerate, 2-methylbutyraldehyde, 3-methylbutyraldehyde, 4-methyl-2-oxopentanoate, 3-isopropylmalate, 2-isopropylmalate, 2-oxoisovalerate, 2,3-dihydroxyisovalerate, 2-acetolactate, isobutyraldehyde, 3-keto-C6-acyl-CoA, 3-hydroxy-C6-acyl-CoA, C6-enoyl-CoA, C6-acyl-CoA, 3-keto-C8-acyl-CoA, 3-hydroxy-C8-acyl-CoA, C8-enoyl-CoA, C8-acyl-CoA, octanal, 1-pentanol, 1-hexanal, 1-heptanal, 2-ketohexanoate, 2-ketoheptanoate, 2-ketooctanoate, 2-ethylmalate, 3-ethylmalate, 3-methyl-1-pentanal, 4-methyl-1-hexanal, 5-methyl-1-heptanal, 2-hydroxy-2-ethyl-3-oxobutanoate, 2,3-dihydroxy-3-methylpentanoate, 2-keto-4-methyl-hexanoate, 2-keto-5-methylheptnoate, 2-keto-6-methyl-octanoate, 4-methyl-1-pentanal, 5-methyl-1-hexanal, 6-methyl-1-heptanal, 2-keto-7-methyloctanoate, 2-keto-6-methyl-heptanoate, and 2-keto-5-methyl-hexanoate. According to one of various embodiments, therefore, a further embodiment comprises an additional step of harvesting the intermediate products that can be produced also from an induced transgenic designer organism. The production of an intermediate product can be selectively enhanced by switching off a designer-enzyme activity that catalyzes its consumption in the designer pathways. The production of a said intermediate product can be enhanced also by using a designer organism with one or some of designer enzymes omitted from the designer butanol-production pathways. For example, a designer organism with the butanol dehydrogenase or butyraldehyde dehydrogenase omitted from the designer pathway(s) of FIG. **1** may be used to produce butyraldehyde or butyryl-CoA, respectively.

Designer Calvin-Cycle-Channeled Aerobic Hydrogenotrophic Biofuel Pathways

[0355] According to one of the various embodiments, a designer hydrogenotrophic Calvin-cycle-channeled pathway technology (FIG. **11**) is created that takes hydrogen (H_2), oxygen (O_2) and carbon dioxide (CO_2) to produce advanced biofuels including butanol and related higher alcohols through the designer Calvin-cycle-channeled pathways (FIGS. **1** and **4-10**). As illustrated in FIG. **11**, one of the various embodiments here is the expression of designer oxygen (O_2)-tolerant hydrogenases in a designer microbial cell such as cyanobacteria to generate NAD(P)H and ATP from consumption of hydrogen. The expression of a membrane bound hydrogenase (MBH, 70 and its accessory proteins 72 as listed in Table 1) enables oxidation of H_2 through the respiratory electron transport chain (ETC) system to pump protons (H^+) across the cytoplasm membrane to create transmembrane electrochemical potential for ATP synthesis; whereas the use of a soluble hydrogenase (SH, 71 and its accessory proteins 72) enables generation of NAD(P)H through SH-mediated reduction of $NAD(P)^+$ by H_2. Use of ATP and NAD(P)H drives the designer Calvin-cycle-channeled pathways (FIGS. **1** and **4-10**) for CO_2 fixation and biofuel butanol and related higher alcohol production. Therefore, this represents an innovative application of the designer Calvin-cycle-channeled biofuel-production pathways.

[0356] For example, the expression of a membrane bound hydrogenase (MBH, 70 and its accessory proteins 72) and a soluble hydrogenase (SH, 71 and its accessory proteins 72) in a designer transgenic cyanobacterium that already contains the designer butanol-production-pathway genes of SEQ ID NOS: 58-69 and 72 (and/or 73) can create a hydrogenotrophic Calvin-cycle 3-phophoglycerate-branched 1-butanol production pathway as numerically labeled as 34, 35, 03-05, 36-42, and 12 in FIG. **4**. The net result of the designer hydrogenotrophic pathway is the production of 1-butanol ($CH_3CH_2CH_2CH_2OH$) from hydrogen (H_2), carbon dioxide (CO_2) and oxygen (O_2) according to the following process reaction:

$$(12+2n)H_2+4CO_2+nO_2 \rightarrow CH_3CH_2CH_2CH_2OH+(7+n)H_2O \quad [20]$$

The number (n) of oxygen (O_2) molecules used to oxidize hydrogen (H_2) by the respiratory electron-transport-coupled phosphorylation to support the synthesis of a 1-butuanol was estimated to be about 5 in this example.

[0357] Note, before the designer genes are turned on, the transgenic cyanobacteria (FIG. **11**) can grow photoautotrophically using CO_2, H_2O and sunlight just like their wild-type parental strains. When they are grown and ready for use, they can then be placed into a bioreactor supplied with H_2 (about 85%) and CO_2 (about 10%) with limiting amount of O_2 (about 5%) for hydrogenotrophic synthesis of higher alcohols such as 1-butanol, for example, through the Calvin-cycle-channeled butanol-production pathway of FIG. **1** without requiring any photosynthesis or sunlight. Since hydrogen (H_2) can be made from a number of sources including the electrolysis of water, the designer hydrogenotrophic Calvin-cycle-channeled pathway technology (FIG. **11**) enables utilization of inexpensive industrial CO_2 and electricity from solar photovoltaic, wind and nuclear power stations to produce "drop-in-ready" liquid transportation fuel such as butanol without requiring any arable lands or photosynthesis.

Designer Anaerobic Hydrogenotrophic Reductive-Acetyl-CoA Biofuel-Production Pathways

[0358] According to one of the various embodiments, a designer hydrogenotrophic reductive-acetyl-CoA biofuel-production pathway technology (FIG. **12**) is created that takes hydrogen (H_2) and carbon dioxide (CO_2) to produce advanced biofuels such as butanol and related higher alcohols under anaerobic conditions. As illustrated in FIG. **12**, one of the various embodiments here is the expression of a set of designer genes that confer a designer anaerobic hydrogenotrophic system and a reductive-acetyl-CoA butanol-producing pathway (FIG. **13**) in a microbial host cell such as a cyanobacterium. Designer anaerobic hydrogenotrophic system includes, for example, energy converting hydrogenase (Ech, 91 in Table 1), [NiFe]-hydrogenase Mvh (95), Coenzyme F_{420}-reducing hydrogenase (Frh, 96), native (or heterologous) soluble hydrogenase (SH, 71), NAD(P)H, reduced ferredoxin (Fd_{red}^{2-}), HS-CoM, HS-CoB, and heterodissulfide reductase (Hdr; 94); while designer reductive-acetyl-CoA butanol-producing pathway (as shown with the numerical labels 83-90 and 07-12/43 in FIG. **13**) comprises formylmethanofuran dehydroganse 83, formyl transferase 84, 10-methenyl-tetrahydromethanopterin cyclohydrolase 85, 10-methylene-H_4 methanopterin dehydrogenase 86, 10-methylene-H_4-methanopterin reductase 87, methyl-H_4-methanopterin: corrinoid iron-sulfur protein methyltransferase 88, corrinoid iron-sulfur protein 89, CO dehydrogenase/acetyl-CoA synthase 90, thiolase 07, 3-hydroxybutyryl-CoA dehydrogenase 08, crotonase 09, butyryl-CoA

dehydrogenase 10, butyaldehyde dehydrogenase 11, butanol dehydrogenase 12, and/or alcohol dehydrogenase 43. In this example, the net result of the designer anaerobic hydrogenotrophic reductive-acetyl-CoA butanol-production pathway technology (FIGS. **12** and **13**) is the production of 1-butanol($CH_3CH_2CH_2CH_2OH$) from hydrogen (H_2) and carbon dioxide (CO_2) according to the following process reaction:

$$12H_2+4CO_2 \rightarrow CH_3CH_2CH_2CH_2OH+7H_2O \quad [21]$$

The standard free energy change) ($\Delta_r G^\circ$) for this overall reaction is −244.7 kJ/mol 1-butanol, which demonstrates that this hydrogen-driven butanol-production technology is not in violation of thermodynamic laws. This equation shows that the use of 12 molecules (24 electrons) of hydrogen (H_2) can produce one molecule of 1-butanol from 4 molecules of carbon dioxide (CO_2). To produce 12 molecules of H_2 by electrolysis of water, it uses 24 electrons from electricity. Therefore, if electrolysis of water is used as a hydrogen source, then 24 electrons (from electricity) are sufficient to generate one molecule of 1-butanol from 4 molecules of CO_2 through the designer anaerobic hydrogenotrophic reductive-acetyl-CoA butanol-production pathway technology (FIGS. **12** and **13**).

[0359] Therefore, in one of the various embodiments, a designer autotrophic organism comprises a set of designer genes (e.g., designer DNA constructs) that express a set of enzymes conferring the designer anaerobic hydrogenotrophic butanol-production-pathway system (as shown in FIGS. **12** and **13**) that comprises: energy converting hydrogenase (Ech) 91, [NiFe]-hydrogenase (Mvh) 95, Coenzyme F_{420}-reducing hydrogenase (Frh) 96, native (or heterologous) soluble hydrogenase (SH) 71, heterodissulfide reductase (Hdr) 94, formylmethanofuran dehydroganse 83, formyl transferase 84, 10-methenyl-tetrahydromethanopterin cyclohydrolase 85, 10-methylene-H_4 methanopterin dehydrogenase 86, 10-methylene-H_4-methanopterin reductase 87, methyl-H_4-methanopterin: corrinoid iron-sulfur protein methyltransferase 88, corrinoid iron-sulfur protein 89, CO dehydrogenase/acetyl-CoA synthase 90, thiolase 07, 3-hydroxybutyryl-CoA dehydrogenase 08, crotonase 09, butyryl-CoA dehydrogenase 10, butyaldehyde dehydrogenase 11, butanol dehydrogenase 12 and/or alcohol dehydrogenase 43.

[0360] Before the designer genes are turned on, the designer transgenic cyanobacteria (FIG. **12**) can grow photoautotrophically using CO_2, H_2O and sunlight just like their wild-type parental strains. When they are grown and ready for use, they can then be placed into a bioreactor for butanol production from H_2 and CO_2 under anaerobic conditions without requiring any photosynthesis or any respiratory oxidation of H_2 by molecular oxygen (O_2). A unique feature of this designer reductive-acetyl-CoA butanol-production pathway (FIG. **13**) is that it does not require any ATP; this pathway uses reduced ferredoxin (Fd_{red}^{2-}), $F_{420}H_2$ and NAD(P)H that the designer anaerobic hydrogenotrophic system (FIG. **12**) can supply from H_2 employing certain electro-proton-coupled bioenergetics bifurcating mechanism. In accordance with one of the various embodiments, this designer pathway (FIG. **13**) represents one of the most energy-efficient butanol-production processes identified so for. The standard free energy change (ΔG°) of this specific anaerobic hydrogenotrophic butanol-production process [Eq. 21] is −20.4 kJ/mol per H_2 used. Its maximum hydrogen (H_2)-to-butanol energy conversion efficiency was estimated to be about 91.4%.

[0361] According to one of the various embodiments, another designer anaerobic reductive-acetyl-CoA butanol-production pathway (as shown with the numerical labels 74-81 and 07-12/43 in FIG. **14**) is created that can produce 1-butanol from H_2 and CO_2 through use of a set of enzymes comprising: formate dehydroganse 74, 10-formyl-H_4 folate synthetase 75, methenyltetrahydrofolate cyclohydrolase 76, 10-methylene-H_4 folate dehydrogenase 77, 10-methylene-H_4 folate reductase 78, methyl-H_4 folate: corrinoid iron-sulfur protein methyltransferase 79, corrinoid iron-sulfur protein 80, CO dehydrogenase/acetyl-CoA synthase 81, thiolase 07, 3-hydroxybutyryl-CoA dehydrogenase 08, crotonase 09, butyryl-CoA dehydrogenase 10, butyaldehyde dehydrogenase 11, butanol dehydrogenase 12, and/or alcohol dehydrogenase 43.

[0362] This designer pathway is similar to that of FIG. **13**, except that it requires consumption of ATP at the step of 10-formyl-H_4 folate synthetase 75 (FIG. **14**). Therefore, it requires ATP supply from other cellular processes in order to operate. According to one of the various embodiments, this pathway (FIG. **14**) can be supported by a designer methanogenic hydrogenotrophic cell system (FIG. **15**) that produces ATP, Fd_{red}^{2-}, $F_{420}H_2$, and NAD(P)H. This designer autotrophic organism comprises a set of designer genes (e.g., designer DNA constructs) that express the designer methanogenic hydrogenotrophic butanol-production-pathway system (as shown in FIGS. **14** and **16**) comprising: methyl-H4MPT: coenzyme-M methyltransferase Mtr 92, native (or heterologous) A_1A_o-ATP synthase 97, methyl-coenzyme M reductase Mcr 93, energy converting hydrogenase (Ech) 91, [NiFe]-hydrogenase (Mvh) 95, Coenzyme F_{420}-reducing hydrogenase (Frh) 96, native (or heterologous) soluble hydrogenase (SH) 71, heterodissulfide reductase (Hdr) 94, formylmethanofuran dehydroganse 83, formyl transferase 84, 10-methenyl-tetrahydromethanopterin cyclohydrolase 85, 10-methylene-H_4 methanopterin dehydrogenase 86, 10-methylene-H_4-methanopterin reductase 87, methyl-H_4-methanopterin: corrinoid iron-sulfur protein methyltransferase 88, corrinoid iron-sulfur protein 89, CO dehydrogenase/acetyl-CoA synthase 90, thiolase 07, 3-hydroxybutyryl-CoA dehydrogenase 08, crotonase 09, butyryl-CoA dehydrogenase 10, butyaldehyde dehydrogenase 11, butanol dehydrogenase 12 and/or alcohol dehydrogenase 43.

[0363] For example, the designer methanogenic hydrogenotrophic system (FIG. **15**) comprises methyl-H4MPT: coenzyme-M methyltransferase Mtr 92, A_1A_o-ATP synthase 97, energy converting hydrogenase (Ech; 91 in Table 1), [NiFe]-hydrogenase Mvh (95), Coenzyme F_{420}-reducing hydrogenase (Frh, 96), native (or heterologous) soluble hydrogenase (SH, 71), NAD(P)H, reduced ferredoxin (Fd_{red}^{2-}), HS-CoM, HS-CoM, methyl-coenzyme M reductase Mcr 93, and heterodissulfide reductase (Hdr, 94). The Mtr 92 in this system can take a fraction of the CH_3—H_4MPT intermediate to produce methane and generate a transmembrane electrochemical potential for synthesis of ATP, which can support the ATP-requiring anaerobic reductive-acetyl-CoA butanol-production pathway of FIG. **14**. Therefore, the combination of the methanogenic hydrogenotrophic system (FIG. **15**) and the ATP-requiring anaerobic reductive-acetyl-CoA butanol-production pathway (FIG. **14**) results in a combined pathway (FIG. **16**) for production of both butanol and methane. The net result is the production of both butanol and methane (CH_4) from hydrogen (H_2) and carbon dioxide

(CO_2) according to the following process reaction where m is the number of CH_4 molecules co-generated per 1-butanol produced:

$$(12+4m)H_2+(4+m)CO_2 \rightarrow CH_3CH_2CH_2CH_2OH+(7+m)H_2O+mCH_4 \quad [22]$$

[0364] The non-ATP-requiring anaerobic reductive-acetyl-CoA butanol-production pathway (FIG. **13**) can, of course, operate with this designer methanogenic hydrogenotrophic system (FIG. **15**) as well, resulting in another combined pathway for production of both butanol and methane (FIG. **17**). Therefore, in one of the various embodiments, a designer autotrophic organism comprises a set of designer genes (e.g., designer DNA constructs) that express a designer methanogenic hydrogenotrophic butanol-production-pathway system (as shown in FIGS. **15**,**13**, and **17**) comprising: methyl-H4MPT: coenzyme-M methyltransferase Mtr 92, native (or heterologous) A_1A_o-ATP synthase 97, methyl-coenzyme M reductase Mcr 93, energy converting hydrogenase (Ech) 91, [NiFe]-hydrogenase (Mvh) 95, Coenzyme F_{420}-reducing hydrogenase (Frh) 96, native (or heterologous) soluble hydrogenase (SH) 71, heterodissulfide reductase (Hdr) 94, formate dehydroganse 74, 10-formyl-H_4 folate synthetase 75, methenyltetrahydrofolate cyclohydrolase 76, 10-methylene-H_4 folate dehydrogenase 77, 10-methylene-H_4 folate reductase 78, methyl-H_4 folate: corrinoid iron-sulfur protein methyltransferase 79, corrinoid iron-sulfur protein 80, CO dehydrogenase/acetyl-CoA synthase 81, thiolase 07, 3-hydroxybutyryl-CoA dehydrogenase 08, crotonase 09, butyryl-CoA dehydrogenase 10, butyaldehyde dehydrogenase 11, butanol dehydrogenase 12, and/or alcohol dehydrogenase 43.

[0365] Some of these enzymes may naturally exist in some of the host organisms depending on their genetic background; some of these native enzymes may be used in constructing part of the designer pathways (FIGS. **12**-**17**) along with designer genes. Therefore, according to one of the various embodiments, a designer autotrophic organism for production of biofuels such as butanol through anaerobic hydrogenotrophic reductive-acetyl-CoA biofuel-production-pathway(s) comprises designer genes that can express at least one of the enzymes selected from the group consisting of: energy converting hydrogenase (Ech) 91, methyl-H4MPT: coenzyme-M methyltransferase Mtr 92, methyl-coenzyme M reductase Mcr 93, heterodissulfide reductase (Hdr) 94, [NiFe]-hydrogenase (Mvh) 95, Coenzyme F_{420}-reducing hydrogenase (Frh) 96, soluble hydrogenase (SH) 71, A_1A_o-ATP synthase 97, formate dehydroganse 74, 10-formyl-H_4 folate synthetase 75, methenyltetrahydrofolate cyclohydrolase 76, 10-methylene-H_4 folate dehydrogenase 77, 10-methylene-H_4 folate reductase 78, methyl-H_4 folate: corrinoid iron-sulfur protein methyltransferase 79, corrinoid iron-sulfur protein 80, CO dehydrogenase/acetyl-CoA synthase 81, formylmethanofuran dehydroganse 83, formyl transferase 84, 10-methenyl-tetrahydromethanopterin cyclohydrolase 85, 10-methylene-H_4 methanopterin dehydrogenase 86, 10-methylene-H_4-methanopterin reductase 87, methyl-H_4-methanopterin: corrinoid iron-sulfur protein methyltransferase 88, corrinoid iron-sulfur protein 89, CO dehydrogenase/acetyl-CoA synthase 90, thiolase 07, 3-hydroxybutyryl-CoA dehydrogenase 08, crotonase 09, butyryl-CoA dehydrogenase 10, butyaldehyde dehydrogenase 11, butanol dehydrogenase 12 and/or alcohol dehydrogenase 43.

[0366] SEQ ID NOS. 166-198 present examples for designer DNA constructs of designer enzymes for creation of designer hydrogenotrophic biofuel-producing organisms such as designer cyanobacteria with reductive-acetyl-CoA biofuel-production pathways. Briefly, SEQ ID NO: 166 presents example 166 of a designer hox-promoter-controlled Formylmethanofuran dehydrogenase (Fmd; 83) DNA construct (6110 bp) that includes a PCR FD primer (sequence 1-20), a 172-bp *Nostoc* (*Anabaena* PCC 7120) hox promoter (21-192), an enzyme-encoding sequence (193-5659) selected/modified from the sequence of formylmethanofuran dehydrogenase subunits B, C, E (GenBank: ADL58895, ADL58894, ADL58893) of *Methanothermobacter marburgensis* and formylmethanofuran dehydrogenase subunits subunits A, D, and G (GenBank: ABC56660, ABC56658, ABC56657) of *Methanosphaera stadtmanae*, a 432-bp *Nostoc* sp. strain PCC 7120 gor terminator (5659-6090), and a PCR RE primer (6091-6110) at the 3' end.

[0367] SEQ ID NO: 167 presents example 167 of a designer hox-promoter-controlled Formyl transferase (84) DNA construct (1538 bp) that includes a PCR FD primer (sequence 1-20), a 172-bp *Nostoc* (*Anabaena* PCC 7120) hox promoter (21-192), an enzyme-encoding sequence (193-1086) selected/modified from the sequence of a formylmethanofuran-tetrahydromethanopterin formyltransferase (GenBank: ADL59225) of *Methanothermobacter marburgensis*, a 432-bp *Nostoc gor* terminator (1087-1518), and a PCR RE primer (1519-1538).

[0368] SEQ ID NO: 168 presents example 168 of a designer hox-promoter-controlled 5,10-Methenyl-tetrahydromethanopterin (H_4 methanopterin) cyclohydrolase (85) DNA construct (1631 bp) that includes a PCR FD primer (sequence 1-20), a 172-bp *Anabaena* PCC 7120 hox promoter (21-192), an enzyme-encoding sequence (193-1179) selected from the sequence of a N(5),N(10)-methenyltetrahydromethanopterin cyclohydrolase (GenBank: ABC57615) of *Methanosphaera stadtmanae*, a 432-bp *Nostoc gor* terminator (1180-1161), and a PCR RE primer (1162-1631).

[0369] SEQ ID NO: 169 presents example 169 of a designer hox-promoter-controlled 5,10-Methylene-H_4-methanopterin dehydrogenase (86) DNA construct (1475 bp) that includes a PCR FD primer (sequence 1-20), a 172-bp *Anabaena* PCC 7120 hox promoter (21-192), an enzyme-encoding sequence (193-1023) selected from the sequence of a F_{420}-dependent methylene-5,6,7,8-tetrahydromethanopterin dehydrogenase (GenBank: ADL57660) of *Methanothermobacter marburgensis*, a 432-bp *Nostoc* gor terminator (1023-1455), and a PCR RE primer (1456-1475).

[0370] SEQ ID NO: 170 presents example 170 of a designer hox-promoter-controlled Methylenetetrahydrofolate reductase and/or Methylene-H_4-methanopterin reductase (78, 87) DNA construct (2594 bp) that includes a PCR FD primer (sequence 1-20), a 172-bp *Nostoc* sp. strain PCC 7120 (*Anabaena* PCC 7120) hox promoter (21-192), an enzyme-encoding sequence (193-2142) selected/modified from the sequence of a methylenetetrahydrofolate reductase (GenBank: YP_430048) of *Moorella thermoacetica* and a coenzyme F_{420}-dependent N(5),N(10)-methenyltetrahydromethanopterin reductase (GenBank: ADN36752) of *Methanoplanus petrolearius*, a 432-bp *Nostoc* gor terminator (2143-2574), and a PCR RE primer (2575-2594).

[0371] SEQ ID NO: 171 presents example 171 of a designer hox-promoter-controlled Methyltetrahydrofolate:corrinoid/iron-sulfur protein methyltransferase (79, 88) DNA construct (2819 bp) that includes a PCR FD primer (sequence 1-20), a 172-bp *Nostoc* (*Anabaena* PCC 7120) hox promoter (21-192), an enzyme-encoding sequence (193-2467) selected/

modified from the sequence of a methyltetrahydrofolate:corrinoid/iron-sulfur protein methyltransferase (GenBank: YP_430950) of *Moorella thermoacetica*, and acetyl-CoA decarbonylase/synthase, subunit gamma (GenBank: ADL57900) of *Methanothermobacter marburgensis*, a 432-bp *Nostoc* sp. strain PCC 7120 gor terminator (2468-2899), and a PCR RE primer (2900-2819).

[0372] SEQ ID NO: 172 presents example 172 of a designer hox-promoter-controlled Corrinoid iron-sulfur protein (80, 89) DNA construct (2771 bp) that includes a PCR FD primer (sequence 1-20), a 172-bp *Nostoc* (*Anabaena* PCC 7120) hox promoter (21-192), an enzyme-encoding sequence (193-2319) selected/modified from the sequence of a small subunit corrinoid iron-sulfur protein (GenBank: AAA23255) of *Moorella thermoacetica*, and acetyl-CoA decarbonylase/synthase subunit delta (GenBank: ADL57899) of *Methanothermobacter marburgensis*, a 432-bp *Nostoc gor* terminator (2319-2751), and a PCR RE primer (2752-2771).

[0373] SEQ ID NO: 173 presents example 173 of a designer hox-promoter-controlled CO dehydrogenase/acetyl-CoA synthase (81, 90) DNA construct (7061 bp) that includes a PCR FD primer (sequence 1-20), a 172-bp *Nostoc* (*Anabaena* PCC 7120) hox promoter (21-192), an enzyme-encoding sequence (193-6609) selected/modified from the sequence of acetyl-CoA decarbonylase/synthase beta subunit/acetyl-CoA decarbonylase/synthase alpha subunit (GenBank: ABC19516) of *Moorella thermoacetica*, and acetyl-CoA decarbonylase/synthase subunits alpha, beta, epsilon (GenBank: ADL57895, ADL59006, ADL57897) of *Methanothermobacter marburgensis*, a 432-bp *Nostoc* sp. strain PCC 7120 gor terminator (6610-7041), and a PCR RE primer (7042-7061).

[0374] SEQ ID NO: 174 presents example 174 of a designer hox-promoter-controlled Thiolase (07) DNA construct (1847 bp) that includes a PCR FD primer (sequence 1-20), a 172-bp *Nostoc* (*Anabaena* PCC 7120) hox promoter (21-192), an enzyme-encoding sequence (193-1395) selected/modified from the sequence of thiolase (GenBank: AB190764) of *Butyrivibrio fibrisolvens*, a 432-bp *Nostoc gor* terminator (1396-1827), and a PCR RE primer (1828-1847).

[0375] SEQ ID NO: 175 presents example 175 of a designer hox-promoter-controlled 3-Hydroxybutyryl-CoA dehydrogenase (08) DNA construct (1514 bp) that includes a PCR FD primer (sequence 1-20), a 172-bp *Nostoc* (*Anabaena* PCC 7120) hox promoter (21-192), an enzyme-encoding sequence (193-1062) selected/modified from the sequence of 3-hydroxybutyryl coenzyme A dehydrogenase (GenBank: Z92974) of *Thermoanaerobacterium*, a 432-bp *Nostoc gor* terminator (1063-1494), and a PCR RE primer (1495-1514).

[0376] SEQ ID NO: 176 presents example 176 of a designer hox-promoter-controlled Crotonase (09) DNA construct (1430 bp) that includes a PCR FD primer (sequence 1-20), a 172-bp *Nostoc* (*Anabaena* PCC 7120) hox promoter (21-192), an enzyme-encoding sequence (193-978) selected from the sequence of crotonase (GenBank: AF494018) of *Clostridium beijerinckii*, a 432-bp *Nostoc gor* terminator (979-1410), and a PCR RE primer (1411-1430).

[0377] SEQ ID NO: 177 presents example 177 of a designer hox-promoter-controlled Butyryl-CoA dehydrogenase (10) DNA construct (1784 bp) that includes a PCR FD primer (sequence 1-20), a 172-bp *Nostoc* (*Anabaena* PCC 7120) hox promoter (21-192), an enzyme-encoding sequence (193-1332) selected/modified from the sequence of butyryl-CoA dehydrogenase (GenBank: AF494018) of *Clostridium beijerinckii*, a 432-bp *Nostoc gor* terminator (1333-1764), and a PCR RE primer (1765-1784).

[0378] SEQ ID NO: 178 presents example 178 of a designer hox-promoter-controlled Butyraldehyde dehydrogenase (11) DNA construct (2051 bp) that includes a PCR FD primer (sequence 1-20), a 172-bp *Nostoc* (*Anabaena* PCC 7120) hox promoter (21-192), an enzyme-encoding sequence (193-1599) selected/modified from the sequence of butyraldehyde dehydrogenase (GenBank: AY251646) of *Clostridium saccharoperbutylacetonicum*, a 432-bp *Nostoc gor* terminator (1600-2031), and a PCR RE primer (2032-2051).

[0379] SEQ ID NO: 179 presents example 179 of a designer hox-promoter-controlled NADH-dependent Butanol dehydrogenase (12) DNA construct (1808 bp) that includes a PCR FD primer (sequence 1-20), a 172-bp *Nostoc* (*Anabaena* PCC 7120) hox promoter (21-192), an enzyme-encoding sequence (193-1356) selected/modified from the sequence of NADH-dependent butanol dehydrogenase (GenBank: YP_148778) of *Geobacillus kaustophilus*, a 432-bp *Nostoc* sp. strain PCC 7120 gor terminator (1367-1788), and a PCR RE primer (1789-1808) at the 3' end.

[0380] Note, use of SEQ ID NOS. 166-179 in genetic transformation of a microbial host cell including (but not limited to) bacterial cells such as a cyanobacterium *Anabaena* PCC 7120 can create a designer cyanobacterium such as designer *Anabaena* with a designer reductive-acetyl-CoA biofuel-production pathway (numerically labeled as 83-90 and 07-12 in FIG. **13**) for production of 1-butanol from hydrogen and carbon dioxide without requiring photosynthesis or sunlight. That is, the expression of SEQ ID NOS. 166-179 in a bacterium such as *Anabaena* PCC 7120 represents a designer organism with the designer hydrogenotrophic reductive-acetyl-CoA biofuel-production pathway (83-90 and 07-12 in FIG. **13**) that can operate for anaerobic chemolithoautotrophic production of butanol from hydrogen and carbon dioxide even if it is in complete darkness.

[0381] SEQ ID NO: 180 presents example 180 of a designer hox-promoter-controlled Energy converting hydrogenase (Ech) (91) DNA construct (10538 bp) that includes a PCR FD primer (sequence 1-20), a 172-bp *Nostoc* (*Anabaena* PCC 7120) hox promoter (21-192), an enzyme-encoding sequence (193-10086) selected/modified from the sequence of Energy converting hydrogenase subunits (EchA, B, C, D, E. F, G, H, I, J, K, L, M, N, O, P, Q) (GenBank: ABC57807, and ABC57812-ABC57827) of *Methanosphaera stadtmanae* DSM 3091, a 432-bp *Nostoc gor* terminator (10087-10518), and a PCR RE primer (10519-10538).

[0382] SEQ ID NO: 181 presents example 181 of a designer hox-promoter-controlled [NiFe]-hydrogenase MvhADG (95) DNA construct (3416 bp) that includes a PCR FD primer (sequence 1-20), a 172-bp *Nostoc* (*Anabaena* PCC 7120) hox promoter (21-192), an enzyme-encoding sequence (193-2964) selected/modified from the sequence of [NiFe]-hydrogenase MvhADG (GenBank: ADL59096, ADL59098, ADL59097) of *Methanothermobacter marburgensis*, a 432-bp *Nostoc* sp. strain PCC 7120 gor terminator (2965-3396), and a PCR RE primer (3397-3416).

[0383] SEQ ID NO: 182 presents example 182 of a designer hox-promoter-controlled Heterodisulfide reductases (HdrABC, HdrDE) (94) DNA construct (6695 bp) that includes a PCR FD primer (sequence 1-20), a 172-bp *Anabaena* PCC 7120 hox promoter (21-192), an enzyme-encoding sequence (193-6243) selected/modified from the

sequence of Heterodisulfide reductases (HdrABC, HdrDE) (GenBank: AET63985, AET63982, AET63983, AET64166, AET64165) of *Methanosaeta harundinacea*, a 432-bp *Nostoc gor* terminator (6244-6675), and a PCR RE primer (6676-6695).

[0384] SEQ ID NO: 183 presents example 183 of a designer hox-promoter-controlled Coenzyme F_{420}-reducing hydrogenase (Frh) (96) DNA construct (3407 bp) that includes a PCR FD primer (sequence 1-20), a 172-bp *Nostoc* sp. strain PCC 7120 (*Anabaena* PCC 7120) hox promoter (21-192), an enzyme-encoding sequence (193-2955) selected/modified from the sequence of Coenzyme F_{420}-reducing hydrogenase (FrhB1-3) (GenBank: YP_003357229, YP_003357467, YP_003357509) of *Methanocella paludicola* SANAE, a 432-bp *Nostoc* sp. strain PCC 7120 gor terminator (2956-3387), and a PCR RE primer (3388-3407) at the 3' end.

[0385] Note, use of SEQ ID NOS. 180-183 in genetic transformation of a microbial host cell including (but not limited to) bacterial cells such as a cyanobacterium *Anabaena* PCC 7120 can confer an anaerobic chemolithoautotrophic hydrogen (H_2) utilization system [which, as shown in FIG. **12**, comprises Energy converting hydrogenase (Ech) (91), [NiFe]-hydrogenase MvhADG (95), Coenzyme F_{420}-reducing hydrogenase (Frh) (96), and Coenzyme F_{420}-reducing hydrogenase (Frh) (96)] that can produce reducing power (Fd_{red}^{2-} and $F_{420}H_2$) from H_2 in support of the designer reductive-acetyl-CoA butanol-production pathway (83-90 and 07-12 in FIG. **13**). Therefore, the expression of SEQ ID NOS. 180-183 along with SEQ ID NOS. 166-179 in a bacterium such as *Anabaena* PCC 7120 represents a designer organism (such as designer Anabaena) with a full designer reductive-acetyl-CoA biofuel-production pathway system (FIGS. **12** and **13**) that can operate for anaerobic chemolithoautotrophic production of butanol from hydrogen and carbon dioxide without requiring photosynthesis or aerobic respiration. The net result in this example is the anaerobic chemolithoautotrophic production of butanol from hydrogen and carbon dioxide as shown in the process equation [21].

[0386] Also note, these designer genes (SEQ ID NOS. 166-183) are controlled by a designer hox anaerobic promoter. Therefore, under aerobic conditions such as in an open pond mass culture, the designer *Anabaena* in this example can quickly grow photoautotrophically using air carbon dioxide and water as the sources of carbon and electrons just like the wild-type parental strain. When the designer *Anabaena* cells cultures are grown and ready for use (as catalysts in this application), they can then be placed into an anaerobic reactor supplied with industrial CO_2 and H_2 gas for induction of the designer genes expression for anaerobic chemolithoautotrophic production of butanol (as shown in FIGS. **12** and **13**) in dark.

[0387] SEQ ID NO: 184 presents example 184 of a designer hox-promoter-controlled Methyl-H4MPT: coenzyme M methyltransferase (MtrA-H) (92) DNA construct (5417 bp) that includes a PCR FD primer (sequence 1-20), a 172-bp *Anabaena* PCC 7120 hox promoter (21-192), an enzyme-encoding sequence (193-4965) selected/modified from the sequence of Methyl-H4MPT: coenzyme M methyltransferase (MtrA-H) (GenBank: ABC56714, ABC56713,YP_447360, YP_447354, YP_447359,YP_447355) of *Methanosphaera stadtmanae*, and mtrEF (AET65445, NC_009051) of *Methanosaeta harundinacea* and *Methanoculleus marisnigri*, a 432-bp *Nostoc* sp. strain PCC 7120 gor terminator (4966-5397), and a PCR RE primer (5398-5417).

[0388] SEQ ID NO: 185 presents example 185 of a designer hox-promoter-controlled Methyl-coenzyme M reductase (Mcr) (93) DNA construct (5042 bp) that includes a PCR FD primer (sequence 1-20), a 172-bp *Nostoc* sp. strain PCC 7120 (*Anabaena* PCC 7120) hox promoter (21-192), an enzyme-encoding sequence (193-4590) selected/modified from the sequence of methylcoenzyme M reductase subunits A, B. C, G (GenBank: CAE48306, CAE48303, ABC56709, CAE48305) of *Methanosphaera stadtmanae*, a 432-bp *Nostoc* sp. strain PCC 7120 gor terminator (4591-5022), and a PCR RE primer (5023-5042).

[0389] Note, use of SEQ ID NOS. 184 and 185 along with SEQ ID NOS. 180-183 in genetic transformation of a microbial host cell including bacterial cells such as a cyanobacterium *Anabaena* PCC 7120 can confer a methanogenic hydrogenotrophic system which, as shown in FIG. **15**, comprises Methyl-H4MPT: coenzyme M methyltransferase (MtrA-H) (92), Methyl-coenzyme M reductase (Mcr) (93), Energy converting hydrogenase (Ech) (91), [NiFe]-hydrogenase MvhADG (95), Coenzyme F_{420}-reducing hydrogenase (Frh) (96), Coenzyme F_{420}-reducing hydrogenase (Frh) (96). These enzymes along with a native ATPase 97 can produce ATP and reducing power (Fd_{red}^{2-} and $F_{420}H_2$) from H_2 in support of the designer reductive-acetyl-CoA methanogenic butanol-production pathways (FIGS. **16** and **17**). Therefore, the expression of SEQ ID NOS. 180-185 along with SEQ ID NOS. 166-179 in a bacterium such as *Anabaena* PCC 7120 represents a designer organism (such as designer *Anabaena*) with a designer hydrogenotrophic reductive-acetyl-CoA methanogenic biofuel-production pathway system (FIGS. **15** and **17**) that can operate for anaerobic production of both butanol and methane from hydrogen and carbon dioxide without requiring any photosynthesis. The net result in this example is the anaerobic chemolithoautotrophic production of butanol and methane from hydrogen and carbon dioxide as shown in the process equation [22].

[0390] SEQ ID NO: 186 presents example 186 of a designer hox-promoter-controlled Formate dehydrogenase (74) DNA construct (5450 bp) that includes a PCR FD primer (sequence 1-20), a 172-bp *Nostoc* sp. strain PCC 7120 (*Anabaena* PCC 7120) hox promoter (21-192), an enzyme-encoding sequence (193-4998) selected/modified from the sequence of formate dehydrogenase alpha and beta subunits (GenBank: AAB18330, AAB18329) of *Moorella thermoacetica*, a 432-bp *Nostoc* sp. strain PCC 7120 gor terminator (4999-5430), and a PCR RE primer (5431-5450).

[0391] SEQ ID NO: 187 presents example 187 of a designer hox-promoter-controlled 10-Formyl-H_4 folate synthetase (75) DNA construct (2324 bp) that includes a PCR FD primer (sequence 1-20), a 172-bp *Nostoc* (*Anabaena* PCC 7120) hox promoter (21-192), an enzyme-encoding sequence (193-1872) selected/modified from the sequence of 10-formyltetrahydrofolate synthetase (GenBank: YP_428991) of *Moorella thermoacetica*, a 432-bp *Nostoc* sp. strain PCC 7120 gor terminator (1873-2304), and a PCR RE primer (2305-2324).

[0392] SEQ ID NO: 188 presents example 188 of a designer hox-promoter-controlled 10-Methenyl-H_4 folate cyclohydrolase (76) DNA construct (1487 bp) that includes a PCR FD primer (sequence 1-20), a 172-bp *Nostoc* (*Anabaena* PCC 7120) hox promoter (21-192), an enzyme-encoding sequence

(193-1035) selected/modified from the sequence of methenyltetrahydrofolate cyclohydrolase (GenBank: YP_430368) of *Moorella thermoacetica* ATCC 39073, a 432-bp *Nostoc gor* terminator (1036-1467), and a PCR RE primer (1468-1487).

[0393] SEQ ID NO: 189 presents example 189 of a designer hox-promoter-controlled 10-Methylene-H_4 folate dehydrogenase (77) DNA construct (1487 bp) that includes a PCR FD primer (sequence 1-20), a 172-bp *Nostoc* (*Anabaena* PCC 7120) hox promoter (21-192), an enzyme-encoding sequence (193-1035) selected/modified from the sequence of methenyltetrahydrofolate cyclohydrolase/5,10-methylenetetrahydrofolate dehydrogenase (GenBank: ABC19825) of *Moorella thermoacetica*, a 432-bp *Nostoc* sp. strain PCC 7120 gor terminator (1036-1467), and a PCR RE primer (1468-1487).

[0394] SEQ ID NO: 190 presents example 190 of a designer hox-promoter-controlled 10-Methylene-H_4 folate reductase (78) DNA construct (1565 bp) that includes a PCR FD primer (sequence 1-20), a 172-bp *Nostoc* (*Anabaena* PCC 7120) hox promoter (21-192), an enzyme-encoding sequence (193-1113) selected/modified from the sequence of methylenetetrahydrofolate reductase (GenBank: ABC19505) of *Moorella thermoacetica*, a 432-bp *Nostoc gor* terminator (1114-1545), and a PCR RE primer (1546-1565).

[0395] SEQ ID NO: 191 presents example 191 of a designer hox-promoter-controlled Methyl-H_4 folate: corrinoid iron-sulfur protein Methyltransferase (79) DNA construct (1442 bp) that includes a PCR FD primer (sequence 1-20), a 172-bp *Anabaena* PCC 7120 hox promoter (21-192), an enzyme-encoding sequence (193-690) selected/modified from the sequence of methyltetrahydrofolate:corrinoid/iron-sulfur protein methyltransferase (GenBank: YP_430174) of *Moorella thermoacetica*, a 432-bp *Nostoc gor* terminator (691-1122), and a PCR RE primer (1123-1442).

[0396] SEQ ID NO: 192 presents example 192 of a designer hox-promoter-controlled Corrinoid iron-sulfur protein (80) DNA construct (2942 bp) that includes a PCR FD primer (sequence 1-20), a 172-bp *Anabaena* hox promoter (21-192), an enzyme-encoding sequence (193-2490) selected/modified from the sequence of corrinoid iron-sulfur protein large and small subunits (GenBank: AEI90745, AEI90746) of *Clostridium autoethanogenum*, a 432-bp *Nostoc* sp. strain PCC 7120 gor terminator (2491-2922), and a PCR RE primer (2923-2942).

[0397] SEQ ID NO: 193 presents example 193 of a designer hox-promoter-controlled CO dehydrogenase/acetyl-CoA synthase (81) DNA construct (4859 bp) that includes a PCR FD primer (sequence 1-20), a 172-bp *Anabaena* PCC 7120 hox promoter (21-192), an enzyme-encoding sequence (193-4407) selected/modified from the sequence of carbon monoxide dehydrogenase alpha subunit alpha and beta subunits (GenBank: AAA23229, AAA23228) of *Moorella thermoacetica*, a 432-bp *Nostoc gor* terminator (4408-4839), and a PCR RE primer (4840-4859).

[0398] Note, use of SEQ ID NOS. 186-193 along with SEQ ID NOS. 174-179 in genetic transformation of a microbial host cell such as a cyanobacterium *Anabaena* PCC 7120 confers an ATP-requiring reductive-acetyl-CoA butanol-production pathway (74-81 and 07-12/42 in FIG. **14**). Similarly, the expression of SEQ ID NOS. 186-193 and SEQ ID NOS. 180-185 along with SEQ ID NOS. 174-179 in a bacterium such as *Anabaena* PCC 7120 represents a designer organism (such as designer *Anabaena*) with a designer ATP-requiring reductive-acetyl-CoA methanogenic biofuel-production pathway and a hydrogenotrophic methanogenesis-coupled ATP-generating system (FIGS. **15** and **16**) that can operate for production of both butanol and methane from hydrogen and carbon dioxide. The net result in this example is the anaerobic chemolithotrophic production of both butanol and methane from hydrogen and carbon dioxide as shown in the process equation [22].

[0399] SEQ ID NO: 194 presents example 194 of a designer hox-promoter-controlled F_{420} synthesis enzymes (99) DNA construct (6428 bp) that includes a PCR FD primer (sequence 1-20), a 172-bp *Anabaena* PCC 7120 hox promoter (21-192), enzymes-encoding sequence (193-4976) selected/modified from the sequence of lactaldehyde dehydrogenase CofA (GenBank: ADC46523,) of *Methanobrevibacter ruminantium,* 2-phospho-l-lactate guanylyltransferase (GenBank: ADL58588) of *Methanothermobacter Marburgensis,* 2-phospho-L-lactate transferase (GenBank: NP_987524) of *Methanococcus maripaludis*, coenzyme F420-0 gamma-glutamyl ligase (YP_001030766) of *Methanocorpusculum labreanum*, FO synthase subunits 1 and 2 (YP_003357513, YP_003357511) of *Methanocella paludicolam*, a 432-bp *Nostoc* sp. strain PCC 7120 gor terminator (4977-6408), and a PCR RE primer (6409-6428).

[0400] SEQ ID NO: 195 presents example 195 of a designer hox-promoter-controlled Pyridoxal phosphate-dependent L-tyrosine decarboxylase(mfnA for methanofuran synthesis) (100) DNA construct (1778 bp) that includes a PCR FD primer (sequence 1-20), a 172-bp *Anabaena* PCC 7120 hox promoter (21-192), an enzyme-encoding sequence (193-1326) selected/modified from the sequence of L-tyrosine decarboxylase (GenBank: YP_003355454) of *Methanocella paludicola*, a 432-bp *Nostoc gor* terminator (1327-1758), and a PCR RE primer (1759-1778).

[0401] SEQ ID NO: 196 presents example 196 of a designer hox-promoter-controlled Methanopterin synthesis enzymes (101) DNA construct (3215 bp) that includes a PCR FD primer (sequence 1-20), a 172-bp *Anabaena* PCC 7120 hox promoter (21-192), an enzymes-encoding sequence (193-2763) selected/modified from the sequence of GTP cyclohydrolase (GenBank: YP_447347) of *Methanosphaera stadtmanae* DSM 3091, cyclic phosphodiesterase MptB (AB035741) of *Methanococcus maripaludis* C5, beta-ribofuranosylaminobenzene 5'-phosphate synthase (YP_003356610) of *Methanocella paludicola* SANAE, a 432-bp *Nostoc* sp. strain PCC 7120 gor terminator (2764-3195), and a PCR RE primer (3195-3215).

[0402] SEQ ID NO: 197 presents example 197 of a designer hox-promoter-controlled Coenzyme M synthesis enzymes (102) DNA construct (4226 bp) that includes a PCR FD primer (sequence 1-20), a 172-bp *Nostoc* sp. strain PCC 7120 (*Anabaena* PCC 7120) hox promoter (21-192), an enzymes-encoding sequence (193-3774) selected/modified from the sequence of phosphosulfolactate synthase, 2-phosphosulfolactate phosphatase and sulfolactate dehydrogenase (GenBank: ADL57861, YP_003850451, ADL59162) of *Methanothermobacter marburgensis*, and sulfopyruvate decarboxylase (YP_003357048) of *Methanocella paludicola* SANAE, a 432-bp *Nostoc* sp. strain PCC 7120 gor terminator (3775-4026), and a PCR RE primer (4027-4226).

[0403] SEQ ID NO: 198 presents example 198 of a designer hox-promoter-controlled Coenzyme B synthesis enzymes (103) DNA construct (5198 bp) that includes a PCR FD primer (sequence 1-20), a 172-bp *Anabaena* PCC 7120 hox

promoter (21-192), an enzymes-encoding sequence (193-4746) selected/modified from the sequence of isopropylmalate synthase, isopropylmalate dehydrogenase (GenBank: AAM01606, NP_614498) of *Methanopyrus kandleri*, isopropylmalate isomerase large and small subunits (ADP98363, ADP98362) of *Marinobacter adhaerens*, a 432-bp *Nostoc gor* terminator (4747-5178), and a PCR RE primer (5179-5198).

[0404] Note, the expression of SEQ ID NOS. 194-198 in a microbial host cell such as cyanobacterium *Anabaena* PCC 7120 provides the ability of synthesizing some of the cofactors such as F_{420}, methanofuran, methanopterin, Coenzyme M, and Coenzyme B that are needed for the designer hydrogenotrophic reductive-acetyl-CoA biofuel-production pathways (of FIGS. **13**,**14**,**16** and **17**) to properly operate. Depending on the genetic backgrounds of various host cells such as cyanobacteria, many of them may or may not possess some of these enzymes to synthesize this type of special cofactors. Therefore, in one of the various embodiments, it is a preferred practice to express this type of designer cofactor-synthesis enzymes (e.g., SEQ ID NOS. 194-198) along with the hydrogenotrophic designer reductive-acetyl-CoA biofuel-production pathway genes (e.g., SEQ ID NOS. 166-193) as shown in these examples.

[0405] Note, many of the hydrogenotrophic bacteria and methanogens such as *Methanocella paludicola* SANAE naturally possess certain hydrogenotrophic and/or reductive acetyl-CoA pathway(s) and the ability of synthesizing the associated cofactors including F420, methanofuran, methanopterin, Coenzyme M, and Coenzyme B. Therefore, in one of the various embodiments, it is also a preferred practice to express certain designer genes of biofuel-production-pathways (FIGS. **1**, **4**, **5**, **6**, **7**, **8**, **10**, **13**, and **14**) such as SEQ ID NOS. 174-179 in a hydrogenotrophic and/or methanogenic host cell for chemolithotrophic production of advanced biofuels such as 1-buatanol from hydrogen (H_2) and carbon dioxide (CO_2). According to one of the various embodiments, a hydrogenotrophic and/or methanogenic host organism for this specific application is selected from the group consisting of: *Methanocella paludicola* SANAE, *Acinetobacter baumannii* ABNIH3, *Acinetobacter baumannii* ABNIH4, *Acinetobacter* sp. DR1, *Agrobacterium* sp. H13-3; *Agrobacterium vitis* S4, *Alcaligenes* sp., *Allochromatium vinosum* DSM 180, *Amycolatopsis mediterranei* S699, *Anoxybacillus flavithermus* WK1, *Aquifex aeolicus* VF5, *Archaeoglobus fulgidus* DSM 4304, *Archaeoglobus veneficus* SNP6, *Azospirillum* sp. B510, *Burkholderia cenocepacia* HI2424, *Caldicellulosiruptor bescii* DSM 6725, *Carboxydothermus hydrogenoformans, Centipeda periodontii* DSM 2778, *Clostridium autoethanogenum, Clostridium ragsdalei, Clostridium sticklandii* DSM 519, *Clostridium sticklandii, Corynebacterium glutamicum, Cupriavidus metallidurans* CH34, *Cupriavidus necator* N-1, *Desulfobacca acetoxidans* DSM 11109, *Exiguobacterium* sp. AT1b, *Ferrimonas balearica* DSM 9799, *Ferroglobus placidus* DSM 10642, *Geobacillus kaustophilus* HTA426, *Helicobacter bilis* ATCC 43879, *Herbaspirillum seropedicae* SmR1, *Hydrogenobacter thermophilus* TK-6, *Hydrogenovibrio marinus, Klebsiella variicola* At-22, *Methanobacterium* sp. SWAN-1, *Methanobrevibacter ruminantium* M1, *Methanocaldococcus fervens* AG86, *Methanocaldococcus infernus* ME, *Methanocaldococcus jannaschii, Methanocaldococcus* sp. FS406-22, *Methanocaldococcus vulcanius* M7, *Methanococcus aeolicus* Nankai-3, *Methanococcus maripaludis* C6, *Methanococcus maripaludis* S2, *Methanococcus voltae* A3, *Methanocorpusculum labreanum* Z, *Methanoculleus marisnigri* JR1, *Methanohalophilus mahii* DSM 5219, *Methanolinea tarda* NOBI-1, *Methanoplanus petrolearius* DSM 11571, *Methanoplanus petrolearius, Methanopyrus kandleri* AV19, *Methanoregula boonei* 6A8, *Methanosaeta harundinacea* 6Ac, *Methanosalsum zhilinae* DSM 4017, *Methanosarcina acetivorans* C2A, *Methanosarcina barkeri* str. *Fusaro, Methanosarcina mazei* Go1, *Methanosphaera stadtmanae, Methanospirillum hungatei* JF-1, *Methanothermobacter marburgensis* str. *Marburg, Methanothermobacter marburgensis, Methanothermobacter thermautotrophicus, Methanothermococcus okinawensis* IH1, *Methanothermus fervidus* DSM 2088, *Methylobacillus flagellates, Methylobacterium organophilum, Methylococcus capsulatus, Methylomicrobium kenyense, Methylomonas methanica* MC09, *Methylomonas* sp. LW13, *Methylosinus* sp. LW2, *Methylosinus trichosporium* OB3b, *Methylotenera mobilis* JLW8, *Methylotenera versatilis* 301, *Methylovorus glucosetrophus* SIP3-4, *Moorella thermoacetica* ATCC 39073, *Moorella thermoacetica, Oligotropha carboxidovorans* OM5, *Paenibacillus terse* HPL-003, *Pelotomaculum thermopropionicum* SI *Planctomyces brasiliensis* DSM 5305, *Pyrococcus furiosus* DSM 3638, *Pyrococcus horikoshii* OT3, *Pyrococcus yayanosii* CH1, *Ralstonia eutropha* H16, *Rubrivivax* sp., *Selenomonas noxia* ATCC 43541, *Shewanella baltica* BA175, *Stenotrophomonas* sp. SKA14, *Synechococcus* sp. JA-2-3B' a(2-13), *Synechococcus* sp. JA-3-3Ab, *Thermococcus gammatolerans* EJ3, *Thermococcus kodakarensis* KOD1, *Thermococcus onnurineus* NA1, *Thermococcus* sp. 4557, *Thermodesulfatator indicus* DSM 15286, *Thermofilum pendens* Hrk 5, *Thermotoga lettingae* TMO, *Thermotoga petrophila* RKU-1, *Thiocapsa roseopersicina, Thiomonas intermedia* K12, *Xanthobacter autotrophicus, Yersinia pestis Antigua*, and combinations thereof.

[0406] While the present invention has been illustrated by description of several embodiments and while the illustrative embodiments have been described in considerable detail, it is not the intention of the applicant to restrict or in any way limit the scope of the appended claims to such detail. Additional advantages and modifications will readily appear to those skilled in the art. The invention in its broader aspects is therefore not limited to the specific details, representative apparatus and methods, and illustrative examples shown and described. Accordingly, departures may be made from such details without departing from the spirit or scope of applicant's general inventive concept.

SEQUENCE LISTING

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gcgctgaagc ccgccgtcaa ggctgccccc gtggctgccc cggctcaggc caaccagatg 420

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cttccagagg ttttaaaaag atatggtaaa aatatattac ttgcatatgg tggtggaagt 540

ataaaaaaga atggactcta tgatactatc caaaagctat tgaaagattt taatattgtt 600

gaattaagtg gtattgaacc aaatccaaga attgaaactg taagacgtgg agttgaactt 660

tgcagaaaaa ataaagtaga tgttatttta gctgttggtg gagggagtac aatagactgc 720

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ccagctaaaa taggtgaggt tttaccaata gtgacagttt taacaatggc agctactggt 840

tctgaaatga atagaaatgc tgttatttca aagatggata caaatgaaaa gcttggaaca 900

ggatcaccta agatgatccc tcaaacttct attttagatc cagaatattt gtatacattg 960

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designer Butyraldehyde-Dehydrogenase DNA construct (2067 bp)

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aaccagatga atttccaatt aactagagaa caacaattag tacaacaaat ggttagagaa 480

ttcgcagtaa atgaagttaa gccaatagct gctgaaatcg acgaaacaga aagattccct 540

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gaaaataaga tggggatcag agcatcttca actactgagt tagttatgga aaactgcata 1080

gtaccaaaag aaaacctact tagcaaagaa ggtaagggat ttggtatagc aatgaaaact 1140

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gaagaagctg ttaactatat gaaagaaaga aaacaatttg gtaaaccatt atcagcattc 1260

caaggattac aatggtatat agctgaaatg gatgttaaaa tccaagctgc taaatactta 1320

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tgcgaaatct acgaaggaac ttcagaagtt caaaagatgg ttatcgcagg aagcatttta 1560

agataatcta gataaatgga ggcgctcgtt gatctgagcc ttgccccctg acgaacggcg 1620

gtggatggaa gatactgctc tcaagtgctg aagcggtagc ttagctcccc gtttcgtgct 1680

gatcagtctt tttcaacacg taaaaagcgg aggagttttg caattttgtt ggttgtaacg 1740

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ttgtgcgcgc attagggctt cgggtcgcaa gcaagacgat acctcgagca tatggccgcc 300

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aaccagatgg aattaaaaaa tgttattctt gaaaaagaag ggcatttagc tattgttaca 480

atcaatagac caaaggcatt aaatgcattg aattcagaaa cactaaaaga tttaaatgtt 540

gttttagatg atttagaagc agacaacaat gtgtatgcag ttatagttac tggtgctggt 600

gagaaatctt ttgttgctgg agcagatatt tcagaaatga aagatcttaa tgaagaacaa 660

ggtaaagaat ttggtatttt aggaaataat gtcttcagaa gattagaaaa attggataag 720

ccagttatcg cagctatatc aggatttgct cttggtggtg gatgtgaact tgctatgtca 780

tgtgacataa gaatagcttc agttaaagct aaatttggtc aaccagaagc aggacttgga 840

ataactccag gatttggtgg aactcaaaga ttagcaagaa tagttggacc aggaaaagct 900

aaagaattaa tttatacttg tgaccttata aatgcagaag aagcttatag aataggctta 960

gttaataaag tagttgaatt agaaaaattg atggaagaag caaaagcaat ggctaacaag 1020

attgcagcta atgctccaaa agcagttgca tattgtaaag atgctataga cagaggaatg 1080

caagttgata tagatgcagc tatattaata gaagcagaag actttgggaa gtgctttgca 1140

acagaagatc aaacagaagg aatgactgcg ttcttagaaa gaagagcaga aaagaatttt 1200

caaaataaag gctgctgccc cggctgctgc taatctagat aaatggaggc gctcgttgat 1260

ctgagccttg ccccctgacg aacggcggtg gatggaagat actgctctca agtgctgaag 1320

cggtagctta gctccccgtt tcgtgctgat cagtcttttt caacacgtaa aaagcggagg 1380

agttttgcaa ttttgttggt tgtaacgatc ctccgttgat tttggcctct ttctccatgg 1440

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<210> SEQ ID NO 5
<211> LENGTH: 1367
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 5, Example 5: designer 3-Hydroxybutyryl-CoA-Dehydrogenase DNA construct (1367 bp)

<400> SEQUENCE: 5

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ccgtcattgc caagtcctcc gtctccgcgg ccgtggctcg cccggcccgc tccagcgtgc 180

gccccatggc cgcgctgaag cccgccgtca aggctgcccc cgtggctgcc ccggctcagg 240

ccaaccagat gaaaaagatt tttgtacttg gagcaggaac tatgggtgct ggtatcgttc 300

aagcattcgc tcaaaaaggt tgtgaggtaa ttgtaagaga cataaaggaa gaatttgttg 360

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acagaggaat agctggaatc actaaaggat tagaaaagca agttgctaaa ggaaaaatgt 420

ctgaagaaga taaagaagct atactttcaa gaatttcagg aacaactgat atgaagttag 480

ctgctgactg tgatttagta gttgaagctg caatcgaaaa catgaaaatt aagaaggaaa 540

tctttgctga gttagatgga atttgtaagc cagaagcgat tttagcttca aacacttcat 600

ctttatcaat tactgaagtt gcttcagcta caaagagacc tgataaagtt atcggaatgc 660

atttctttaa tccagctcca gtaatgaagc ttgttgaaat tattaaagga atagctactt 720

ctcaagaaac ttttgatgct gttaaggaat tatcagttgc tattggaaaa gaaccagtag 780

aagttgcaga agctccagga ttcgttgtaa acggaatctt aatcccaatg attaacgaag 840

cttcattcat ccttcaagaa ggaatagctt cagttgaaga tattgataca gctatgaaat 900

atggtgctaa ccatccaatg ggacctttag ctttaggaga tcttattgga ttagatgttt 960

gcttagctat catggatgtt ttattcactg aaacaggtga taacaagtac agagctagca 1020

gcatattaag aaaatatgtt agagctggat ggcttggaag aaaatcagga aaaggattct 1080

atgattattc taaaggctgc tgccccggct gctgctaatc tagataaatg gaggcgctcg 1140

ttgatctgag ccttgccccc tgacgaacgg cggtggatgg aagatactgc tctcaagtgc 1200

tgaagcggta gcttagctcc ccgtttcgtg ctgatcagtc tttttcaaca cgtaaaaagc 1260

ggaggagttt tgcaattttg ttggttgtaa cgatcctccg ttgattttgg cctctttctc 1320

catgggcggg ctgggcgtat ttgaagcggt tctctcttct gccgtta 1367

<210> SEQ ID NO 6
<211> LENGTH: 1721
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 6, Example 6: designer Thiolase DNA construct (1721 bp)

<400> SEQUENCE: 6

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caaacgaccc cgccgtacga acttttgtcg gggggcgctc ccggctcgag catatggccg 120

ccgtcattgc caagtcctcc gtctccgcgg ccgtggctcg cccggcccgc tccagcgtgc 180

gccccatggc cgcgctgaag cccgccgtca aggctgcccc cgtggctgcc ccggctcagg 240

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ctcttaaccg cgcaggtgtt aaacctgaag atgttgatca cgtatacatg ggatgcgtta 420

ttcaggcagg acagggacag aacgttgctc gtcaggcttc tatcaaggct ggtcttcctg 480

tagaagtacc tgcagttaca actaacgttg tatgtggttc aggtcttaac tgtgttaacc 540

aggcagctca gatgatcatg gctggagatg ctgatatcgt tgttgccggt ggtatggaaa 600

acatgtcact tgcaccattt gcacttccta atggccgtta cggatatcgt atgatgtggc 660

caagccagag ccagggtggt cttgtagaca ctatggttaa ggatgctctt tgggatgctt 720

tcaatgatta tcatatgatc cagacagcag acaacatctg cacagagtgg ggtcttacac 780

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ctacattcgt agctggagca cttgctggtg ttcgtcctga agttatgggt atcggtcctg   1140

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tcatcgaggc taacgaagca ttcgcagctc agtctgtagc agttggtaag gatcttggaa   1260

tcgacgtcca caagcagctc aatcctaacg gtggtgctat cgctcttgga cacccagttg   1320

gagcttcagg tgctcgtatc cttgttacac ttcttcacga gatgcagaag aaagacgcta   1380

agaagggtct tgctacactt tgcatcggtg gcggtatggg atgcgctact atcgttgaga   1440

agtacgaagg ctgctgcccc ggctgctgct aatctagata aatggaggcg ctcgttgatc   1500

tgagccttgc cccctgacga acggcggtgg atggaagata ctgctctcaa gtgctgaagc   1560

ggtagcttag ctccccgttt cgtgctgatc agtctttttc aacacgtaaa aagcggagga   1620

gttttgcaat tttgttggtt gtaacgatcc tccgttgatt ttggcctctt tctccatggg   1680

cgggctgggc gtatttgaag cggttctctc ttctgccgtt a                       1721
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<210> SEQ ID NO 7
<211> LENGTH: 4211
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 7, Example 7: designer Pyruvate-Ferredoxin-Oxidoreductase DNA construct (4211 bp)

<400> SEQUENCE: 7

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gaccccgcgc gacttggaag ggttcaaacg accccgccgt acgaactttt gtcgggggggc    180

gctcccggct cgagcatatg gccgccgtca ttgccaagtc ctccgtctcc gcggccgtgg    240

ctcgcccggc ccgctccagc gtgcgcccca tggccgcgct gaagcccgcc gtcaaggctg    300

cccccgtggc tgccccggct caggccaacc agatggcgca gaggtgcaag gagcccgtcg    360

acggaacgac agccacgacg cacgtggcct acttcatgag cgacagcgcg ttcatcttcc    420

ccatcacgcc cagctcggtc atgtccgagg tcgcccacga gtggtccatg aacggccgca    480

agaacgcctt cggccagccc acgatggtcc gccagatgca gagcgaggct gggtctgccg    540

gcgccctgca cggcgcgctc agcgagggag cgctggcgac gacgttcacg agcagccagg    600

gcctgctgct catgatcccc aacatgtaca agatcgccgg cgagctcctg ccctgcgtca    660

tgcacatcgc cgcccgcacc gtcgccaccg aggccctctc tatcttcggc gaccacacgg    720

atgtctacgc ggtgaggtcg acggggttcg cgttcctgtg ctccgcgacc gtccaggagt    780

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agctgatcgc gcgcacgagt ttctggatcc tcggtggcga cgggtgggcg tacgacatcg 3300

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ttctgccgtt a 4211

<210> SEQ ID NO 8
<211> LENGTH: 2021
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 8, Example 8: designer Pyruvate-Kinase DNA construct (2021 bp)

<400> SEQUENCE: 8

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caaacgaccc cgccgtacga acttttgtcg gggggcgctc ccggctcgag catatggccg 120

ccgtcattgc caagtcctcc gtctccgcgg ccgtggctcg cccggcccgc tccagcgtgc 180

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ttgctttgag aaaggctggt ttgaacattg tccgtatgaa cttctctcac ggttcttacg 420

aataccacaa gtctgtcatt gacaacgcca gaaagtccga agaattgtac ccaggtagac 480

cattggccat tgctttggac accaagggtc cagaaatcag aactggtacc accaccaacg 540

atgttgacta cccaatccca ccaaaccacg aaatgatctt caccaccgat gacaagtacg 600

ctaaggcttg tgacgacaag atcatgtacg ttgactacaa gaacatcacc aaggtcatct 660

ccgctggtag aatcatctac gttgatgatg gtgttttgtc tttccaagtt ttggaagtcg 720

ttgacgacaa gactttgaag gtcaaggctt tgaacgccgg taagatctgt tcccacaagg 780

gtgtcaactt accaggtacc gatgtcgatt tgccagcttt gtctgaaaag gacaaggaag 840

atttgagatt cggtgtcaag aacggtgtcc acatggtctt cgcttctttc atcagaaccg 900

ccaacgatgt tttgaccatc agagaagtct tgggtgaaca aggtaaggac gtcaagatca 960

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acggtgttat ggttgccaga ggtgacttgg gtattgaaat cccagcccca gaagtcttgg 1080

ctgtccaaaa gaaattgatt gctaagtcta acttggctgg taagccagtt atctgtgcta 1140

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ctatcgctta cttgccaaac tacgatgaca tgagaaactg tactccaaag ccaacctcca 1380

ccaccgaaac cgtcgctgcc tccgctgtcg ctgctgtttt cgaacaaaag gccaaggcta 1440

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cttacgtttc catccaaggt ttcaaggccg gtgctggtca ctccaacact ttgcaagtct 1740

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ggtagcttag ctccccgttt cgtgctgatc agtctttttc aacacgtaaa aagcggagga 1920

gttttgcaat tttgttggtt gtaacgatcc tccgttgatt ttggcctctt tctccatggg 1980

cgggctgggc gtatttgaag cggttctctc ttctgccgtt a 2021

<210> SEQ ID NO 9
<211> LENGTH: 1815
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 9, Example 9: designer Enolase DNA construct (1815 bp)

<400> SEQUENCE: 9

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gcgcatgaaa atgcattcgc ttccatagga cgctgcattg tggcttgaag gttcaaggga 180

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ggtgccgctg agaagggcgt gcccctgtac aagcacattg cggacctggc cggcaacagc 660

aagctgatcc tgcccgtgcc ctcgttcaac atcatcaacg gcggcagcca cgccggcaac 720

gccctggcta tgcaggagtt catgatcctg cccgttggcg cctcgagctt ctctgaggcc 780

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ttcaagaacc agcccaacga tggctcgcag aagaagacca aggagcagat gctggagctg 1080

tacaacgagt tctgcaagaa gtacccggtc atctccatcg aggacccctt cgagcaggac 1140

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gccaaggagg ccggctgggg tgtcatgacc agccaccgct cgggtgagac tgaggactct 1380

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tgctaatcta gataaatgga ggcgctcgtt gatctgagcc ttgccccctg acgaacggcg 1620

gtggatggaa gatactgctc tcaagtgctg aagcggtagc ttagctcccc gtttcgtgct 1680

gatcagtctt tttcaacacg taaaaagcgg aggagttttg caattttgtt ggttgtaacg 1740

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<210> SEQ ID NO 10
<211> LENGTH: 2349
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 10, Example 10: designer Phosphoglycerate-Mutase DNA construct (2349 bp)

<400> SEQUENCE: 10

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agggttcaaa cgaccccgcc gtacgaactt ttgtcggggg gcgctcccgg ccccgggctc 240

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gtcattgcca agtcctccgt ctccgcggcc gtggctcgcc cggcccgctc cagcgtgcgc 360

cccatggccg cgctgaagcc cgccgtcaag gctgcccccg tggctgcccc ggctcaggcc 420

aaccagatgg cgcacgacta caagctgaag gcccacccgg cgattcctgc gcccgagggc 480

ccgctgctgg tctgcattct ggacggcttc ggcgagaacg agtacaagga tgagttcaac 540

gccgtgcacg tggctaagac gcccactgtg gacgcgctgc gcgctgtgcc ccatcgcttc 600

cgttccatca aggcgcacgg aaaggctgtg ggcctgccca gcgatgccga catgggcaac 660

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gtgaagcgcg gctgggacgc gcacgtgctg ggcaaggcgc cccactactt caaggacgcc 1140

aagaccgcgg tcaccaccct gcgcggctcc gaggacgcgc cggtgtctga ccagtacgtg 1200

gccccctttg tgattgtgga cgaggcggac aagccggtgg gcaccattga ggacggcgac 1260

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tacgaggacg gcttcaccgc ctttgagcgc gagcgcttcc ccaagggcct gcgcttcgtg 1380

ggcatgatgc agtacgacgg cgacctgaag ctgcccgcca acttcctggt gccgccgccc 1440

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tccgagactc agaagttcgg gcacgtgacg ttcttctgga acggcaaccg ctccggctac 1560

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gctccggaca tgaaggcgcg cgagatcacc gccgccggca ttgaggcgct caagagcggc 1680

aagtacaagg tggtgcgcat caactacgcc aacccggaca tggtcggcca caccggcgac 1740

atggctgcca ccgtccgcgc ctgcgagacc gtggacgggt gcgtgaagga gctgctggag 1800

gtggtggaca gcctgaacgg ccgctggatc gtcacgtccg accacggcaa cgccgacgac 1860

atggtgcagc gcgacaagaa gggcaagccc ctgctgggcg aggacggcaa gccgctgccc 1920

ctgaccagcc acacgctggc gcccgtgccg ttcttcatcg gcggcaaggg cctgccggac 1980

ggcgtggtgc tgcgcgacga cctgccggac gccgggctgg ccaacgtggc cgccaccacc 2040

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tctagataaa tggaggcgct cgttgatctg agccttgccc cctgacgaac ggcggtggat 2160

ggaagatact gctctcaagt gctgaagcgg tagcttagct ccccgtttcg tgctgatcag 2220

tctttttcaa cacgtaaaaa gcggaggagt tttgcaattt tgttggttgt aacgatcctc 2280

cgttgatttt ggcctctttc tccatgggcg ggctgggcgt atttgaagcg gttctctctt 2340

ctgccgtta 2349

<210> SEQ ID NO 11
<211> LENGTH: 1908
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 11, Example 11: designer Phosphoglycerate-Kinase DNA construct (1908 bp)

<400> SEQUENCE: 11

agaaaatctg gcaccacacc tatatggtag ggtgcgagtg accccgcgcg acttggagct 60

cgatggcccc gggttgtttg gggcgtccgc ctctcgcgct attctgagct ggagaccgag 120

gcgcatgaaa atgcattcgc ttccatagga cgctgcattg tggcttgaag gttcaaggga 180

agggttcaaa cgaccccgcc gtacgaactt ttgtcggggg gcgctcccgg ccccgggctc 240

ttgtgcgcgc attagggctt cgggtcgcaa gcaagacgat acatggccct ctctatgaag 300

atgcgcgcca acgcgcgcgt gtccggtcgc cgcgtcgccg ctgtggcccc ccgcgtggtg 360

cccttctcgt cggcctccag ctccgtgctg cgctctggct tcgcgctgag gtgtctgtgg 420

acatccgccg cgtgggccgc tctcgcatcc gtcgtcgagg cggtgaagaa gtcggttggc 480

gacctgcaca aggctgacct ggagggcaag cgcgtgttcg tccgcgcgga cctgaacgtg 540

cctcttgaca aggccaccct ggccatcacc gacgacaccc gcattcgcgc ggccgtcccc 600

accctgaagt acctgctgga caacggtgct aaggtcctgc tgacctcgca cctgggtcgc 660

ccgaagggcg gtcccgagga caagtaccgc ctgacccccg tggtggcccg cctgtcggag 720

ctgctgggca agcccgtgac caaggtcgat gactgcatcg gccccgaggt ggagaaggcg 780

gtgggcgcca tgaagaacgg cgagctgctg ctgctggaga actgccgctt ctacaaggag 840

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gaggagaaga acgagcccga gttcgccaag aagctggccg ccaacgccga cctgtacgtg 900

aacgacgcgt tcggcactgc ccaccgcgcc cacgcctcca ccgagggtgt gaccaagttc 960

ctgaagccct ccgtggccgg cttcctgctg cagaaggagc tggactacct tgatggcgcc 1020

gtgtccaacc ccaagcgccc cttcgtggcc attgtgggcg gctccaaggt gtcctccaag 1080

atcaccgtca ttgaggcgct gatggagaag tgcgacaaga tcatcatcgg cggtggcatg 1140

atcttcacct tctacaaggc ccgcgcgctg aaggtgggct cctcgctggt tgaggacgac 1200

aagatcgagc tggccaagaa gctggaggag atggccaagg ccaagggtgt gcagctgctg 1260

ctgcccaccg acgtggtggt ggccgacaag ttcgacgcca acgccaacac ccagaccgtg 1320

cccatcaccg ccatccccga tggctggatg ggtctggaca ttggcccgga ctccgtcaag 1380

accttcaacg acgccctggc cgacgccaag accgttgtgt ggaacggccc catgggtgtg 1440

ttcgagtttc cccaagttcg ccaacgcacc gtgtcgatcg ccaacaccct ggccggcctg 1500

acgcccaagg gctgcatcac catcattggt ggcggtgact ccgtggctgc cgtcgagcag 1560

gccggcgttg ccgagaagat gagccacatc tccaccggcg gcggtgcctc cctggagctg 1620

ctggagggca aggtcctgcc cggcgtggcc gccctggacg agaagtaaat ggaggcgctc 1680

gttgatctga gccttgcccc ctgacgaacg gcggtggatg gaagatactg ctctcaagtg 1740

ctgaagcggt agcttagctc cccgtttcgt gctgatcagt ctttttcaac acgtaaaaag 1800

cggaggagtt ttgcaatttt gttggttgta acgatcctcc gttgattttg gcctctttct 1860

ccatgggcgg gctgggcgta tttgaagcgg ttctctcttc tgccgtta 1908

<210> SEQ ID NO 12
<211> LENGTH: 1677
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 12, Example 12: designer NAD-dependent Glyceraldehyde-3-Phosphate-Dehydrogenase DNA construct (1677 bp)

<400> SEQUENCE: 12

agaaaatctg gcaccacacc tatatggtag ggtgcgagtg accccgcgcg acttggagct 60

cgatggcccc gggttgtttg gggcgtccgc ctctcgcgct attctgagct ggagaccgag 120

gcgcatgaaa atgcattcgc ttccatagga cgctgcattg tggcttgaag gttcaaggga 180

agggttcaaa cgaccccgcc gtacgaactt ttgtcggggg gcgctcccgg ccccgggctc 240

ttgtgcgcgc attagggctt cgggtcgcaa gcaagacgat acatggccgc cgtcattgcc 300

aagtcctccg tctccgcggc cgtggctcgc ccggcccgct ccagcgtgcg ccccatggcc 360

gcgctgaagc ccgccgtcaa ggctgccccc gtggctgccc cggctcaggc caaccagatg 420

gctcccatca agatcggcat caatggtttt ggtcgtattg gccgcctcgt gtggcgtgcc 480

actcttaacc gtgacgatgt cgaggtcgtc gccatcaatg atccattcat tgatgtgcca 540

tacatggtct acatggccaa gtatgactcg gtccacggca acctgaccca cgacgttcag 600

caaggcgacg gcaagctgat ggtcaatggc aagtcaatca ccatcttcgg caagatggat 660

gccaaggaga tcccatggaa ggaggccggc gcgaccttcg tcgttgagtc gactggtgtg 720

ttcaccaccc tggagggcgc cagctctcac ctggtcggcg gtgctgagac cgtcgtcatc 780

tccgccccat caaacgatgc ccccatgttc gtcatgggtg tcaacgagga gggctacaag 840

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ccagacatga aagtggtgtc caacgcgtct tgcaccacca actgcctggg ccccctggcc 900

aaggtcatcc accttaagtt cggcatcctg gagggcctga tgaccaccgt ccacgcgacc 960

accgccaccc agaagaccgt cgacgggccg tccaagaagg actggcgcgg cgggcgcggc 1020

atcctggaca acatcatccc ctcggcgact ggtgccgcca aggccgtcgg caaggtgctg 1080

cctgccctga acggcaagct caccggcatg gccttccgcg tgcccacccc cgatgtctcg 1140

gtcgtcgatc tgaccgtgcg cctggagaag ggtgcgtcgt acgacgccat caaggccgag 1200

atcaagcgcg cgagcgagaa cgagctcaag ggcatcctgg cctacaccga ggatgccgtg 1260

gtctccaccg acttcatcgg caacaagcac agctccatct tcgacgccga ggccggcatc 1320

gccctcaacg acaactttgt caagctggtc tcctggtacg acaacgagtg gggctactcc 1380

aaccgtgtcg tcgacctgat cgcgcacatg gccaaggtca aggccgccag ccactaaatg 1440

gaggcgctcg ttgatctgag ccttgccccc tgacgaacgg cggtggatgg aagatactgc 1500

tctcaagtgc tgaagcggta gcttagctcc ccgtttcgtg ctgatcagtc tttttcaaca 1560

cgtaaaaagc ggaggagttt tgcaattttg ttggttgtaa cgatcctccg ttgattttgg 1620

cctctttctc catgggcggg ctgggcgtat ttgaagcggt tctctcttct gccgtta 1677

<210> SEQ ID NO 13
<211> LENGTH: 2351
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 13, Example 13: designer HydA1-promoter-linked Phosphoglycerate-Mutase DNA construct (2351 bp)

<400> SEQUENCE: 13

agaaaatctg gcaccacacc gagctgtcat gcgttgttcc gttatgtgtc gtcaaacgcc 60

ttcgagcgct gcccggaaca atgcgtacta gtataggagc catgaggcaa gtgaacagaa 120

gcgggctgac tggtcaaggc gcacgatagg gctgacgagc gtgctgacgg ggtgtaccgc 180

cgagtgtccg ctgcattccc gccggattgg gaaatcgcga tggtcgcgca taggcaagct 240

cgcaaatgct gtcagcttat cttacatgaa cacacaaaca ctctcgcagg cactagcctc 300

aaatggccgc cgtcattgcc aagtcctccg tctccgcggc cgtggctcgc ccggcccgct 360

ccagcgtgcg ccccatggcc gcgctgaagc ccgccgtcaa ggctgccccc gtggctgccc 420

cggctcaggc caaccagatg gcgcacgact acaagctgaa ggcccacccg gcgattcctg 480

cgcccgaggg cccgctgctg gtctgcattc tggacggctt cggcgagaac gagtacaagg 540

atgagttcaa cgccgtgcac gtggctaaga cgcccactgt ggacgcgctg cgcgctgtgc 600

cccatcgctt ccgttccatc aaggcgcacg gaaaggctgt gggcctgccc agcgatgccg 660

acatgggcaa cagcgaggtg gggcacaacg ccctgggctc gggccaggtg gtggaccaag 720

gcgcgcgcct ggtggacctg gcgctggaga ccggccgtat gttctcggac cccggctgga 780

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gcggcgtgca ctcgcgcgcc gatcagctgc acggctgcct gcgcggcgcc gtggagcgcg 900

gcgccaagcg cgtgcgcgtg cacatcctga ctgacggccg cgacgtgccg gacggcagca 960

gcatccggtt cgtggaggag ctggaggcgg tgctggcgga gctgcgcggc aagggctgcg 1020

acatcgccat cgcctcgggc ggcggccgca tgcaggtcac catggaccgc tacgaggcgg 1080

actggagcat ggtgaagcgc ggctgggacg cgcacgtgct gggcaaggcg ccccactact 1140

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tcaaggacgc caagaccgcg gtcaccaccc tgcgcggctc cgaggacgcg ccggtgtctg 1200

accagtacgt ggcccccttt gtgattgtgg acgaggcgga caagccggtg ggcaccattg 1260

aggacggcga cgcggtggtg ctgttcaact tccgcgcgga ccgcatggtg gagatcagca 1320

aggccttcga gtacgaggac ggcttcaccg cctttgagcg cgagcgcttc cccaagggcc 1380

tgcgcttcgt gggcatgatg cagtacgacg gcgacctgaa gctgcccgcc aacttcctgg 1440

tgccgccgcc cctgattgag cacgtgtcgg gcgagtacct gtgcaagaac gggctgagca 1500

ccttcgcctg ctccgagact cagaagttcg ggcacgtgac gttcttctgg aacggcaacc 1560

gctccggcta cctggacgcc aagcaggagc agtacctgga gatcccgtcg gacaagatcg 1620

agttcaacaa ggctccggac atgaaggcgc gcgagatcac cgccgccggc attgaggcgc 1680

tcaagagcgg caagtacaag gtggtgcgca tcaactacgc caacccggac atggtcggcc 1740

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acgccgacga catggtgcag cgcgacaaga agggcaagcc cctgctgggc gaggacggca 1920

agccgctgcc cctgaccagc cacacgctgg cgcccgtgcc gttcttcatc ggcggcaagg 1980

gcctgccgga cggcgtggtg ctgcgcgacg acctgccgga cgccgggctg gccaacgtgg 2040

ccgccaccac cttcaacctg ctgggcttcg aggcgcccgg catctacaag cccagcatgg 2100

tcaaggcgta aatggaggcg ctcgttgatc tgagccttgc cccctgacga acggcggtgg 2160

atggaagata ctgctctcaa gtgctgaagc ggtagcttag ctccccgttt cgtgctgatc 2220

agtctttttc aacacgtaaa aagcggagga gttttgcaat tttgttggtt gtaacgatcc 2280

tccgttgatt ttggcctctt tctccatggg cgggctgggc gtatttgaag cggttctctc 2340

ttctgccgtt a 2351

<210> SEQ ID NO 14
<211> LENGTH: 1796
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 14, Example 14: designer HydA1-promoter-linked Enolase DNA construct (1796 bp)

<400> SEQUENCE: 14

agaaaatctg gcaccacacc gagctgtcat gcgttgttcc gttatgtgtc gtcaaacgcc 60

ttcgagcgct gcccggaaca atgcgtacta gtataggagc catgaggcaa gtgaacagaa 120

gcgggctgac tggtcaaggc gcacgatagg gctgacgagc gtgctgacgg ggtgtaccgc 180

cgagtgtccg ctgcattccc gccggattgg gaaatcgcga tggtcgcgca taggcaagct 240

cgcaaatgct gtcagcttat cttacatgaa cacacaaaca ctctcgcagg cactagcctc 300

aaatggccgc cgtcattgcc aagtcctccg tctccgcggc cgtggctcgc ccggcccgct 360

ccagcgtgcg ccccatggcc gcgctgaagc ccgccgtcaa ggctgccccc gtggctgccc 420

cggctcaggc caaccaggtg accaaggctg ttgagaacat caacgctatt attgcccccg 480

ccctgaaggg catggacccc gtcaagcagg cggagattga ccagaagatg aaggacctgg 540

acggcactga caacaagggc aagctgggtg ccaacgccat cctggccgtc tccatggccg 600

tgtgcaaggc cggtgccgct gagaagggcg tgcccctgta caagcacatt gcggacctgg 660

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ccggcaacag caagctgatc ctgcccgtgc cctcgttcaa catcatcaac ggcggcagcc 720

acgccggcaa cgccctggct atgcaggagt tcatgatcct gcccgttggc gcctcgagct 780

tctctgaggc catgcgcatg ggctgcgagg tgtaccacgc cctgaagggc ctgatcaagg 840

ccaagtacgg ccaggacgcc tgcaacgtgg gtgatgaggg tggcttcgcc cccaacatcg 900

gctccaacga tgagggcctg aacttggtga acgaggccat cgagaaggcc ggctacaccg 960

gcaaggtgaa gatcggcatg gacgtggcct cgtcggagtt ctacaccgag gacggcatgt 1020

acgacctgga cttcaagaac cagcccaacg atggctcgca gaagaagacc aaggagcaga 1080

tgctggagct gtacaacgag ttctgcaaga agtacccggt catctccatc gaggacccct 1140

tcgagcagga cgactgggag ccctgcgcca agctgaccac cgagaacatc tgccaggtgg 1200

tcggcgacga catcctggtg accaaccccg tgcgcgtgaa gaaggccatc gacgccaagg 1260

ccgtcaacgc tctgctgctc aaggtcaacc agatcggtac cattaccgag tccattgagg 1320

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ctgaggactc tttcatcgcc gacctggcgg tgggcctggc ctccggccag atcaagaccg 1440

gcgccccctg ccgctcggag cgcaatgcca agtacaacca gctgctgcgc atcgaggagg 1500

agctgggcga gaacgctgtg tacgctggcg agagctggcg ccacatcggc tggtaaatgg 1560

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ctcaagtgct gaagcggtag cttagctccc cgtttcgtgc tgatcagtct ttttcaacac 1680

gtaaaaagcg gaggagtttt gcaattttgt tggttgtaac gatcctccgt tgattttggc 1740

ctctttctcc atgggcgggc tgggcgtatt tgaagcggtt ctctcttctg ccgtta 1796

<210> SEQ ID NO 15
<211> LENGTH: 1832
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 15, Example 15: designer HydA1-promoter-linked Pyruvate-Kinase DNA construct (1832 bp)

<400> SEQUENCE: 15

agaaaatctg gcaccacacc gagctgtcat gcgttgttcc gttatgtgtc gtcaaacgcc 60

ttcgagcgct gcccggaaca atgcgtacta gtataggagc catgaggcaa gtgaacagaa 120

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cgagtgtccg ctgcattccc gccggattgg gaaatcgcga tggtcgcgca taggcaagct 240

cgcaaatgct gtcagcttat cttacatgaa cacacaaaca ctctcgcagg cactagcctc 300

aaatggccgc cgtcattgcc aagtcctccg tctccgcggc cgtggctcgc ccggcccgct 360

ccagcgtgcg ccccatggcc gcgctgaagc ccgccgtcaa ggctgccccc gtggctgccc 420

cggctcaggc caaccagatg tgcgagatgc tggacgcggg cgtggtgggc tgccgcgtgg 480

acctgacgtg gggcccgctg gagttccacc gcaagtcgct tgccaatctg cagcaggcca 540

tgcgcaagag ccgccgcctg tgttgcacca tggtggacac gctgggccgc gagctcatga 600

tccgccgcca gagaggggca ggctggaccc agcgccagag gggtggggtg atcatcacca 660

cgcgcacgga cgtggacgcc agcagcaacg tgctgcccat cacttacagc aagttcacgg 720

agatggcggt caagggcgac accatctaca tcggccgcta cctggtgtgc ggcgcagaca 780

gcgcctcgct gtacctggag gtcatggacg tgcagggcga cgacgtgtac tgcatcgcca 840

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ggctggccaa cgtgcagaac gacctgccgc tgctgtccga ctacgacaag gagtgcctgc 960

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gccagtgcct catcagtcgc gcgctgctgc cggtgctggc cgcgccctcg cccagcggcg 1260

accagctgct gcaggaggcg gtggccatgg cgggccgcgt caagctggtc aagccgcacg 1320

accacgtggt gtgcgtgcag cgcatccacg acgacttctg cgtcaagatc atctccgtgg 1380

acgacatggg cgcgggcatc aagcgcgacg acacggtcat gtcgcacagc gtgtttggca 1440

gcagccccat ggccgtgcag ggctcgtccg gctacgactc gccgcgcgtg cacaacaacc 1500

ccatcggcaa caagttcggc cccatgccgc ccgccatcat caccaccggc aatagcttca 1560

ccctgggcgg catgggcgtg ggcgtgctgt aaatggaggc gctcgttgat ctgagccttg 1620

ccccctgacg aacggcggtg gatggaagat actgctctca agtgctgaag cggtagctta 1680

gctccccgtt tcgtgctgat cagtcttttt caacacgtaa aaagcggagg agttttgcaa 1740

ttttgttggt tgtaacgatc ctccgttgat tttggcctct ttctccatgg gcgggctggg 1800

cgtatttgaa gcggttctct cttctgccgt ta 1832

<210> SEQ ID NO 16
<211> LENGTH: 4376
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 16, Example 16: designer HydA1-promoter-linked Pyruvate-Ferredoxin-Oxidoreductase DNA construct (4376 bp)

<400> SEQUENCE: 16

agaaaatctg gcaccacacc gagctgtcat gcgttgttcc gttatgtgtc gtcaaacgcc 60

ttcgagcgct gcccggaaca atgcgtacta gtataggagc catgaggcaa gtgaacagaa 120

gcgggctgac tggtcaaggc gcacgatagg gctgacgagc gtgctgacgg ggtgtaccgc 180

cgagtgtccg ctgcattccc gccggattgg gaaatcgcga tggtcgcgca taggcaagct 240

cgcaaatgct gtcagcttat cttacatgaa cacacaaaca ctctcgcagg cactagcctc 300

aaatggccgc cgtcattgcc aagtcctccg tctccgcggc cgtggctcgc ccggcccgct 360

ccagcgtgcg ccccatggcc gcgctgaagc ccgccgtcaa ggctgccccc gtggctgccc 420

cggctcaggc caaccagatg ggaaagaaaa tgatgacgac tgatggcaat acagcgacag 480

cgcacgtggc gtatgccatg agcgaagtcg ccgccatcta ccccatcacc ccttcctcga 540

ccatgggcga ggaggctgac gactgggcgg cgcaaggacg caagaacatc tttggccaga 600

ccctgaccat acgcgaaatg cagtccgagg ccggcgccgc cggcgcggtg cacggggccc 660

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<210> SEQ ID NO 17
<211> LENGTH: 6092
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 17, Example 17: designer HydA1-promoter-linked Pyruvate-NADP+-Oxidoreductase DNA construct (6092 bp)

<400> SEQUENCE: 17

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<210> SEQ ID NO 18
<211> LENGTH: 1856
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 18, Example 18: designer HydA1-promoter-linked Thiolase DNA construct (1856 bp)

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<210> SEQ ID NO 19
<211> LENGTH: 1550
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 19, Example 19: designer HydA1-promoter-linked 3-Hydroxybutyryl-CoA-Dehydrogenase DNA construct (1550 bp)

<400> SEQUENCE: 19

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tcgttgatct gagccttgcc ccctgacgaa cggcggtgga tggaagatac tgctctcaag 1380

tgctgaagcg gtagcttagc tccccgtttc gtgctgatca gtctttttca acacgtaaaa 1440

agcggaggag ttttgcaatt ttgttggttg taacgatcct ccgttgattt tggcctcttt 1500

ctccatgggc gggctgggcg tatttgaagc ggttctctct tctgccgtta 1550

<210> SEQ ID NO 20
<211> LENGTH: 1457
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 20, Example 20: designer HydA1-promoter-linked Crotonase DNA construct (1457 bp)

<400> SEQUENCE: 20

agaaaatctg gcaccacacc gagctgtcat gcgttgttcc gttatgtgtc gtcaaacgcc 60

ttcgagcgct gcccggaaca atgcgtacta gtataggagc catgaggcaa gtgaacagaa 120

gcgggctgac tggtcaaggc gcacgatagg gctgacgagc gtgctgacgg ggtgtaccgc 180

cgagtgtccg ctgcattccc gccggattgg gaaatcgcga tggtcgcgca taggcaagct 240

cgcaaatgct gtcagcttat cttacatgaa cacacaaaca ctctcgcagg cactagcctc 300

aaatggccgc cgtcattgcc aagtcctccg tctccgcggc cgtggctcgc ccggcccgct 360

ccagcgtgcg ccccatggcc gcgctgaagc ccgccgtcaa ggctgccccc gtggctgccc 420

cggctcaggc caaccagatg gattttaata atgttttatt aaataaggat gatgggatag 480

ctctcatcat tataaatcgt ccaaaggctt taaatgcatt aaactatgag acactaaaag 540

agttagatag tgtgcttgat atagttgaaa atgataaaga gataaaagtt ttaattataa 600

ctggcagcgg tgaaaaaacc ttcgttgcag gtgctgatat agctgagatg agtaatatga 660

caccacttga agcgaagaag ttctctcttt atggacagaa agtatttagg aagatagaaa 720

tgctaagtaa gcctgttata gcagcggtaa atggttttgc acttggtggt ggatgcgagc 780

tttctatggc atgtgacata cgtattgcaa gtaaaaatgc aaaatttggt caacctgaag 840

taggacttgg aataatacct ggcttttcag gaactcaaag attaccacgt cttataggca 900

cttctaaagc taaagagctt attttcacag gtgacatgat aaattctgat gaagcatata 960

aaataggcct tatatctaaa gttgttgaac tatctgatct cattgaagaa gcaaaaaaac 1020

tcgcgaaaaa aatgatgtca aaaagtcaaa tagcaatttc tctagcaaag gaagcaataa 1080

ataagggaat ggaaacagac ttagatacag gcaatactat agaagctgag aaattttcct 1140

tatgttttac aacagatgat caaaaagaag gtatgattgc gttttctgaa aagagggcgc 1200

ctaaatttgg caaataaatg gaggcgctcg ttgatctgag ccttgccccc tgacgaacgg 1260

cggtggatgg aagatactgc tctcaagtgc tgaagcggta gcttagctcc ccgtttcgtg 1320

ctgatcagtc tttttcaaca cgtaaaaagc ggaggagttt tgcaattttg ttggttgtaa 1380

cgatcctccg ttgattttgg cctctttctc catgggcggg ctgggcgtat ttgaagcggt 1440

tctctcttct gccgtta 1457

<210> SEQ ID NO 21
<211> LENGTH: 1817
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 21, Example

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21: designer HydA1-promoter-linked Butyryl-CoA-Dehydrogenase DNA construct (1817 bp)

<400> SEQUENCE: 21

agaaaatctg gcaccacacc gagctgtcat gcgttgttcc gttatgtgtc gtcaaacgcc 60

ttcgagcgct gcccggaaca atgcgtacta gtataggagc catgaggcaa gtgaacagaa 120

gcgggctgac tggtcaaggc gcacgatagg gctgacgagc gtgctgacgg ggtgtaccgc 180

cgagtgtccg ctgcattccc gccggattgg gaaatcgcga tggtcgcgca taggcaagct 240

cgcaaatgct gtcagcttat cttacatgaa cacacaaaca ctctcgcagg cactagcctc 300

aaatggccgc cgtcattgcc aagtcctccg tctccgcggc cgtggctcgc ccggcccgct 360

ccagcgtgcg ccccatggcc gcgctgaagc ccgccgtcaa ggctgccccc gtggctgccc 420

cggctcaggc caaccagatg gacttttcat taacaaagga gcaagaaatg gtaaggcgtg 480

ttgtgagaga attcgctgaa aaagaagttg ctcctaaagc aaaagaaata gatatcacag 540

aagagtttcc atgggataca gtaagaaaaa tggctcaaaa cgatatgatg ggtattcctt 600

atccagaaga gtatggtgga gcaggtggag attacttgag ttatatcata gctgttgaag 660

agatatcaag agcttgtgct acgactggag taattttatc tgctcatact tcattgggaa 720

gttttccaat atatcaatgg ggaacagaag aacaaaaaag aaaatatcta gtgccacttg 780

caaaaggtga aaaattgggc gcttttggcc ttacagaacc taacgcaggt acagatgcag 840

ctggacagca gacaactgca gtattagatg gtgatcacta cgtattaaac ggctcaatat 900

ttattacaaa cggaggaaaa gctgacatat atataatctt tgcaatgaca gacaaatcaa 960

aaggcacaag aggcattagt gcatttatag ttgagaaaga ttttccgggt tttagcattg 1020

gcaaaattga agaaaaaatg ggtataagag cttcatcaac tgccgaactt gtgtttgaag 1080

attgtattgt accaaaagaa aatttacttg gtaaagaagg agaaggtttt aaaattgcga 1140

tggctacact agatggtgga agaataggaa tagcagcgca acgccttgga atagctcagg 1200

ctgctttaga tgaagagata aaatatgcaa aggaaagaca acagtttgga agaccaattg 1260

gaaaatttca aggcattcaa tggtatatag ctgatatggc aacgagaata aatgcttcaa 1320

gatggcttgt atacaatgcc gcttggagaa agcaggtagg tcttccgtac acaatggaag 1380

cagctatggc aaaattatat gcttccgaaa cagcaatgtt tgtaacgaca aaaacagttc 1440

agatatttgg cggctatggc tttacaaaag attatccagt ggaaagattt atgagagatg 1500

caaaaataac agaaatttat gaaggcacat cggaagtcca gaaaatggtt atttccggta 1560

acctattgaa aatgtaaatg gaggcgctcg ttgatctgag ccttgccccc tgacgaacgg 1620

cggtggatgg aagatactgc tctcaagtgc tgaagcggta gcttagctcc ccgtttcgtg 1680

ctgatcagtc tttttcaaca cgtaaaaagc ggaggagttt tgcaattttg ttggttgtaa 1740

cgatcctccg ttgattttgg cctctttctc catgggcggg ctgggcgtat ttgaagcggt 1800

tctctcttct gccgtta 1817

<210> SEQ ID NO 22
<211> LENGTH: 2084
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 22, Example 22: designer HydA1-promoter-linked Butyraldehyde-Dehydrogenase DNA construct (2084 bp)

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<400> SEQUENCE: 22

agaaaatctg gcaccacacc gagctgtcat gcgttgttcc gttatgtgtc gtcaaacgcc 60

ttcgagcgct gcccggaaca atgcgtacta gtataggagc catgaggcaa gtgaacagaa 120

gcgggctgac tggtcaaggc gcacgatagg gctgacgagc gtgctgacgg ggtgtaccgc 180

cgagtgtccg ctgcattccc gccggattgg gaaatcgcga tggtcgcgca taggcaagct 240

cgcaaatgct gtcagcttat cttacatgaa cacacaaaca ctctcgcagg cactagcctc 300

aaatggccgc cgtcattgcc aagtcctccg tctccgcggc cgtggctcgc ccggcccgct 360

ccagcgtgcg ccccatggcc gcgctgaagc ccgccgtcaa ggctgccccc gtggctgccc 420

cggctcaggc caaccagatg attaaagaca cgctagtttc tataacaaaa gatttaaaat 480

taaaaacaaa tgttgaaaat gccaatctaa agaactacaa ggatgattct tcatgtttcg 540

gagttttcga aaatgttgaa aatgctataa gcaatgccgt acacgcacaa aagatattat 600

cccttcatta tacaaaagaa caaagagaaa aaatcataac tgagataaga aaggccgcat 660

tagaaaataa agagattcta gctacaatga ttcttgaaga aacacatatg ggaagatatg 720

aagataaaat attaaagcat gaattagtag ctaaatacac tcctgggaca gaagatttaa 780

ctactactgc ttggtcagga gataacgggc ttacagttgt agaaatgtct ccatatggcg 840

ttataggtgc aataactcct tctacgaatc caactgaaac tgtaatatgt aatagtatag 900

gcatgatagc tgctggaaat actgtggtat ttaacggaca tccaggcgct aaaaaatgtg 960

ttgcttttgc tgtcgaaatg ataaataaag ctattatttc atgtggtggt cctgagaatt 1020

tagtaacaac tataaaaaat ccaactatgg actctctaga tgcaattatt aagcaccctt 1080

caataaaact actttgcgga actggagggc caggaatggt aaaaaccctc ttaaattctg 1140

gtaagaaagc tataggtgct ggtgctggaa atccaccagt tattgtagat gatactgctg 1200

atatagaaaa ggctggtaag agtatcattg aaggctgttc ttttgataat aatttacctt 1260

gtattgcaga aaaagaagta tttgtttttg agaacgttgc agatgattta atatctaaca 1320

tgctaaaaaa taatgctgta attataaatg aagatcaagt atcaaagtta atagatttag 1380

tattacaaaa aaataatgaa actcaagaat actctataaa taagaaatgg gtcggaaaag 1440

atgcaaaatt attcttagat gaaatagatg ttgagtctcc ttcaagtgtt aaatgcataa 1500

tctgcgaagt aagtgcaagg catccatttg ttatgacaga actcatgatg ccaatattac 1560

caattgtaag agttaaagat atagatgaag ctattgaata tgcaaaaata gcagaacaaa 1620

atagaaaaca tagtgcctat atttattcaa aaaatataga caacctaaat aggtttgaaa 1680

gagaaatcga tactactatc tttgtaaaga atgctaaatc ttttgccggt gttggttatg 1740

aagcagaagg ctttacaact ttcactattg ctggatccac tggtgaagga ataacttctg 1800

caagaaattt tacaagacaa agaagatgtg tactcgccgg ttaaatggag gcgctcgttg 1860

atctgagcct tgccccctga cgaacggcgg tggatggaag atactgctct caagtgctga 1920

agcggtagct tagctccccg tttcgtgctg atcagtcttt ttcaacacgt aaaaagcgga 1980

ggagttttgc aattttgttg gttgtaacga tcctccgttg attttggcct ctttctccat 2040

gggcgggctg ggcgtatttg aagcggttct ctcttctgcc gtta 2084

<210> SEQ ID NO 23
<211> LENGTH: 1733
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

-continued

<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 23, Example 23: designer HydA1-promoter-linked Butanol-Dehydrogenase DNA construct (1733 bp)

<400> SEQUENCE: 23

agaaaatctg gcaccacacc gagctgtcat gcgttgttcc gttatgtgtc gtcaaacgcc 60

ttcgagcgct gcccggaaca atgcgtacta gtataggagc catgaggcaa gtgaacagaa 120

gcgggctgac tggtcaaggc gcacgatagg gctgacgagc gtgctgacgg ggtgtaccgc 180

cgagtgtccg ctgcattccc gccggattgg gaaatcgcga tggtcgcgca taggcaagct 240

cgcaaatgct gtcagcttat cttacatgaa cacacaaaca ctctcgcagg cactagcctc 300

aaatggccgc cgtcattgcc aagtcctccg tctccgcggc cgtggctcgc ccggcccgct 360

ccagcgtgcg ccccatggcc gcgctgaagc ccgccgtcaa ggctgccccc gtggctgccc 420

cggctcaggc caaccagatg aaaggttttg caatgctagg tattaataag ttaggatgga 480

tcgaaaaaga aaggccagtt gcgggttcat atgatgctat tgtacgccca ttagcagtat 540

ctccgtgtac atcagatata catactgttt ttgagggagc tcttggagat aggaagaata 600

tgattttagg gcatgaagct gtaggtgaag ttgttgaagt aggaagtgaa gtgaaggatt 660

ttaaacctgg tgacagagtt atagttcctt gtacaactcc agattggaga tctttggaag 720

ttcaagctgg ttttcaacag cactcaaacg gtatgctcgc aggatggaaa ttttcaaatt 780

tcaaggatgg agtttttggt gaatattttc atgtaaatga tgcggatatg aatcttgcga 840

ttctacctaa agacatgcca ttagaaaatg ctgttatgat aacagatatg atgactactg 900

gatttcatgg agcagaactt gcagatattc aaatgggttc aagtgttgtg gtaattggca 960

ttggagctgt tggcttaatg ggaatagcag gtgctaaatt acgtggagca ggtagaataa 1020

ttggagtggg gagcaggccg atttgtgttg aggctgcaaa attttatgga gcaacagata 1080

ttctaaatta taaaaatggt catatagttg atcaagttat gaaattaacg aatggaaaag 1140

gcgttgaccg cgtaattatg gcaggcggtg gttctgaaac attatcccaa gcagtatcta 1200

tggttaaacc aggaggaata atttctaata taaattatca tggaagtgga gatgctttac 1260

taataccacg tgtagaatgg ggatgtggaa tggctcacaa gactataaaa ggaggtcttt 1320

gtcctggggg acgtttgaga gcagaaatgt taagagatat ggtagtatat aatcgtgttg 1380

atctaagtaa attagttaca catgtatatc atggatttga tcacatagaa gaagcactgt 1440

tattaatgaa agacaagcca aaagacttaa ttaaagcagt agttatatta taaatggagg 1500

cgctcgttga tctgagcctt gccccctgac gaacggcggt ggatggaaga tactgctctc 1560

aagtgctgaa gcggtagctt agctccccgt ttcgtgctga tcagtctttt tcaacacgta 1620

aaaagcggag gagttttgca attttgttgg ttgtaacgat cctccgttga ttttggcctc 1680

tttctccatg ggcgggctgg gcgtatttga agcggttctc tcttctgccg tta 1733

<210> SEQ ID NO 24
<211> LENGTH: 1556
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 24, Example 24: designer Fructose-Diphosphate-Aldolase DNA construct (1556 bp)

<400> SEQUENCE: 24

agaaaatctg gcaccacacc atggtagggt gcgagtgacc ccgcgcgact tggaagggtt 60

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caaacgaccc cgccgtacga acttttgtcg gggggcgctc ccggatggta gggtgcgagt 120

gaccccgcgc gacttggaag ggttcaaacg accccgccgt acgaactttt gtcgggggggc 180

gctcccggat ggccctgatg atgaagtcgt cggccagcct gaaggctgtg tcgctggccg 240

ctctcgccgc gccgtcgttg tgcgcgccgg gcaagtacga tgaggagctg attaagaccg 300

ctggcaccgt tgcctccaag ggccgcggta tcctggccat ggacgagtca aacgccacct 360

gcggcaaacg cctggactcc atcggcgtgg agaacaccga ggagaaccgc cgcgcctacc 420

gcgagctgct ggtgaccgcc cccggcctgg gccagtacat ctccggcgct atcctgttcg 480

aggagaccct gtatcagtcc accgcctccg gcaagaagtt cgtcgatgtg atgaaggagc 540

agaacatcgt gcccggcatc aaggtcgaca agggcctggt gccctgtcca acaccaacga 600

tgagctggtg catgggcctg gacggctgga caagcgctgc tgagtactac aaggccggcg 660

ctcgcttcgc caagtggcgc tcggtcgtct cgatccccca cggcccctcg atcatgctgc 720

cgcgactggc ctacggcctg gcccgctacg ccgccatcgc ccagaacgcc ggtctggtgc 780

ccattgtgga gcccgaggtc ctgctggacg gtgagcacga catcgaccgc tgcctggagg 840

tgcaggaggc catctgggcc gagaccttca agtacatggc cgacaacaag gtcatgttgc 900

agggtatcct gctgaagccc gccatggtca cccccggcgc tgactgcaag aacaaggccg 960

gccccgccaa ggttgccgag tacaccctga agatgctggc cgcgcgtgcc cccccggtcc 1020

ccggcatcat gttcctgtcg ggcggccagt ccgagctgga gtcgaccctg aacctgaacg 1080

ccatgaacca gagccccaac ccgtggcacg tgtcgttctc gtacgcccgc gctctgacga 1140

acaccgttct gaagacctgg caggcaagcc cgagaacggt ccaggcgccc aggctcgctg 1200

ctcaagcgcg caaggccaac tcggacgctc agcagggcaa gtacgacgcc accaccgagg 1260

gcaaggaggc tgcccagggc atgtacgaga agggaaaagg ctacgtctac taataaatgg 1320

aggcgctcgt tgatctgagc cttgcccccc gacgaacggc ggtggatgga agatactgct 1380

ctcaagtgct gaagcggtag cttagctccc cgtttcgtgc tgatcagtct ttttcaacac 1440

gtaaaaagcg gaggagtttt gcaattttgt tggttgtaac gatcctccgt tgattttggc 1500

ctctttctcc atgggcgggc tgggcgtatt tgaagcggtt ctctcttctg ccgtta 1556

<210> SEQ ID NO 25
<211> LENGTH: 1379
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 25, Example 25: designer Triose-Phosphate-Isomerase DNA construct (1379 bp)

<400> SEQUENCE: 25

agaaaatctg gcaccacacc atggtagggt gcgagtgacc ccgcgcgact tggaagggtt 60

caaacgaccc cgccgtacga acttttgtcg gggggcgctc ccggatggta gggtgcgagt 120

gaccccgcgc gacttggaag ggttcaaacg accccgccgt acgaactttt gtcgggggggc 180

gctcccggat ggcagctacc tctctcactg cccctccttc tttctccggt ctccgccgca 240

tttctcccaa gctcgacgct gccgccgtct cctcccacca atccttcttc caccgcgtca 300

attcctctac ccgtctcgtt tcttcctctt cttcttctca tcgctccccc agaggtgttg 360

ttgccatggc tggatccgga aagtttttcg ttggaggaaa ctggaagtgt aacgggacta 420

aggactccat cgccaagctt atctccgatc tcaacagtgc aaccttggaa gcagatgtag 480

-continued

atgttgttgt gtcacctcca tttgtctaca tcgaccaggt caaatcctcg ttgacagacc 540

gtattgacat atcaggtcag aactcttggg ttgggaaagg tggagccttc actggtgaaa 600

tcagcgtgga acagctcaaa gaccttggct gcaagtgggt cattcttggg cattccgaac 660

ggagacatgt catcggagaa aaagatgagt ttatcgggaa gaaagctgca tatgcattga 720

gtgagggtct tggagtgata gcttgtattg gggaaaagct agaagagagg gaagcaggca 780

agacgtttga tgtttgcttc gcgcaactga aggcgtttgc tgatgctgtg cctagctggg 840

acaatatagt tgttgcatac gagcctgtat gggcaattgg aactggtaaa gttgcatctc 900

ctcagcaagc acaagaagtc catgtagctg tccgcggttg gctaaagaag aatgtctctg 960

aggaagttgc ttccaaaacg agaatcatat atggaggttc tgtcaatgga ggcaacagtg 1020

cagagcttgc caaagaagaa gacattgatg gatttcttgt tggtggtgcc tccttgaagg 1080

gtcctgagtt tgcaaccatt gtgaactcag tcacgtcgaa gaaagttgct gcttgataaa 1140

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gctctcaagt gctgaagcgg tagcttagct ccccgtttcg tgctgatcag tctttttcaa 1260

cacgtaaaaa gcggaggagt tttgcaattt tgttggttgt aacgatcctc cgttgatttt 1320

ggcctctttc tccatgggcg ggctgggcgt atttgaagcg gttctctctt ctgccgtta 1379

<210> SEQ ID NO 26
<211> LENGTH: 2156
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 26, Example 26: designer Phosphofructose-Kinase DNA construct (2156 bp)

<400> SEQUENCE: 26

agaaaatctg gcaccacacc atggtagggt gcgagtgacc ccgcgcgact tggaagggtt 60

caaacgaccc cgccgtacga acttttgtcg gggggcgctc ccggatggta gggtgcgagt 120

gaccccgcgc gacttggaag ggttcaaacg accccgccgt acgaactttt gtcgggggggc 180

gctcccggat ggccgccgtc attgccaagt cctccgtctc cgcggccgtg gctcgcccgg 240

cccgctccag cgtgcgcccc atggccgcgc tgaagcccgc cgtcaaggct gcccccgtgg 300

ctgccccggc tcaggccaac cagatggaag cttcgatttc gtttctgggg tcaacaaaac 360

ccaatatttc cttgtttaac ccttcttcaa acgtccttcc tcgtagagat ttccctcttc 420

ctgctttgaa attgaagaaa gtttcagtgc tgcctcgaat cttgcaccag aaacgactca 480

tcagagctca gtgctctgat ggattcaaac cagaggaaga cgatgggttt gtcctagaag 540

acgttcctca cttgaccaaa tttctccctg atttaccgtc atatccaaat ccattgaaag 600

aaagccaagc atatgccatt gttaagcgaa cttttgtcag ttccgaagat gtggttgcgc 660

aaaatattgt agtccagaag ggaagtaagc gaggagtaca ctttaggcga gcagggcctc 720

gagaaagagt gtacttcaga tcagatgaag taaaagcttg catagtgact tgtgggggct 780

tgtgccctgg aatcaatact gttatacggg aaattgtatg tggattgaac aatatgtatg 840

gtgttaataa cattctcggc attcagggag gatatagagg cttttactcc aaaaacacta 900

tgaacctgac acctaaagta gttaacgata ttcataaacg cggtggcact tttcttcaaa 960

cctcaagagg aggacatgat acagcgaaga ttgttgataa tattcaagat agaggaataa 1020

atcaggtata tattattgga ggtggtggga cgcaaaaggg tgcagagaag atatacgagg 1080

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aagttgagag gcgtggtctt caagtggcgg tttctggcat tcctaagaca attgataatg 1140

atattgctgt gattgacaaa tcatttggct ttgatacggc ggttgaggaa gcacaacgag 1200

ctattaatgc tgcacatgta gaggtcgaga gcgtggaaaa tggagttggt atcgttaaac 1260

tcatgggcag atacagtggt tttattgcca tgattgcaac tttagcgaat cgtgatgtgg 1320

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ttattgaaga acgactcaaa gagaataggc acatggttat tgtgatagct gaaggagctg 1440

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ttcggaaaat gatgataaat atgaagtaca tagacccaac gtatatgata agagcaatac 1620

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caatggctgg gtactcaggt ttcactgtag gaccagttaa cagtagacat gcttacatcc 1740

caatttctgt gacggaagtg acaaatacgg tgaagttaac tgataggatg tgggctagac 1800

tccttgcatc gacaaatcaa ccgagtttct tgactggtga aggagcattg cagaatgtga 1860

tcgacatgga aactcaagaa aagatcgata acatgaagat ctcttctatc taataaatgg 1920

aggcgctcgt tgatctgagc cttgcccccc gacgaacggc ggtggatgga agatactgct 1980

ctcaagtgct gaagcggtag cttagctccc cgtttcgtgc tgatcagtct ttttcaacac 2040

gtaaaaagcg gaggagtttt gcaattttgt tggttgtaac gatcctccgt tgattttggc 2100

ctctttctcc atgggcgggc tgggcgtatt tgaagcggtt ctctcttctg ccgtta 2156

<210> SEQ ID NO 27
<211> LENGTH: 860
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 27, Example 27: designer Nia1-promoter-linked Starch-Synthase-iRNA DNA construct (860 bp)

<400> SEQUENCE: 27

agaaaatctg gcaccacacc tatatggtag ggtgcgagtg accccgcgcg acttggagct 60

cgatggcccc gggttgtttg gggcgtccgc ctctcgcgct attctgagct ggagaccgag 120

gcgcatgaaa atgcattcgc ttccatagga cgctgcattg tggcttgaag gttcaaggga 180

agggttcaaa cgaccccgcc gtacgaactt ttgtcggggg gcgctcccgg ccccgggctc 240

ttgtgcgcgc attagggctt cgggtcgcaa gcaagacgat acatgccagc cggctcacca 300

ccgccaccag cggcttgcgg gggtccacct ccaggcccag acccttctgc agaaactcct 360

tgcacagcgc cttcccggcg gggcggtcgg cgtcgaagtt ggctggcagc agcgcgtcag 420

tggccgggtt ccactcctca cagtcaatgc cgttcaggat gccgtggaac ttggagcgca 480

gctcggggcg cgcgaaggtg gatctcgccg tcccagcggt agcccttggg cacctcgatg 540

tcgcattcgt gcttgaggcc ctcaatctgg tccttgggca ggcactcgta gaacggcagc 600

atgaccgtca cgaagtgtaa atggaggcgc tcgttgatct gagccttgcc ccctgacgaa 660

cggcggtgga tggaagatac tgctctcaag tgctgaagcg gtagcttagc tccccgtttc 720

gtgctgatca gtctttttca acacgtaaaa agcggaggag ttttgcaatt ttgttggttg 780

taacgatcct ccgttgattt tggcctcttt ctccatgggc gggctgggcg tatttgaagc 840

-continued

ggttctctct tctgccgtta 860

<210> SEQ ID NO 28
<211> LENGTH: 1328
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 28, Example 28: designer HydA1-promoter-linked Starch-Synthase-iRNA DNA construct (1328 bp)

<400> SEQUENCE: 28

agaaaatctg gcaccacacc gagctgtcat gcgttgttcc gttatgtgtc gtcaaacgcc 60

ttcgagcgct gcccggaaca atgcgtacta gtataggagc catgaggcaa gtgaacagaa 120

gcgggctgac tggtcaaggc gcacgatagg gctgacgagc gtgctgacgg ggtgtaccgc 180

cgagtgtccg ctgcattccc gccggattgg gaaatcgcga tggtcgcgca taggcaagct 240

cgcaaatgct gtcagcttat cttacatgaa cacacaaaca ctctcgcagg cactagcctc 300

aaatgaagag cttcatgcgg agggatgcgc tcggcgcggg gctccgcggt gcagccagca 360

caaagcccgt ctcaagggtc gccagcgtga ggcctgcgcc taccgcctac cgcactgcct 420

gccaagttgc gaaggtggat gaaatggtgt cggtggatga ggagcttact cgtctccgca 480

aggagaacga gctcctgcgc gcccaactgg cgctgtacca gcagaaccag cagccgtccg 540

tgggtgccgc tgccgttgcc ccgcctgctg ccgccacgaa ggtgctggag aagccggcgc 600

cgtaagtaac ctaacggtga gcagcatgca atattttagc gtcgatactc ggaaactata 660

ggagcgcatc agccgaccga tgttcgcgtt gctgtcgcag gcccaaccgt gccaccgccg 720

tggtgtgcaa ggcgcagaag gcggccaggc cgccgctgcc gctgctctgg ccataagtaa 780

cctaacggcg ccggcttctc cagcaccttc gtggcggcag caggcggggc aacggcagcg 840

gcacccacgg acggctgctg gttctgctgg tacagcgcca gttgggcgcg caggagctcg 900

ttctccttgc ggagacgagt aagctcctca tccaccgaca ccatttcatc caccttcgca 960

acttggcagg cagtgcggta ggcggtaggc gcaggcctca cgctggcgac ccttgagacg 1020

ggctttgtgc tggctgcacc gcggagcccc gcgccgagcg catccctccg catgaagctc 1080

ttcattaaat ggaggcgctc gttgatctga gccttgcccc ctgacgaacg gcggtggatg 1140

gaagatactg ctctcaagtg ctgaagcggt agcttagctc cccgtttcgt gctgatcagt 1200

ctttttcaac acgtaaaaag cggaggagtt ttgcaatttt gttggttgta acgatcctcc 1260

gttgattttg gcctctttct ccatgggcgg gctgggcgta tttgaagcgg ttctctcttc 1320

tgccgtta 1328

<210> SEQ ID NO 29
<211> LENGTH: 1889
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 29, Example 29: designer Amylase DNA construct (1889 bp)

<400> SEQUENCE: 29

agaaaatctg gcaccacacc atggtagggt gcgagtgacc ccgcgcgact tggaagggtt 60

caaacgaccc cgccgtacga acttttgtcg gggggcgctc ccggatggta gggtgcgagt 120

gaccccgcgc gacttggaag ggttcaaacg accccgccgt acgaactttt gtcgggggggc 180

-continued

gctcccggct cgagcatatg gccgccgtca ttgccaagtc ctccgtctcc gcggccgtgg 240

ctcgcccggc ccgctccagc gtgcgcccca tggccgcgct gaagcccgcc gtcaaggctg 300

cccccgtggc tgccccggct caggccaacc agatggcgaa caaacacatg tccctttctc 360

tcttcatcgt cctccttggc ctctcgtgca gcttggcctc cgggcaagtc ctgtttcagg 420

gttttaactg ggagtcgtgg aagcacaatg gcgggtggta caacttcctg atgggcaagg 480

tggacgacat cgccgccgct ggcgtcacgc acgtgtggct ccccccggcg tcgcagtccg 540

tcgccgagca agggtacatg ccgggccggc tctacgacct ggacgcctcc aagtacggca 600

acaaggcgca gctcaagtcc ctcatcggcg cgctccacgg caagggcgtc aaggccatcg 660

ccgacatcgt catcaaccac cgcacggcgg agcgcaagga cggccggggc atctactgca 720

tcttcgaggg cggcaccccg gacgcgcgcc tcgactgggg cccccacatg atctgccgcg 780

acgaccggcc ctacgccgac ggcaccggca acccggacac cggcgccgac ttcggggccg 840

cgccggacat cgaccacctc aacccgcgcg tccagaagga gctcgtcgag tggctcaact 900

ggctcaggac cgacgtcggc ttcgacggct ggcgcttcga cttcgccaag ggctactccg 960

cggacgtggc caagatctac gtcgaccgct ccgagcccag cttcgccgtc gccgagatat 1020

ggacgtcgct ggcgtacggc ggggacggca agccgaacct caaccaggac ccgcaccggc 1080

aggagctggt gaactgggtg aacaaggtgg gcggctccgg ccccgccacc acgttcgact 1140

tcaccaccaa gggcatcctc aacgtggccg tggagggcga gctgtggcgc ctgcgcggca 1200

ccgacggcaa ggcgccgggc atgatcgggt ggtggccggc caaggcggtg accttcgtcg 1260

acaaccacga caccggctcc acgcagcaca tgtggccctt cccttccgac agggtcatgc 1320

agggatatgc ctacatcctc acgcacccag ggaccccatg catcttctac gatcatttct 1380

tcgactgggg cttgaaggag gagatcgatc gtctggtgtc aatcaggacc cgacagggga 1440

tacacagtga gagcaagctg cagatcatgg aggccgacgc cgacctttac cttgccgaga 1500

tcgacggcaa ggtcatcgtc aagctcgggc caagatacga tgtcggacac ctcattcctg 1560

aaggcttcaa ggtggtcgcg catggcaatg actatgccgt atgggagaaa gtataaggct 1620

gctgccccgg ctgctgctaa tctagataaa tggaggcgct cgttgatctg agccttgccc 1680

cctgacgaac ggcggtggat ggaagatact gctctcaagt gctgaagcgg tagcttagct 1740

ccccgtttcg tgctgatcag tctttttcaa cacgtaaaaa gcggaggagt tttgcaattt 1800

tgttggttgt aacgatcctc cgttgatttt ggcctctttc tccatgggcg ggctgggcgt 1860

atttgaagcg gttctctctt ctgccgtta 1889

<210> SEQ ID NO 30
<211> LENGTH: 3089
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 30, Example 30: designer Starch-Phosphorylase DNA construct (3089 bp)

<400> SEQUENCE: 30

agaaaatctg gcaccacacc atggtagggt gcgagtgacc ccgcgcgact tggaagggtt 60

caaacgaccc cgccgtacga acttttgtcg gggggcgctc ccggatggta gggtgcgagt 120

gaccccgcgc gacttggaag ggttcaaacg accccgccgt acgaactttt gtcgggggcc 180

gctcccggat ggccgccgtc attgccaagt cctccgtctc cgcggccgtg gctcgcccgg 240

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cccgctccag cgtgcgcccc atggccgcgc tgaagcccgc cgtcaaggct gcccccgtgg 300

ctgccccggc tcaggccaac cagatggcgg atgcgaaagc aaacggaaag aatgaggcgg 360

ccaaactggc gaaaattccg gcggctgcga atccattggc taatgaacca tcggcgattg 420

catcaaatat aagttaccac gtgcagtaca gtcctcattt ctcgccgact aagttcgagc 480

cggagcaagc tttctttgcc acggcggagg ttgtccgcga tcgtcttatt caacaatgga 540

atgagacata ccaccatttt aataaagttg atccgaagca aacatactac ctatcaatgg 600

aatttcttca aggaaggact ttgactaatg caattggcag tttggacatt cagaatgcat 660

atgctgatgc tttaaataat ttggggcatg tccttgagga gatagctgaa caggaaaaag 720

atgctgcact aggaaatggt gggctgggca ggctagcttc atgcttctta gactccatgg 780

caacattgaa tttgcctgca tggggttatg gtttgagata ccggtatggg ctgttcaagc 840

agaagatcac caagcagggt caagaagaag ttgctgaaga ttggcttgag aaatttagtc 900

cttgggaagt tgtcaggcat gatgtggtat ttccggtcag attttttggg agtgttatgg 960

ttaatccaaa tggaacgaga aaatgggttg ggggtgaagt tgtccaagcc gtagcttatg 1020

atataccaat tccagggtac aaaaccaaga acactatcag tcttcgtctc tgggacgcta 1080

aagctagcgc tgaggatttc aatttatttc agtttaatga tggacaatac gaatctgctg 1140

cacagcttca ttctcgagct caacagattt gtgctgtgct ctaccccggg gattctactg 1200

aagaagggaa gcttttaagg ctgaaacaac aattctttct ctgcagtgct tcacttcagg 1260

atatgattct tagattcaag gagaggaaaa gtggaaggca gtggtctgaa tttcccagca 1320

aggtagctgt acaactgaat gatactcatc caacacttgc aattccagag ttgatgcgat 1380

tgctaatgga tgaggaagga cttggatggg atgaagcatg ggatataaca acaaggactg 1440

ttgcttatac caatcacaca gtacttcctg aagcacttga gaagtggtca caagcagtaa 1500

tgtggaagct tcttcctcgc catatggaaa taattgaaga gattgacaag agattcattg 1560

caatggtccg ctccacaagg agtgaccttg agagtaagat tcccagcatg tgcatcttgg 1620

ataataatcc caaaaagccg gttgttagga tggcaaactt atgtgtagta tctgcgcata 1680

cggtaaatgg tgttgctcag ttgcacagtg atatcttaaa ggccgacttg ttcgctgact 1740

atgtttctct atggccaaac aaactccaaa ataaaactaa tggcattact cctcgtcgat 1800

ggctccggtt ttgcaatcct gagctcagca aaattatcac aaaatggtta aaaaccgatc 1860

agtgggttac gaaccttgac ctgcttgtag gtcttcgtca gtttgctgac aacacagaac 1920

tccaagctga atgggaatct gctaagatgg ccagtaagaa acatttggca gactacatat 1980

ggcgagtaac cggtgtaacg attgatccta atagcttatt tgacatacaa gtcaagcgca 2040

ttcatgaata caagagacaa ctgctaaata ttttgggcgc aatctacaga tacaagaagt 2100

tgaaggagat gagccctcag gagcggaaga aaactactcc acgcaccatt atgtttggag 2160

ggaaagcatt tgcaacatat acaaacgcaa aaagaatagt aaagttggtt aatgatgttg 2220

gtgaagtcgt caacaccgat cctgaggtca atagttattt gaaggtggta tttgttccaa 2280

attacaatgt ctctgttgcg gagttgctta ttccaggaag tgagctatct cagcatatta 2340

gcacagcagg catggaggca agtggcacaa gcaacatgaa attttctcta aatggttgcc 2400

tcattatagg aacattggat ggagctaatg tggaaatcag gcaggagata ggagaggaga 2460

atttctttct ctttggtgca ggagcagacc aagtccctaa gctgcggaag gaaagagaag 2520

atggattgtt caaaccagat cctcggtttg aagaggccaa gcaatttata agaagtggag 2580

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catttggaag ctatgactac aacccgcttc ttgattccct ggaggggaac actggttatg 2640

gtcgtggtga ttattttcta gttggttatg acttcccaag ttacttagag gctcaggaca 2700

gagttgacca agcttacaag gaccggaaga agtggctgaa gatgtctata ttaagtacag 2760

ctggcagtgg gaaattcagc agtgatcgca caattgcaca gtatgctaag gaaatctgga 2820

acataacaga atgccgtaca tcatgataaa tggaggcgct cgttgatctg agccttgccc 2880

cctgacgaac ggcggtggat ggaagatact gctctcaagt gctgaagcgg tagcttagct 2940

ccccgtttcg tgctgatcag tctttttcaa cacgtaaaaa gcggaggagt tttgcaattt 3000

tgttggttgt aacgatcctc cgttgatttt ggcctctttc tccatgggcg ggctgggcgt 3060

atttgaagcg gttctctctt ctgccgtta 3089

<210> SEQ ID NO 31
<211> LENGTH: 1949
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 31, Example 31: designer Hexose-Kinase DNA construct (1949 bp)

<400> SEQUENCE: 31

agaaaatctg gcaccacacc atggtagggt gcgagtgacc ccgcgcgact tggaagggtt 60

caaacgaccc cgccgtacga acttttgtcg gggggcgctc ccggatggta gggtgcgagt 120

gaccccgcgc gacttggaag ggttcaaacg accccgccgt acgaactttt gtcgggggggc 180

gctcccggat ggccgccgtc attgccaagt cctccgtctc cgcggccgtg gctcgcccgg 240

cccgctccag cgtgcgcccc atggccgcgc tgaagcccgc cgtcaaggct gcccccgtgg 300

ctgccccggc tcaggccaac cagatggcta taacaccccg ccgaaaacct tcccggaagg 360

gatcaatggc tgatatgccg aaggatgtgc ttgaccagct caagacgctg gaagagctct 420

tcacagttga ccaggagaag ctgaagcaga tcgttgagca tttcatcaag gagttacaga 480

agggcctcag tgtcgaaggc ggaaacattc ccatgaacgt gacttgggtt ctgggatttc 540

ccactggcca tgagaaaggt acatttctgg ctctggacat ggggggcacc aacctgcgcg 600

tctgcgaaat tgagctctcc gaagagaagg gcgagtttga tgtcacacag tccaagtatc 660

gaatccccga agagctcaag agcggtgaat catcagaact atgggaatat attgccgact 720

gtgtacagca gttcatagaa tactaccatg acggttgcac ggctttgcca gacctgccgc 780

tgggctttac cttttcgtac cctgctactc aagaatatgt tgaccacggt gtcctacaga 840

gatggaccaa gggttttgat attgacggcg tcgagggcaa agacgtcgtc ccaatgttag 900

aagaagcttt ggctaagaag gttaaaaatt cagctctttc cccatttttc tttggctata 960

tggtgctaat tactttacag ggtctcccca ttaaagttgc cgctctagta aacgacacga 1020

ctggcacact tattgcttcc gcctacactg acccagagat gaaaatcggc tgtatcttcg 1080

gcacaggcgt caacgccgcc tacatggaaa atgcgggctc tatccctaaa atagcccact 1140

acaatttacc tcccgacacc ccagtcgcta tcaactgcga atacggcgcc ttcgacaacg 1200

aactcattgt cctcccccga acgcagtatg acgacgtatc ccaactacgt aaaccatact 1260

ccctggactc ctccttccta gccttcatcg aagaagatcc cttcgagaac ctgtcagaaa 1320

cgcgagatct cttcgaacgc accctgggga tctacgcatt gccctcggag ctagaattct 1380

gcagacgcct ggcggaattg atcggcacac gtgccgcacg cctctccgct tgcggtgttg 1440

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cggccatctg caagaagaaa aatatcaccc attgccatgt cggagcggac gggtcggtgt 1500

tcgagaagta cccgcatttc aaggccaggg gcgccagagc cctgcgggag atccttgact 1560

ggccagatag tgaaccggat cgggttgtga tgagcggagc ggaggatggg tctggcgttg 1620

gtgcggcgct tattgcggct ttgacgcttg agagggttaa acaagcttct tgggaatgga 1680

agtacatcgg aagcggtctg tcttaataaa tggaggcgct cgttgatctg agccttgccc 1740

cctgacgaac ggcggtggat ggaagatact gctctcaagt gctgaagcgg tagcttagct 1800

ccccgtttcg tgctgatcag tctttttcaa cacgtaaaaa gcggaggagt tttgcaattt 1860

tgttggttgt aacgatcctc cgttgatttt ggcctctttc tccatgggcg ggctgggcgt 1920

atttgaagcg gttctctctt ctgccgtta 1949

<210> SEQ ID NO 32
<211> LENGTH: 2249
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 32, Example 32: designer Phosphoglucomutase DNA construct (2249 bp)

<400> SEQUENCE: 32

agaaaatctg gcaccacacc atggtagggt gcgagtgacc ccgcgcgact tggaagggtt 60

caaacgaccc cgccgtacga acttttgtcg gggggcgctc ccggatggta gggtgcgagt 120

gaccccgcgc gacttggaag ggttcaaacg accccgccgt acgaactttt gtcgggggggc 180

gctcccggat ggccgccgtc attgccaagt cctccgtctc cgcggccgtg gctcgcccgg 240

cccgctccag cgtgcgcccc atggccgcgc tgaagcccgc cgtcaaggct gcccccgtgg 300

ctgccccggc tcaggccaac cagatgtccg atttctccgt ccagaccatt gccaccacgg 360

ccttcacaga ccaaaagcct ggaacctctg gtctcagaaa gaaagttact gtgtttcaac 420

agcctcacta cactgaaaac ttcattcagg ctattctcga tgccattccg gaaggtgccc 480

aaggtgccac tcttgttgta ggaggtgatg gccgtttcta caacgacaag gtcatcaact 540

tgatcgccaa aatcgcctcg gccaacggag tttccaagtt gattttgggt caagacggga 600

ttctttccac tccagcaact tcgcatgtaa tcaggatcag gggtgcaact ggaggaatta 660

ttctcactgc ttcacacaac cccggaggcc ccaaaaacga tttgggtatt aagtacaact 720

tgggaaacgg tgcaccagct ccagaatcgg ttaccaacaa gatctatgat gtctccaagg 780

aattgacttc gtacaagctc attgatttac ccgacattga tttgtccaaa acccagaccg 840

tgcaattggg ccctcttgaa gtggaaatca ttgactccac ctctgattac gtagccatgt 900

tgaaggatat ctttgacttc cccttgatca agtcgttcct cgagactgcc actaaggagc 960

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tcgataagga gaatattgcc tttggtgctg catctgatgg tgacggtgac agaaacatga 1200

tctacggtgc tggtaccttt gtttcgcctg gtgactctgt agccatcatc tcggaatacg 1260

ccgattccat cccttacttc aagaagcaag gtgtctacgg tttggccaga tccatgccta 1320

cctctggagc catcgatttg gtagcaaagg ctaaaggatt gaatgtttac gaagtgccaa 1380

ccggttggaa gttcttctgc aacctttttcg acgctgacaa gttgagtatc tgtggtgaag 1440

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agtcgtttgg aacaggctcc aaccacatca gagaaaagga cggcctttgg gctgtagttg   1500

cctggttgaa cgtgctagca gattacaacg tcaagaatcc agaatccaag acatctattt   1560

ctgtagtgca gaactcgttt tggaagaaat acggaagaac tttcttcact agatatgact   1620

acgaaaacgt atcgtctgaa ggtgctgccg agctcatcaa cttgttgtct tctattgttg   1680

actctaagaa accaggaagt agcttagctg atggctacgt cgtcaaggaa gctgctaact   1740

tctcgtacac cgatttggac ggctctgttt cgtccaacca aggtttgttc atcaagtttg   1800

aaagcggctt gagattcata gtaagattgt ctggtactgg atcatccggt gctacagtca   1860

gattatatct cgaaaagcac tctgccgacg aatccaccta tggcttaggc gtagaccagt   1920

acttagttga tgacatcaag tttgtcttgg acttgttgaa gttcaagcag ttcttgggaa   1980

aggatgaacc agatgttcgt acctagtaaa tggaggcgct cgttgatctg agccttgccc   2040

cctgacgaac ggcggtggat ggaagatact gctctcaagt gctgaagcgg tagcttagct   2100

ccccgtttcg tgctgatcag tctttttcaa cacgtaaaaa gcggaggagt tttgcaattt   2160

tgttggttgt aacgatcctc cgttgatttt ggcctctttc tccatgggcg ggctgggcgt   2220

atttgaagcg gttctctctt ctgccgtta                                     2249
```

<210> SEQ ID NO 33
<211> LENGTH: 2231
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 33, Example 33: designer Glucosephosphate-Isomerase DNA construct (2231 bp)

<400> SEQUENCE: 33

```
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caaacgaccc cgccgtacga acttttgtcg gggggcgctc ccggatggta gggtgcgagt    120

gaccccgcgc gacttggaag ggttcaaacg accccgccgt acgaactttt gtcgggggggc   180

gctcccggat ggccgccgtc attgccaagt cctccgtctc cgcggccgtg gctcgcccgg    240

cccgctccag cgtgcgcccc atggccgcgc tgaagcccgc cgtcaaggct gcccccgtgg    300

ctgccccggc tcaggccaac cagatgtcca ataactcatt cactaacttc aaactggcca    360

ctgaattgcc agcctggtct aagttgcaaa aaatttatga atctcaaggt aagactttgt    420

ctgtcaagca agaattccaa aaagatgcca agcgttttga aaaattgaac aagactttca    480

ccaactatga tggttccaaa atcttgttcg actactcaaa gaacttggtc aacgatgaaa    540

tcattgctgc attgattgaa ctggccaagg aggctaacgt caccggtttg agagatgcta    600

tgttcaaagg tgaacacatc aactccactg aagatcgtgc tgtctaccac gtcgcattga    660

gaaacagagc taacaagcca atgtacgttg atggtgtcaa cgttgctcca gaagtcgact    720

ctgtcttgaa gcacatgaag gagttctctg aacaagttcg ttctggtgaa tggaagggtt    780

ataccggtaa gaagatcacc gatgttgtta acatcggtat tggtggttcc gatttgggtc    840

cagtcatggt cactgaggct ttgaagcact acgctggtgt cttggatgtc cacttcgttt    900

ccaacattga cggtactcac attgctgaaa ccttgaaggt tgttgaccca gaaactactt    960

tgtttttgat tgcttccaag actttcacta ccgctgaaac tatcactaac gctaacactg   1020

ccaagaactg gttcttgtcg aagacaggta atgatccatc tcacattgct aagcatttcg   1080

ctgctttgtc cactaacgaa accgaagttg ccaagttcgg tattgacacc aaaaacatgt   1140
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ttggtttcga aagttgggtc ggtggtcgtt actctgtctg gtcggctatt ggtttgtctg 1200

ttgccttgta cattggctat gacaactttg aggctttctt gaagggtgct gaagccgtcg 1260

acaaccactt cacccaaacc ccattggaag acaacattcc attgttgggt ggtttgttgt 1320

ctgtctggta caacaacttc tttggtgctc aaacccattt ggttgctcca ttcgaccaat 1380

acttgcacag attcccagcc tacttgcaac aattgtcaat ggaatctaac ggtaagtctg 1440

ttaccagagg taacgtgttt actgactact ctactggttc tatcttgttt ggtgaaccag 1500

ctaccaacgc tcaacactct ttcttccaat tggttcacca aggtaccaag ttgattccat 1560

ctgatttcat cttagctgct caatctcata acccaattga gaacaaatta catcaaaaga 1620

tgttggcttc aaacttcttt gctcaagctg aagctttaat ggttggtaag gatgaagaac 1680

aagttaaggc tgaaggtgcc actggtggtt tggtcccaca caaggtcttc tcaggtaaca 1740

gaccaactac ctctatcttg gctcaaaaga ttactccagc tactttgggt gctttgattg 1800

cctactacga acatgttact ttcactgaag gtgccatttg gaatatcaac tctttcgacc 1860

aatggggtgt tgaattgggt aaagtcttgg ctaaagtcat cggcaaggaa ttggacaact 1920

cctccaccat ttctacccac gatgcttcta ccaacggttt aatcaatcaa ttcaaggaat 1980

ggatgtgata aatggaggcg ctcgttgatc tgagccttgc cccctgacga acggcggtgg 2040

atggaagata ctgctctcaa gtgctgaagc ggtagcttag ctccccgttt cgtgctgatc 2100

agtctttttc aacacgtaaa aagcggagga gttttgcaat tttgttggtt gtaacgatcc 2160

tccgttgatt ttggcctctt tctccatggg cgggctgggc gtatttgaag cggttctctc 2220

ttctgccgtt a 2231

<210> SEQ ID NO 34
<211> LENGTH: 1709
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 34, Example 34: designer oxyphotobacterial Butanol Dehydrogenase DNA construct (1709 bp)

<400> SEQUENCE: 34

agaaaatctg gcaccacacc atccaaactc gccacccgca aaccaatggc atggccgagc 60

gctgcaacgg tcgcattgcc aagattctgc gtgctgagcg ctttgtctcc gctgctgatc 120

tgcaagagac gctcacgcga tacctctggg cgtgcaatca ccgcattccc caacgcgctt 180

tgggccacat gacccccatc gagagactcc gaacgtggca aatggaggga ccagagttgt 240

tcagttcaca ggtagataat gtcgcgggtc ttgatagtta gcaataaata cagtttcaga 300

atatctgtaa tacaaaaact gtatcgagac aagaaaaaag tagcaaaatt tacaaatgtt 360

catgattcat ctggctaaat tggatgttca actgacccat tgaagacaag ggcaacaacc 420

atggagaatt ttagatttaa tgcatataca gagatgcttt ttggaaaggg acaaatagag 480

aagcttccag aggttttaaa aagatatggt aaaaatatat tacttgcata tggtggtgga 540

agtataaaaa agaatggact ctatgatact atccaaaagc tattgaaaga ttttaatatt 600

gttgaattaa gtggtattga accaaatcca agaattgaaa ctgtaagacg tggagttgaa 660

ctttgcagaa aaaataaagt agatgttatt ttagctgttg gtggagggag tacaatagac 720

tgctcaaagg ttataggggc aggttattat tatgctggag atgcatggga ccttgtaaaa 780

-continued

aatccagcta aaataggtga ggttttacca atagtgacag ttttaacaat ggcagctact 840

ggttctgaaa tgaatagaaa tgctgttatt tcaaagatgg atacaaatga aaagcttgga 900

acaggatcac ctaagatgat ccctcaaact tctattttag atccagaata tttgtataca 960

ttgccagcaa ttcaaacagc tgcaggttgt gctgatatta tgtcacacat atttgaacaa 1020

tattttaata aaactacaga tgcttttgta caagataaat ttgcggaagg tttgttgcaa 1080

acttgtataa aatattgccc tgttgcttta aaggaaccaa agaattatga agctagagca 1140

aatataatgt gggctagttc aatggctctt aacggacttt taggaagtgg gaaagctgga 1200

gcttggactt gtcatccaat agaacatgaa ttaagtgcat tttatgatat aactcatgga 1260

gtaggtcttg caattttaac tccaagttgg atgagatata tcttaagtga tgtaacagtt 1320

gataagtttg ttaacgtatg gcatttagaa caaaaagaag ataaatttgc tcttgcaaat 1380

gaagcaatag atgcaacaga aaaattcttt aaagcttgtg gtattccaat gactttaact 1440

gaacttggaa tagataaagc aaactttgaa aagatggcaa aagctgcagt agaacatggt 1500

gctttagaat atgcatatgt ttcattaaat gccgaggatg tatataaaat tttagaaatg 1560

tccctttaat aaggctgaga tcttcttcag tgcattgtag ttgaatgaag ggttaggggg 1620

gaaatgcccc cctatttttt gtctagccat cctgccacgt ttgacagggt agcaatttcg 1680

acacgatagg gttctctctt ctgccgtta 1709

<210> SEQ ID NO 35
<211> LENGTH: 1967
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 35, Example 35: designer oxyphotobacterial Butyraldehyde Dehydrogenase DNA construct (1967 bp)

<400> SEQUENCE: 35

agaaaatctg gcaccacacc atccaaactc gccacccgca aaccaatggc atggccgagc 60

gctgcaacgg tcgcattgcc aagattctgc gtgctgagcg ctttgtctcc gctgctgatc 120

tgcaagagac gctcacgcga tacctctggg cgtgcaatca ccgcattccc caacgcgctt 180

tgggccacat gacccccatc gagagactcc gaacgtggca aatggaggga ccagagttgt 240

tcagttcaca ggtagataat gtcgcgggtc ttgatagtta gcaataaata cagtttcaga 300

atatctgtaa tacaaaaact gtatcgagac aagaaaaaag tagcaaaatt tacaaatgtt 360

catgattcat ctggctaaat tggatgttca actgacccat tgaagacaag ggcaacaacc 420

atgattaaag acacgctagt ttctataaca aaagatttaa aattaaaaac aaatgttgaa 480

aatgccaatc taaagaacta caaggatgat tcttcatgtt tcggagtttt cgaaaatgtt 540

gaaaatgcta taagcaatgc cgtacacgca caaaagatat tatcccttca ttatacaaaa 600

gaacaaagag aaaaaatcat aactgagata agaaaggccg cattagaaaa taaagagatt 660

ctagctacaa tgattcttga agaaacacat atgggaagat atgaagataa aatattaaag 720

catgaattag tagctaaata cactcctggg acagaagatt taactactac tgcttggtca 780

ggagataacg ggcttacagt tgtagaaatg tctccatatg gcgttatagg tgcaataact 840

ccttctacga atccaactga aactgtaata tgtaatagta taggcatgat agctgctgga 900

aatactgtgg tatttaacgg acatccaggc gctaaaaaat gtgttgcttt tgctgtcgaa 960

atgataaata aagctattat ttcatgtggt ggtcctgaga atttagtaac aactataaaa 1020

-continued

aatccaacta tggactctct agatgcaatt attaagcacc cttcaataaa actactttgc 1080

ggaactggag ggccaggaat ggtaaaaacc ctcttaaatt ctggtaagaa agctataggt 1140

gctggtgctg gaaatccacc agttattgta gatgatactg ctgatataga aaaggctggt 1200

aagagtatca ttgaaggctg ttcttttgat aataatttac cttgtattgc agaaaaagaa 1260

gtatttgttt ttgagaacgt tgcagatgat ttaatatcta acatgctaaa aaataatgct 1320

gtaattataa atgaagatca agtatcaaag ttaatagatt tagtattaca aaaaaataat 1380

gaaactcaag aatactctat aaataagaaa tgggtcggaa aagatgcaaa attattctta 1440

gatgaaatag atgttgagtc tccttcaagt gttaaatgca taatctgcga agtaagtgca 1500

aggcatccat ttgttatgac agaactcatg atgccaatat taccaattgt aagagttaaa 1560

gatatagatg aagctattga atatgcaaaa atagcagaac aaaatagaaa acatagtgcc 1620

tatatttatt caaaaaatat agacaaccta aataggtttg aaagagaaat cgatactact 1680

atctttgtaa agaatgctaa atcttttgcc ggtgttggtt atgaagcaga aggctttaca 1740

actttcacta ttgctggatc cactggtgaa ggaataactt ctgcaagaaa ttttacaaga 1800

caaagaagat gtgtactcgc cggttaataa ggctgagatc ttcttcagtg cattgtagtt 1860

gaatgaaggg ttaggggga aatgcccccc tatttttgt ctagccatcc tgccacgttt 1920

gacagggtag caatttcgac acgatagggt tctctcttct gccgtta 1967

<210> SEQ ID NO 36
<211> LENGTH: 1602
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 36, Example 36: designer oxyphotobacterial Butyryl-CoA Dehydrogenase DNA construct (1602 bp)

<400> SEQUENCE: 36

agaaaatctg gcaccacacc tgatctgcaa gagacgctca cgcgatacct ctgggcgtgc 60

aatcaccgca ttccccaacg cgctttgggc cacatgaccc ccatcgagag actccgaacg 120

tggcaaatgg agggaccaga gttgttcagt tcacaggtag ataatgtcgc gggtcttgat 180

agttagcaat aaatacagtt tcagaatatc tgtaatacaa aaactgtatc gagacaagaa 240

aaaagtagca aaatttacaa atgttcatga ttcatctggc taaattggat gttcaactga 300

cccattgaag acaagggcaa caaccatgaa tttccaatta actagagaac aacaattagt 360

acaacaaatg gttagagaat tcgcagtaaa tgaagttaag ccaatagctg ctgaaatcga 420

cgaaacagaa agattcccta tggaaaacgt tgaaaaaatg gctaagctta aaatgatggg 480

tatcccattt tctaaagaat ttggtggagc aggcggagat gttctttcat atataatagc 540

tgtggaagaa ttatcaaaag tttgtggtac tacaggagtt attctttcag cgcatacatc 600

attatgtgca tcagtaatta atgaaaatgg aactaacgaa caaagagcaa aatatttacc 660

tgatctttgc agcggtaaaa agatcggtgc tttcggatta actgaaccag gtgctggtac 720

agatgctgca ggacaacaaa caactgctgt attagaaggg gatcattatg tattaaatgg 780

ttcaaaaatc ttcataacaa atggtggagt tgctgaaact ttcataatat ttgctatgac 840

agataagagt caaggaacaa aaggaatttc tgcattcata gtagaaaagt cattcccagg 900

attctcaata ggaaaattag aaaataagat ggggatcaga gcatcttcaa ctactgagtt 960

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agttatggaa aactgcatag taccaaaaga aaacctactt agcaaagaag gtaagggatt 1020

tggtatagca atgaaaactc ttgatggagg aagaattggt atagctgctc aagctttagg 1080

tattgcagaa ggagcttttg aagaagctgt taactatatg aaagaaagaa aacaatttgg 1140

taaaccatta tcagcattcc aaggattaca atggtatata gctgaaatgg atgttaaaat 1200

ccaagctgct aaatacttag tatacctagc tgcaacaaag aagcaagctg gtgagcctta 1260

ctcagtagat gctgcaagag ctaaattatt tgctgcagat gttgcaatgg aagttacaac 1320

taaagcagtt caaatctttg gtggatatgg ttacactaaa gaatacccag tagaaagaat 1380

gatgagagat gctaaaatat gcgaaatcta cgaaggaact tcagaagttc aaaagatggt 1440

tatcgcagga agcattttaa gataaggctg agatcttctt cagtgcattg tagttgaatg 1500

aagggttagg ggggaaatgc ccccctattt tttgtctagc catcctgcca cgtttgacag 1560

ggtagcaatt tcgacacgat agggttctct cttctgccgt ta 1602

<210> SEQ ID NO 37
<211> LENGTH: 1248
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 37, Example 37: designer oxyphotobacterial Crotonase DNA construct (1248 bp)

<400> SEQUENCE: 37

agaaaatctg gcaccacacc tgatctgcaa gagacgctca cgcgatacct ctgggcgtgc 60

aatcaccgca ttccccaacg cgctttgggc cacatgaccc ccatcgagag actccgaacg 120

tggcaaatgg agggaccaga gttgttcagt tcacaggtag ataatgtcgc gggtcttgat 180

agttagcaat aaatacagtt tcagaatatc tgtaatacaa aaactgtatc gagacaagaa 240

aaaagtagca aaatttacaa atgttcatga ttcatctggc taaattggat gttcaactga 300

cccattgaag acaagggcaa caaccatgga attaaaaaat gttattcttg aaaaagaagg 360

gcatttagct attgttacaa tcaatagacc aaaggcatta aatgcattga attcagaaac 420

actaaaagat ttaaatgttg ttttagatga tttagaagca gacaacaatg tgtatgcagt 480

tatagttact ggtgctggtg agaaatcttt tgttgctgga gcagatattt cagaaatgaa 540

agatcttaat gaagaacaag gtaaagaatt tggtatttta ggaaataatg tcttcagaag 600

attagaaaaa ttggataagc cagttatcgc agctatatca ggatttgctc ttggtggtgg 660

atgtgaactt gctatgtcat gtgacataag aatagcttca gttaaagcta aatttggtca 720

accagaagca ggacttggaa taactccagg atttggtgga actcaaagat tagcaagaat 780

agttggacca ggaaaagcta aagaattaat ttatacttgt gaccttataa atgcagaaga 840

agcttataga ataggcttag ttaataaagt agttgaatta gaaaaattga tggaagaagc 900

aaaagcaatg gctaacaaga ttgcagctaa tgctccaaaa gcagttgcat attgtaaaga 960

tgctatagac agaggaatgc aagttgatat agatgcagct atattaatag aagcagaaga 1020

ctttgggaag tgctttgcaa cagaagatca aacagaagga atgactgcgt tcttagaaag 1080

aagagcagaa aagaattttc aaaataaata aggctgagat cttcttcagt gcattgtagt 1140

tgaatgaagg gttaggggggg aaatgccccc ctatttttttg tctagccatc ctgccacgtt 1200

tgacagggta gcaatttcga cacgataggg ttctctcttc tgccgtta 1248

<210> SEQ ID NO 38

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<211> LENGTH: 1311
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 38, Example 38: designer oxyphotobacterial 3-Hydroxybutyryl-CoA Dehydrogenase DNA construct (1311 bp)

<400> SEQUENCE: 38

agaaaatctg gcaccacacc tgatctgcaa gagacgctca cgcgatacct ctgggcgtgc 60

aatcaccgca ttccccaacg cgctttgggc cacatgaccc ccatcgagag actccgaacg 120

tggcaaatgg agggaccaga gttgttcagt tcacaggtag ataatgtcgc gggtcttgat 180

agttagcaat aaatacagtt tcagaatatc tgtaatacaa aaactgtatc gagacaagaa 240

aaaagtagca aaatttacaa atgttcatga ttcatctggc taaattggat gttcaactga 300

cccattgaag acaagggcaa caaccatgaa aaagattttt gtacttggag caggaactat 360

gggtgctggt atcgttcaag cattcgctca aaaaggttgt gaggtaattg taagagacat 420

aaaggaagaa tttgttgaca gaggaatagc tggaatcact aaaggattag aaaagcaagt 480

tgctaaagga aaaatgtctg aagaagataa agaagctata ctttcaagaa tttcaggaac 540

aactgatatg aagttagctg ctgactgtga tttagtagtt gaagctgcaa tcgaaaacat 600

gaaaattaag aaggaaatct ttgctgagtt agatggaatt tgtaagccag aagcgatttt 660

agcttcaaac acttcatctt tatcaattac tgaagttgct tcagctacaa agagacctga 720

taaagttatc ggaatgcatt tctttaatcc agctccagta atgaagcttg ttgaaattat 780

taaaggaata gctacttctc aagaaacttt tgatgctgtt aaggaattat cagttgctat 840

tggaaaagaa ccagtagaag ttgcagaagc tccaggattc gttgtaaacg gaatcttaat 900

cccaatgatt aacgaagctt cattcatcct tcaagaagga atagcttcag ttgaagatat 960

tgatacagct atgaaatatg gtgctaacca tccaatggga cctttagctt taggagatct 1020

tattggatta gatgtttgct tagctatcat ggatgtttta ttcactgaaa caggtgataa 1080

caagtacaga gctagcagca tattaagaaa atatgttaga gctggatggc ttggaagaaa 1140

atcaggaaaa ggattctatg attattctaa ataaggctga gatcttcttc agtgcattgt 1200

agttgaatga agggttaggg gggaaatgcc cccctatttt ttgtctagcc atcctgccac 1260

gtttgacagg gtagcaattt cgacacgata gggttctctc ttctgccgtt a 1311

<210> SEQ ID NO 39
<211> LENGTH: 1665
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 39, Example 39: designer oxyphotobacterial Thiolase DNA construct (1665 bp)

<400> SEQUENCE: 39

agaaaatctg gcaccacacc tgatctgcaa gagacgctca cgcgatacct ctgggcgtgc 60

aatcaccgca ttccccaacg cgctttgggc cacatgaccc ccatcgagag actccgaacg 120

tggcaaatgg agggaccaga gttgttcagt tcacaggtag ataatgtcgc gggtcttgat 180

agttagcaat aaatacagtt tcagaatatc tgtaatacaa aaactgtatc gagacaagaa 240

aaaagtagca aaatttacaa atgttcatga ttcatctggc taaattggat gttcaactga 300

cccattgaag acaagggcaa caaccatggg caaagaaagt agttttagct gtgcatgtcg 360

-continued

tacagccatc ggaacaatgg gtggatctct tagcacaatt cctgcagtag atttaggtgc 420

tatcgttatc aaagaggctc ttaaccgcgc aggtgttaaa cctgaagatg ttgatcacgt 480

atacatggga tgcgttattc aggcaggaca gggacagaac gttgctcgtc aggcttctat 540

caaggctggt cttcctgtag aagtacctgc agttacaact aacgttgtat gtggttcagg 600

tcttaactgt gttaaccagg cagctcagat gatcatggct ggagatgctg atatcgttgt 660

tgccggtggt atggaaaaca tgtcacttgc accatttgca cttcctaatg gccgttacgg 720

atatcgtatg atgtggccaa gccagagcca gggtggtctt gtagacacta tggttaagga 780

tgctctttgg gatgctttca atgattatca tatgatccag acagcagaca acatctgcac 840

agagtggggt cttacacgtg aagagctcga tgagtttgca gctaagagcc agaacaaggc 900

ttgtgcagca atcgaagctg gcgcattcaa ggatgagatc gttcctgtag agatcaagaa 960

gaagaaagag acagttatct tcgatacaga tgaaggccca agacagggtg ttacacctga 1020

atctctttca aagcttcgtc ctatcaacaa ggatggattc gttacagctg gtaacgcttc 1080

aggtatcaac gacggtgctg cagcactcgt agttatgtct gaagagaagg ctaaggagct 1140

cggcgttaag cctatggcta cattcgtagc tggagcactt gctggtgttc gtcctgaagt 1200

tatgggtatc ggtcctgtag cagctactca gaaggctatg aagaaggctg gtatcgagaa 1260

cgtatctgag ttcgatatca tcgaggctaa cgaagcattc gcagctcagt ctgtagcagt 1320

tggtaaggat cttggaatcg acgtccacaa gcagctcaat cctaacggtg gtgctatcgc 1380

tcttggacac ccagttggag cttcaggtgc tcgtatcctt gttacacttc ttcacgagat 1440

gcagaagaaa gacgctaaga agggtcttgc tacactttgc atcggtggcg gtatgggatg 1500

cgctactatc gttgagaagt acgaataagg ctgagatctt cttcagtgca ttgtagttga 1560

atgaagggtt agggggggaaa tgccccccta ttttttgtct agccatcctg ccacgtttga 1620

cagggtagca atttcgacac gatagggttc tctcttctgc cgtta 1665

<210> SEQ ID NO 40
<211> LENGTH: 4071
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 40, Example 40: designer oxyphotobacterial Pyruvate-Ferredoxin Oxidoreductase DNA construct (4071 bp)

<400> SEQUENCE: 40

agaaaatctg gcaccacacc tgatctgcaa gagacgctca cgcgatacct ctgggcgtgc 60

aatcaccgca ttccccaacg cgctttgggc cacatgaccc ccatcgagag actccgaacg 120

tggcaaatgg agggaccaga gttgttcagt tcacaggtag ataatgtcgc gggtcttgat 180

agttagcaat aaatacagtt tcagaatatc tgtaatacaa aaactgtatc gagacaagaa 240

aaaagtagca aaatttacaa atgttcatga ttcatctggc taaattggat gttcaactga 300

cccattgaag acaagggcaa caaccatggc gcagaggtgc aaggagcccg tcgacggaac 360

gacagccacg acgcacgtgg cctacttcat gagcgacagc gcgttcatct tccccatcac 420

gcccagctcg gtcatgtccg aggtcgccca cgagtggtcc atgaacggcc gcaagaacgc 480

cttcggccag cccacgatgg tccgccagat gcagagcgag gctgggtctg ccggcgccct 540

gcacggcgcg ctcagcgagg gagcgctggc gacgacgttc acgagcagcc agggcctgct 600

gctcatgatc cccaacatgt acaagatcgc cggcgagctc ctgccctgcg tcatgcacat 660

-continued

cgccgcccgc accgtcgcca ccgaggccct ctctatcttc ggcgaccaca cggatgtcta 720

cgcggtgagg tcgacggggt tcgcgttcct gtgctccgcg accgtccagg agtgcatcca 780

catgtccgcc gccgcgcacg ccgccaccct gtccagcgag gtcccgttcg cccacttctt 840

cgacggcttc cgcacgtccc acgagatcca gaagatcgac ttcccctcgg acgccgacct 900

gctggcctgc atgaactttg acgacgtccg caggttccgt ggccgctcgc tgtgctgcga 960

gcgcccgctg ctgcgcggga cggcgcagaa ccccgacgtc ttcatgcagg cgtccgagtc 1020

gaacctggcg acgctggcca gggtccccgc ggccatcgac gaggcgctgg ctcgtgtgaa 1080

caaggtgttc gggaccaact acaggaccta cgagtactat ggccaccccg aggccacgga 1140

cgtgatcgtg gccatgggaa gcggcaccga agtggccatc tcgactgcca acttcctcaa 1200

ctcgcgcgac gcgaactcga gggtcggcgt cgtgagggtg cggctgttcc ggccgtttgt 1260

gtcggcggcg tttgtggctg cgctgcccaa gaccgtcaag aggatctgcg ttctggaccg 1320

cgggagggac gggcaggcgg ccgcggaccc cctgcaccag gacgtcctgt cggcgctggg 1380

tctggcagcg cccgggaggg ttcaggtgtg cgtgggaggc gtgtacggtc tgtcgtccaa 1440

ggacttcaac cccgaccacg tgatcgccgt gtacaggaac ctcgcgtcgg cgagccccaa 1500

gaacaggttc agcgtcggca tcgtcgacga cgtgacgcac aacagcctgg acatgggaga 1560

gcacgtggac gcgctgccgc aggggacgaa gcagtgcctg ctgtggggca tcggcggaga 1620

cgggaccatc ggggcgaaca agacggccat caagctgatc gcggaccaca cggagctgca 1680

cgcgcagggg tactttgcgt acgacgccaa caaggccggc ggcctgacag tctcgcacct 1740

gcggttcggc ccgacgcggt tcgaggcgcc gtacctggtg aacgacagca actacgtggc 1800

gtgccacaac ttctcgtacg tgcacaggtt caacctgctg tcgtcgctgc gcaccggggg 1860

cacgttcgtg ctcaactgcc cgtgccggac cgtggaggag ctggacacgg cactcccggt 1920

gcgcctgagg cgcgagatcg ccaggcggca ggccaagttc tatgtgatcg acgcgaccaa 1980

gatcgccaag gacaacggga tgggcccgtt catcaacatg gtcctccagg ccgtgttctt 2040

ctatctgtcc cacgtgctcg atgtgaacga ggcagtggca ctcctgaaga agagcatcca 2100

gaagatgtac gcgcgcaagg gcgaggaggt tgtcaggaag aacgtggcat cggtcgacgc 2160

gtcgctggat cccaaggcgt tgctgcacat cgagtacccc gcagacaggt ggcttgcgct 2220

ggccgacgag cacgtgcccc gcatgggtct gctcactgtc cccgagcgcc tgcagaagtt 2280

caacgccgag ctgtacgagc cgaccctcgc gtacgatggg gagagcatcc cggtcagcag 2340

gttccctcgc ggcggcgaga cgccgacggg cacgactcag ctgggcaagc gtggcatcgc 2400

cgagagcgtg ccgcactgga accacgagaa gtgcgtgcag tgcaaccagt gctcgttcgt 2460

gtgcccgcac gccgtcatcc ggtcgtacca gatcagcgag gaggagatga agaacgcccc 2520

tgccggcttc gacactctta agtcgcgcaa gcccgggtat cgtttccgca tcaacgtcag 2580

cgccctggac tgcactggct gcagcgtgtg cgtggagcag tgcccagtca agtgcctgga 2640

gatgaagcct ctcgagtccg agttcgagat gcagaaggac gccatcaggt tcgtccgcga 2700

gatggtcgcg cccaagcccg agctgggaga ccgcaagact cccgtcggca tcgcgtctca 2760

cacgccgctg ttcgagttcc cgggagcctg cgccgggtgc ggtgagaccc cgctggtgcg 2820

cctcgtgacg cagatgttcg gtgagcgcat ggtcatcgcc gcggccactg ggtgcaactc 2880

gatctgggga gcgtcgttcc cgaacgtgcc gtacacaacc aacgcccgcg gggagggccc 2940

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cgcgtggcac aactcgctgt tcgaggacgc ggcggagctc gggtatggca ttacgtgtgc 3000

gtatcgccag cgccgcgagc gcctcatcgg catcgtgcgg agcgtcgtcg acgatgcggg 3060

atccgtgcag ggtctgtctg ctgagctgaa ggctctgctg gtcgagtggc tcgcgcacgt 3120

cagggacttc gagaagaccc gcgagctccg cgacaggatg aacccctga tcgacgcaat 3180

cccagcgaac gcggactgca gggttctgga gctcagggag aagcacaacc gcgagctgat 3240

cgcgcgcacg agtttctgga tcctcggtgg cgacgggtgg gcgtacgaca tcggcttcgg 3300

tggactggac cacgtgatcg ccaacaacga ggacgtcaac atccttgttc tcgacacgga 3360

ggtctactcc aacactggtg gccagcgctc caagtcgacg ccgctcggcg cccgcgccaa 3420

gtacgctgtg ctgggcaagg acactgggaa gaaggacctg gggcgcatcg cgatgaccta 3480

cgagaccgcg tacgtggcca gcatcgcgca gggagccaac cagcagcagt gcatggacgc 3540

gctgagggag gccgaggcct accagggccc ctcgatcgtc attgcgtaca ctccgtgcat 3600

ggagcaccag atggtccgcg ggatgaagga gagccagaag aaccagaagc tggctgtgga 3660

gacgggctac tggctgctgt accgcttcaa ccccgacctc atccacgagg gcaagaaccc 3720

cttcaccctc gactcgaagc ctccctcgaa gcctcccaag gagttcctgg acacgcaggg 3780

ccgtttcatt actctgcagc gcgagcaccc cgagcaggcc cacctccttc acgaggcact 3840

cacccgctct ctggccaccc gcttcgtgcg ctaccagcgc ctcgtgcagc tgtacgagcc 3900

cgctgcccct gccgcagctc ctgccacgca ttaaggctga gatcttcttc agtgcattgt 3960

agttgaatga agggttaggg gggaaatgcc cccctatttt ttgtctagcc atcctgccac 4020

gtttgacagg gtagcaattt cgacacgata gggttctctc ttctgccgtt a 4071

<210> SEQ ID NO 41
<211> LENGTH: 1806
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 41, Example 41: designer oxyphotobacterial Pyruvate Kinase DNA construct (1806 bp)

<400> SEQUENCE: 41

agaaaatctg gcaccacacc tgatctgcaa gagacgctca cgcgatacct ctgggcgtgc 60

aatcaccgca ttccccaacg cgctttgggc cacatgaccc ccatcgagag actccgaacg 120

tggcaaatgg agggaccaga gttgttcagt tcacaggtag ataatgtcgc gggtcttgat 180

agttagcaat aaatacagtt tcagaatatc tgtaatacaa aaactgtatc gagacaagaa 240

aaaagtagca aaatttacaa atgttcatga ttcatctggc taaattggat gttcaactga 300

cccattgaag acaagggcaa caaccgtgtt cactaaaatt gtagctacat tggggccttc 360

gactgataga ctgccggata taacggccct gttgagcaag gttcacggcg tgcggataaa 420

tatgtctcac gcatcgccat cggaggtaga ggcccgcgtg aacgccgtga ggaagtatga 480

ggagaccagc gggaggtata tagccattat agcggatcta aggggcccca gcgtcaggac 540

cggccttatg cgccctctac agataacggc gggcgcccgc gtctccttta aattagccga 600

gaaggggac ggcttcgtac ctgtgccgcg gcgtgagttc ttcgaagtaa tcgaggaggg 660

agacgaggtt cttatgttag acggaaaact cgtcttgagg ataatcagcg cagcgcagac 720

ctcggccgag gccgagtcgt tatcctccgg cgtcatatcc agcaataagg caatagtggt 780

caaaggcaag gaatatcata tagagcagcc tgtggaggaa gacataaggg cgcttcagac 840

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gctctctcgg ttcagagacg acgtagacta cgtggccctc agccttgtga gagacggagc 900

agacgtgagg aaaatgagga gcgtcgtcga ggaggctggg ctcacctccg gcataatggc 960

caaaatagag acgaagagcg cagtagataa aatcgaggag ataatcaatg cggccgacta 1020

catagttata gcgagaggcg atctggcgct gcactacgga ctggagtaca ttcctaaagt 1080

acagaggctc ttggtggaga gatctctctc ggcaggaagg cccgtggcgg tggccacgca 1140

gcttttggac tctatgcaga ccaacacgac gcccactagg gcggaggtca acgacgtgta 1200

cacaacggcg agtctcggag tggactctct gtggctgacc aacgagactg cgagcggaga 1260

gcacccgtta gaggcagtgg attggctgag gaggatagtg tcgcaggtcg agttcgggag 1320

acttaaggct gcgtcgccgg ccgacgcacg cgataggttc gccaaagccg tggtagatat 1380

ggccgaggac atgggagggg aaatcgcagt atactcaatg acgggaactc tggcgaagag 1440

aatagctaaa tttaggccga tgacgacagt ctacgtcgga gtcaacgaga ggaggctcgc 1500

gaggatgttg gagctccgcg aggatgttgg agctcatatg gggcctagag cctgtggtcg 1560

tgccggcgca tacttacgag gagggcctcg agaggctcct ctccagattc tccgacaaag 1620

tcttgatagc cacgtatggg ctcagaggcg gcacacatac tattaataag gctgagatct 1680

tcttcagtgc attgtagttg aatgaagggt taggggggaa atgccccccct attttttgtc 1740

tagccatcct gccacgtttg acagggtagc aatttcgaca cgatagggtt ctctcttctg 1800

ccgtta 1806

<210> SEQ ID NO 42
<211> LENGTH: 1696
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 42, Example 42: designer oxyphotobacterial Enolase DNA construct (1696 bp)

<400> SEQUENCE: 42

agaaaatctg gcaccacacc tgacccccat cgagagactc cgaacgtggc aaatggaggg 60

accagagttg ttcagttcac aggtagataa tgtcgcgggt cttgatagtt agcaataaat 120

acagtttcag aatatctgta atacaaaaac tgtatcgaga caagaaaaaa gtagcaaaat 180

ttacaaatgt tcatgattca tctggctaaa ttggatgttc aactgaccca ttgaagacaa 240

gggcaacaac cttatttttt cttcaagtta aagaatgcgt tcattccagg ataaacggca 300

atgctgccaa gctcttcttc aattctcaag agctgattgt attttgctac tctgtctgtt 360

cttgacggtg cacctgtctt tatctgacca gcatttactg caacaacaag gtcagcaatt 420

gttgtatctt cagtctcacc tgatctgtgg gatacaactg cagtgtagcc tgctctattt 480

gccatttcaa tagcttctaa agtttctgta agtgttccta tctgattaag cttaatcaat 540

attgagtttg caacgccaag ttctattccc tttgcaagcc tctttgtgtt tgtaacaaac 600

aaatcatcac ccacaagctg aatcttcttg ccaagtgctt cagttagcat cttccagcct 660

tcccagtcct cttctgcaac accgtcttca attgatacaa ttgggtactt ttcaacaagt 720

tttacccaga attctaccat ttcttctttt gttctaactt taccttctct ttcgaaatga 780

tactttccat cttcttcatt gtagagctca gatgttgcag ggtcaagcgc aattgcaata 840

tccttaccag gagtataacc agctttttca attgcttcga caattacttc caatggctct 900

tcgttagact tcaagtttgg tgcaaatcca ccttcatcac ccactgttgt gttgtatcct 960

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cttgccttca atacatttct taattgatgg aatgtctcag cacacatcct gagtgcttcg 1020

ctaaaagatt ttgcaccaac tggcattatc ataaactctt gtaggtcaac agagttgtca 1080

gcatgctttc caccgttcaa aatattcatc attggcacag gtaaatactt tgcattgaca 1140

ccaccaatgt attggtacag tggaagacca agtgcgtttg ccgctgcctt cgcaactgcc 1200

aaagatacac ccaaaattgc atttgcacca agcttgctct tgttctctgt cccatcaagc 1260

tcaatcataa gcctgtcaat ctcaacttgg ttaagagcgt tcattccaat tatttctggc 1320

gcaataacct cgtttacatt ttcgactgct ttgagaaccc cttttcccat atatcttttt 1380

ttatcaccgt ctctgagttc aacagcctcg aacatacctg ttgacgcacc tgatggaaca 1440

gcagctctac ctacaaattc atcatttaca acaacttcta cttcaacagt tgggtttcct 1500

cttgaatcca gaatttctct tgcttttaca gctgtaattg aaagatcaac cttcattaag 1560

gctgagatct tcttcagtgc attgtagttg aatgaagggt taggggggaa atgccccccct 1620

atttttttgtc tagccatcct gccacgtttg acagggtagc aatttcgaca cgatagggtt 1680

ctctcttctg ccgtta 1696

<210> SEQ ID NO 43
<211> LENGTH: 2029
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 43, Example 43: designer oxyphotobacterial Phosphoglycerate-Mutase DNA construct (2029 bp)

<400> SEQUENCE: 43

agaaaatctg gcaccacacc tgacccccat cgagagactc cgaacgtggc aaatggaggg 60

accagagttg ttcagttcac aggtagataa tgtcgcgggt cttgatagtt agcaataaat 120

acagtttcag aatatctgta atacaaaaac tgtatcgaga caagaaaaaa gtagcaaaat 180

ttacaaatgt tcatgattca tctggctaaa ttggatgttc aactgaccca ttgaagacaa 240

gggcaacaac cctacgccgg cgcctgcttc tcctcctgcc ggcagcactt ctccaaaggg 300

tgcacgttcg cttctcttgt aatcagggtc tggccggtca tctcggccgg tttcgggatg 360

cccagcaggt gcaggatggt gggggccaca tcccgcaggc tgccgtcccg cagcgcaatg 420

ccggcggtat cccgcccgat caggatgaac ggcaccgggc tggtggtgtg ggccgtatga 480

ggctgtccct cttcgtccac catctcatcc gcattgccgt ggtctgccgt tatcaggagc 540

gtgccgtcct tttccaggac ggcccgcgcc acctttccaa ggcagcggtc gattgtttct 600

atggcctttа ccgttgcctt catgtcgccg gtatgcccga ccatgtcggg attggcgtaa 660

ttcattatga ttacgtcgta cttgcccgag gccagccgct ccagaaaggt gccggtgacc 720

tcgttggcgc tcatttcggg cttcaggtcg taggtggcca cccgcgggga gggcaccagg 780

atcctgtctt cgccggggta tggcttttct aagccgccgt tgaagaagaa ggtcacatgg 840

gcgtactttt ccgtttcggc caggcggagc tgggtcatgc cgtgcctgct taaaacctcg 900

cccagggtat tgcgcagctc ctgcggctga aacgccaccg gcgccttaat ggtcttgtcg 960

taaagggtca tgcaggtaaa atgcacggca gggtagccct gctttctggc aaacccggtg 1020

aaatcctcgt ccacaaaggc cctggtaatc tggcgggccc ggtccggccg gaagttaaag 1080

aaaataacgg cgtcgccctt cattattttg gcggccggcc cacccgaccc gtttaccacg 1140

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acggtgggct ggataaactc gtcggtttca tcccttccgt accccaggtc aaccgcctcc   1200

agcgggcttg ttgcctgaat gccctcgcct aaaaccattg cgttgtacgc ccgctcggtg   1260

cggtcccagc ggcggtctct gtccatggcg taatagcgcc ccattaccgt tgccaccgcc   1320

ccaaagccca gttcgcccag cttcttcctt aactgctcga agtattcttt tgcgttggcc   1380

ggcggcacgt cgcgcccgtc caggaaggca tggacaaaga cgttgcgcat gttctcgcgg   1440

gcggccaggt ccaggagggc gaaaaggtgg ctgatatggc tgtgcactcc gccgtccgat   1500

aaaagcccca tcaggtgaag ggccttatta ttctccctgg cgtatctcac cgcctccagc   1560

aggacttcgt tcttgaaaaa ggtcccgtcc ttgatggcgc ggcttattct ggtaagctcc   1620

tggtacacca ccctgccggc gcctatgttc aagtgtccca cctcggaatt gcccatctgg   1680

ccctcgggaa gccccacgtc ctcgccggaa cagctcaggg cacagtgggg gtaaccggcc   1740

agaaagctct tgaaattcgg tgtgctggcc agggctatgg cattgccccg gacattggaa   1800

ctgaggcccc agccgtccag aaccaccagc accaggggcc tgccgccggc ataccggccg   1860

cagggcgttg cagctacgtc ttccttcaat aaggctgaga tcttcttcag tgcattgtag   1920

ttgaatgaag ggttaggggg gaaatgcccc cctatttttt gtctagccat cctgccacgt   1980

ttgacagggt agcaatttcg acacgatagg gttctctctt ctgccgtta               2029
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<210> SEQ ID NO 44
<211> LENGTH: 1687
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 44, Example 44: designer oxyphotobacterial Phosphoglycerate Kinase DNA construct (1687 bp)

<400> SEQUENCE: 44

```
agaaaatctg gcaccacacc tgacccccat cgagagactc cgaacgtggc aaatggaggg     60

accagagttg ttcagttcac aggtagataa tgtcgcgggt cttgatagtt agcaataaat    120

acagtttcag aatatctgta atacaaaaac tgtatcgaga caagaaaaaa gtagcaaaat    180

ttacaaatgt tcatgattca tctggctaaa ttggatgttc aactgaccca ttgaagacaa    240

gggcaacaac cttatttatc gagcagcgcc cttactcccg gcagttgctt cccttccaga    300

aactccaggg aagcgccgcc gccggttgag atatgggtca ttttgccggc tacgccggcc    360

ttcttggccg ccgccgccgt gtcaccgccg ccgattacgg tgacggcgtt taattcggcc    420

agcgtccggg ctattgcttc ggtgcccctg gcaaaaggat ccatttcaaa aacgcccatt    480

ggtccgttcc agaccacggt cctggccgcc ctgagggctt cggtgaaaag tctgatggac    540

tcgggcccta tatccagggc catccactcc gccgggattt gatcgaccgg caccgtcctt    600

tgctcctggc cgggcgccgg ccccggcgcc accaccacat ccaccggcag gaggagcttt    660

acttccctgc ttctggcttc tgcaatcagc ttcctggcca ggtcaatctt gtcggcctcc    720

agcagggact taccgacgct gtacccttgt gccttcagaa aggtattggc catcccgccg    780

ccaatgataa ccgtatcgac tttggtcagc aggttgaaaa ttactcccag cttgtcggaa    840

actttcgagc cgcccacgac ggctgcaaaa gggcgctccg ggctggtcag cagcctgccc    900

agtatttcca gctctttttc catcagcagg cctgccacgg ccggcaaaaa cccggcaacg    960

ccctcggtgg aggcgtgggc ccggtgtgcg gttccaaacg catcgtttac aaagacatct   1020

gccagctcag ccagttgccg ggcaaacttc tcgtcgtttt tctcctcctc cgggtggaaa   1080
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cggacgtttt ccagcagcac cacgtccccg tcctgcatct gggcaacggc ggacctggcg 1140

gcttctccca cgcagtcgcc ggccttaacc accgttttcc ccagcagttc ggaaaggcgc 1200

ctggcaacgg gatccatttt gtacctctcg tccaccctgc ccttgggccg gcccaggtgc 1260

gaaaccagaa taaccctggc tttttgtccg ataaggtagt ttatggtggg cacggcctcc 1320

tttattttaa cgtcatcggc cacccggccg ttttccatcg gcacgttgaa gtccacccgc 1380

aacaggaccc gcttgccctt tacatctata tcccttaccg ttttttttggc cactaaggct 1440

gagatcttct tcagtgcatt gtagttgaat gaagggttag gggggaaatg ccccccctatt 1500

ttttgtctag ccatcctgcc acgtttgaca gggtagcaat ttcgacacga tagcgtgctg 1560

tactgttttt tgctcgtcag ggttgggttt tgtcatcgac acccaaggat tggagtcggt 1620

gctcaataat cgccagttgc tgttgggcag ccgccaattg cgcctgaggt tctctcttct 1680

gccgtta 1687

<210> SEQ ID NO 45
<211> LENGTH: 1514
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 45, Example: designer oxyphotobacterial Glyceraldehyde-3-Phosphate Dehydrogenase DNA construct (1514 bp)

<400> SEQUENCE: 45

agaaaatctg gcaccacacc tgatctgcaa gagacgctca cgcgatacct ctgggcgtgc 60

aatcaccgca ttccccaacg cgctttgggc cacatgaccc ccatcgagag actccgaacg 120

tggcaaatgg agggaccaga gttgttcagt tcacaggtag ataatgtcgc gggtcttgat 180

agttagcaat aaatacagtt tcagaatatc tgtaatacaa aaactgtatc gagacaagaa 240

aaaagtagca aaatttacaa atgttcatga ttcatctggc taaattggat gttcaactga 300

cccattgaag acaagggcaa caaccaatgg atttgggcgg atcggacgtt tagcattcag 360

aagaattcaa gatgtagaag gtcttgaagt agttgcagtt aacgacttaa cagatgacga 420

tatgttagct catttattaa aatacgatac tatgcaaggt cgtttcactg gagaagttga 480

agttatcgaa ggtggattcc gtgttaacgt aaaagaaatt aaatcattcg atgaccagat 540

gctgggtaaa ttaccatggg gcgatttaga tatcgacgta gtattagaat gtactggttt 600

ctatactgat aaagaaaaag cacaagctca catcgatgca ggtgctaaaa aagtattaat 660

ctcagctcca gctaaaggtg atgtaaaaac aatcgtattc aacactaacc atgacgcatt 720

agacggttca gaaacagttg tttcaggtgc ttcttgtact actaactcat tagcaccagt 780

tgcaaaagtt ttaagtgatg aattcggttt agttgaaggt ttcatgacta caattcacgc 840

ttacactggt gaccaaaata cacaagacgc acctcacaga aaaggtgaca aacgtcgtgc 900

acgtgcagca gcagaaaata ttatccctaa ctcaacaggt gctgctaaag ctatcggtaa 960

agttattcca gaaatcgatg gtaaattaga cggtggagca caacgtgttc cagttgctac 1020

tgggtcttta actgaattaa ctgtagtatt agacaaacaa gatgtaactg ttgaccaagt 1080

taacagtgct atgaaacaag cttcagacga atcattcggt tacactgaag acgaaatcgt 1140

atcttctgat atcgttggta tgacttacgg ttcattattc gatgcgactc aaactcgtgt 1200

tatgactgtt ggagatcgtc aattagttaa agttgcagct tggtacgaca aagagtgggg 1260

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taaggctgag atcttcttca gtgcattgta gttgaatgaa gggttagggg ggaaatgccc 1320

ccctattttt tgtctagcca tcctgccacg tttgacaggg tagcaatttc gacacgatag 1380

cgtgctgtac tgtttttttgc tcgtcagggt tgggttttgt catcgacacc caaggattgg 1440

agtcggtgct caataatcgc cagttgctgt tgggcagccg ccaattgcgc ctgaggttct 1500

ctcttctgcc gtta 1514

<210> SEQ ID NO 46
<211> LENGTH: 609
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 46, Example 46: designer Nial-promoter-controlled Proton-Channel DNA construct (609 bp)

<400> SEQUENCE: 46

agaaaatctg gcaccacacc tatatggtag ggtgcgagtg accccgcgcg acttggagct 60

cgatggcccc gggttgtttg gggcgtccgc ctctcgcgct attctgagct ggagaccgag 120

gcgcatgaaa atgcattcgc ttccatagga cgctgcattg tggcttgaag gttcaaggga 180

agggttcaaa cgaccccgcc gtacgaactt ttgtcggggg gcgctcccgg ccccgggctc 240

ttgtgcgcgc attagggctt cgggtcgcaa gcaagacgat acatggccgg catcggcgcc 300

gtgctgaagg tcctgaccac cggcctgccc gccctgatca gctggatcaa gcgcaagcgc 360

cagcagtaaa tggaggcgct cgttgatctg agccttgccc cctgacgaac ggcggtggat 420

ggaagatact gctctcaagt gctgaagcgg tagcttagct ccccgtttcg tgctgatcag 480

tctttttcaa cacgtaaaaa gcggaggagt tttgcaattt tgttggttgt aacgatcctc 540

cgttgatttt ggcctctttc tccatgggcg ggctgggcgt atttgaagcg gttctctctt 600

ctgccgtta 609

<210> SEQ ID NO 47
<211> LENGTH: 1360
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 47, Example 47: designer nirA-promoter-controlled NAD-dependent Glyceraldehyde-3-Phosphate-Dehydrogenase DNA construct (1360 bp)

<400> SEQUENCE: 47

agaaaatctg gcaccacacc cttcttgcag aacatgcatg atttacaaaa agttgtagtt 60

tctgttacca attgcgaatc gagaactgcc taatctgccg agtatatgaa cggatttggc 120

aggataggac gactggtgtt gcgggcggcg gtggagaagg gcacggtgga ggtggtggcg 180

gtgaacgatc cgttcatctt cccggacgcg gcgtacgctg cgtacatgct gcagtacgac 240

tcgacgcacg gggcgttccc gggtgaggtg ggcagcgacg gggagcactt ggtggtgaac 300

gggaagaagc tggcgtgctt tgcgatccgc gatccggcgg agatcccgtg gggctcggtc 360

ggcgccgact acgtcgtgga gtccaccggc gtgttcaccg tgaccgagaa ggcgtcgttg 420

cacgtcaagg gcggcgcgaa gaaggtggtt atatcggcgc cgtcgaagga tgcgcccatg 480

tttgtgatgg gcgtgaacca tgacgcctac accaaggact tgacggtggt gtcgaatgcg 540

tcttgcacca ccaacttgtt tggcgccgct ggccaagatc atcgacgagg cgttcggcat 600

cgggatgggc ctcatgagca ccatccacgc ggtgacggcc acgcaaaaga cggtggatgg 660

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gccgagctcc aaagactggc gcggtgtcgc ggcgcgttcc agtcgattat tcccagcagc 720

accggcgctg cgaaagcggt cggcaaggtg tacccgaagc tgaacggcaa gctgaccggc 780

atggcgttcc gcgtgccggt gcccgacgtg tccgtggtag acttgacagt gaccctgaag 840

aaggagacca actacgagga gatcaaaaag gctgtcaagc aggcgtcgca gagcccgcac 900

tacaagggca tcgtggcgta caccgagcac cccatcgtgt cggccgacct ggtgcacaac 960

ccgtactcgt cggtgttcga tgccgaagcc ggtatcatgc tgtcgcccac gtttgtgaaa 1020

ctggtcagct ggtaatagtg atcccggccg ctactaaagc ctgatttgtc ttgatagctg 1080

ctcctgcctt tgggcagggg ctttttttctg tctgccattc ttgaggatgg cggactcttt 1140

ccctttttgct ctacgcccat gaatgcgatc gcagtctccc ctgtccagca cgttggagtg 1200

attggtggtg gccagttagc ttggatgctg gcaccagcag cgcaacagtt ggggatgtcg 1260

ctgcacgttc aaacacccaa tgatcacgac ccagcagtag cgatcgcgga tcaaaccgta 1320

ttagcagcag ttgctgacgc ggttctctct tctgccgtta 1360

<210> SEQ ID NO 48
<211> LENGTH: 1621
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Syntheitc Construct- Sequence No. 48, Example 48: designer nirA-promoter-controlled Phosphoglycerate-Kinase DNA construct (1621 bp)

<400> SEQUENCE: 48

agaaaatctg gcaccacacc cttcttgcag aacatgcatg atttacaaaa agttgtagtt 60

tctgttacca attgcgaatc gagaactgcc taatctgccg agtatatgtc atttgtcttc 120

gagcgcgacg acacccggca gctgttttcc ttccataaac tcgagcgaag cgccgccgcc 180

ggtggagata tgatccattt tgtcggccaa gccgaatttc tcaaccgccg ccgccgaatc 240

cccgccgccg atgaccgaat aggtgtcggg cgcttccgcc agtgcttcgg cgatcgcttt 300

tgtcccatgg gcgaacgctt ccatttcaaa gacgcccatc gggccgttcc agacaacgag 360

cttcgattga cgaatgacat cgcggtacaa ttcgcgcgtt ttcgggccga tgtcaagcgc 420

ctcccaatcg ctcggaatgg cgtcgatggc gacgactttc gtgttggcgt cgttcgcaaa 480

ccggtcggcg acgaccacgt ccaccggcat ataaaaacgg acgccttttt ctttcgcctt 540

ttccataaac gatttggcga gttcgatttt gtcctcctca agcagcgact tgccgacgtc 600

atggccgagc gctttgacga acgtatacgc cagtccgccg ccgatgatca agttgtcgac 660

tttttcaagc aaattgtcga tgacgccgat tttgtctttc actttcgcgc cgccgatgat 720

cgccgtaaac gggcggtccg gattcgagag cgctttgccg agcacttcga gttctttttc 780

catcaaaaac ccggccaccg caggcaagta atgggcgatg ccttccgtcg acgcatgagc 840

gcggtgggcg gcgccgaacg catcgttgac atacagatcc gcgagctccg caaacgcttt 900

ggccagctct ggatcgtttt tctcttcgcc agggtaaaaa cggacgttct caagcaagag 960

cacgtcgcct tcgttcaaac ggtcgaccgc cgctttcacc tcatcgccga ccgcttcatt 1020

cgttttggcg accggccgtt caagcagctc gccgagccgc ttcgcaacgg catccaaacg 1080

caattcttcg accacttttc ctttcgggcg gccgaggtgg ctcgccaaaa tgactttcgc 1140

cccgtgctcg atcaaatagc ggatcgtcgg gagtgcggcg cgaatgcgcg tgtcatcggt 1200

-continued

gatggcgcct tgctccatcg gaacgttgaa atcgacgcgg caaaagacgc gctttcccct 1260

cacctcaacg tcgcggatcg tcttcttgtt cattaatagt gatcccggcc gctactaaag 1320

cctgatttgt cttgatagct gctcctgcct ttgggcaggg gctttttttct gtctgccatt 1380

cttgaggatg gcggactctt tccctttgc tctacgccca tgaatgcgat cgcagtctcc 1440

cctgtccagc acgttggagt gattggtggt ggccagttag cttggatgct ggcaccagca 1500

gcgcaacagt tggggatgtc gctgcacgtt caaacaccca atgatcacga cccagcagta 1560

gcgatcgcgg atcaaaccgt attagcagca gttgctgacg cggttctctc ttctgccgtt 1620

a 1621

<210> SEQ ID NO 49
<211> LENGTH: 1990
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 49, Example 49: designer nirA-promoter-controlled Phosphoglycerate-Mutase DNA construct (1990 bp)

<400> SEQUENCE: 49

agaaaatctg gcaccacacc cttcttgcag aacatgcatg atttacaaaa agttgtagtt 60

tctgttacca attgcgaatc gagaactgcc taatctgccg agtatatgct cgagcattta 120

tttaataata agcgagcttc ccttcatctc tgaaggtttt tctaacccta agatgtctaa 180

gattgttgga gcaatgtctg ctaagattcc atcatctctt aatttaacat tgccatatcc 240

cacaagatac aaaggcacct tatttgttgt atgagctgta tgaggctcac ctgtctcata 300

atcaatcatc tgttcacagt tgccatggtc agcagtaata ataaccactc cacccttttc 360

taaaaccttg ttaacaactt ttccaataca ctcatctaca gcctcaactg cctttattgc 420

agcctctaaa acgcctgtgt gccctaccat gtcaccattt gcatagttac atattatcac 480

atcatattca tctctttcaa ttctctcaag taaagcttct gttacctcgt atgcactcat 540

ctcaggttta agatcatatg ttgcaacctt tggtgatggt accaataccc tgtcttctcc 600

gacatttggt acttccacac cgccgttgaa gaaaaaggtg acatgagcat acttttctgt 660

ctcagcaatt cgaagttgtt ttaaccctaa cttgctaaaa tactctccca aagtgtttgt 720

caggttctct ggtttgaatg caacatggca atttttttatt gtcacatcat actgagtcat 780

gcatacaaag aacacttcga aatatccttt tttcctttca aaaccgtcaa attcaacatc 840

acaaaacgct cttgtaagct gtcttgctct gtcaggtctg aagttaaaga aaataatact 900

gtcatgttca tttattgttg cgacaggttt tccattttca agcacaacag tcggaattac 960

aaactcatca gtgttacctt ttttatacga cttttcaacc gcctctaatc ctgagcttgc 1020

atactcgcct tcaccaaaga ccattgcatt atatgccttt tcaactcttt cccatctttt 1080

gtctctgtcc attgcatagt atctgcccat cactgttgca atcttaccac aaccaatttc 1140

ttttatcttc tgttcaagct cttcaatgta aatttttgcg ctcgaaggtg gaacatctcg 1200

cccatccaaa aagcaatgaa catatacttt ttcaagattg tgcctctttg caagttttaa 1260

aagtgcgtaa agatgtgtgt tgtggctgtg aacaccacca tctgataaaa gtcccatcag 1320

atgaagagaa gagttatatt ttttgcaatt ctctattgcc atcaaaaact cttctttttc 1380

aaaaaaatca ccgtctttaa ttgactttgt tattcttgta aattcttggt aaacaattct 1440

tcctgcaccc aggttcagat gtccaacttc agaattcccc atttgtcctt cgggaagacc 1500

-continued

aacatccata ccactgctac caatcagggt atatgggtaa ttcttttcgt aatagtcaag 1560

gttaggggtc ttacccaaag caacagcgtt tccctcttgc tttgggttat aaccccaacc 1620

gtccatgata atcaacacaa caggtttttt cattaatcta gataatagtg atcccggccg 1680

ctactaaagc ctgatttgtc ttgatagctg ctcctgcctt tgggcagggg ctttttttctg 1740

tctgccattc ttgaggatgg cggactcttt ccctttttgct ctacgcccat gaatgcgatc 1800

gcagtctccc ctgtccagca cgttggagtg attggtggtg gccagttagc ttggatgctg 1860

gcaccagcag cgcaacagtt ggggatgtcg ctgcacgttc aaacacccaa tgatcacgac 1920

ccagcagtag cgatcgcgga tcaaaccgta ttagcagcag ttgctgacgc ggttctctct 1980

tctgccgtta 1990

<210> SEQ ID NO 50
<211> LENGTH: 1765
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 50, Example 50: designer nirA-promoter-controlled Enolase DNA construct (1765 bp)

<400> SEQUENCE: 50

agaaaatctg gcaccacacc cttcttgcag aacatgcatg atttacaaaa agttgtagtt 60

tctgttacca attgcgaatc gagaactgcc taatctgccg agtatatgct cgagcatatg 120

ctaaataaac ccgtcgtttc cattgaagaa attaccgcta gagaaatttt agactctcgt 180

ggccgtccta ccattgaagc agaagtctta ctggaaacag gggctttcgg tattgcccag 240

gttcccagtg gcgcgtcaac tggtagcttc gaggcccacg aattacggga tgatgacccc 300

aaccgctacg gtggtaaagg cgttctcaaa gcggttagta acgttataga cgaaattgcc 360

cctaaaatta tcggaatgga tgggttagat caaactgcga tcgatcacac catgattgag 420

ttagacggtt ctactaataa aaaagaatta ggggccaatg ctatccttgc cgtttcctta 480

gccactgcaa aagctgccgc cgatgaatta gcccttcccc tgtaccgtta tttaggggggt 540

cccttggcca atgtcttacc cgtccccatg atgaacgtga ttaacgggggg ttctcacgcg 600

gataataacg tagacttcca ggagtttatg attatgccag tgggtgcgga ctcttttaaa 660

gaagctttga ggtgggggggc cgaagtgttt gcttccctca gtaaagttct aaaagagcgt 720

aaattgctct ctggggtagg agacgagggg ggatacgccc cgaacctggg atcgaaccag 780

gaagccttag atttgctcat agaagccatt gaaaaggcgg ggtataagcc aggggaacag 840

gtggctttag cgatggatgt ggcttcaagt gagttttata aggatggcga atatatttat 900

gatggttctc cccattcccc tcaagaattt atcgattatt taggtaaatt agtggatcaa 960

tatcctatta tttccattga agatggctta caagaagatg actgggatag ctggaaaagt 1020

ttgaccgata cgttaggatc tcgcattcag ttagttgggg acgatctttt tgtcacgaac 1080

cccactcgtc tgcaaaaagg cattgatatg ggtgtgggta atagtattct cattaaactc 1140

aatcaaattg gtagtttaac ggaaacgtta gatacgattg ctttagcgac tcgtcatcaa 1200

tatagttccg ttatttccca tcgttccgga gaaaccgaag acactaccat tgcagactta 1260

gccgtagcta cacgcgctgg acaaatcaaa accggttctc tgtgtcgtag tgaacgggta 1320

gccaaatata accgactatt acgtattgaa gaagaattag gcgatcgcgc agtttatgct 1380

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gcaaaagtgg gtttaggccc tcaataaggc tgctgccccg gctgctgcta atctagataa 1440

tagtgatccc ggccgctact aaagcctgat ttgtcttgat agctgctcct gcctttgggc 1500

aggggctttt ttctgtctgc cattcttgag gatggcggac tctttccctt ttgctctacg 1560

cccatgaatg cgatcgcagt ctcccctgtc cagcacgttg gagtgattgg tggtggccag 1620

ttagcttgga tgctggcacc agcagcgcaa cagttgggga tgtcgctgca cgttcaaaca 1680

cccaatgatc acgacccagc agtagcgatc gcggatcaaa ccgtattagc agcagttgct 1740

gacgcggttc tctcttctgc cgtta 1765

<210> SEQ ID NO 51
<211> LENGTH: 1888
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 51, Example 51: designer nirA-promoter-controlled Pyruvate-Kinase DNA construct (1888 bp)

<400> SEQUENCE: 51

agaaaatctg gcaccacacc cttcttgcag aacatgcatg atttacaaaa agttgtagtt 60

tctgttacca attgcgaatc gagaactgcc taatctgccg agtatatgct cgagcatatg 120

ttaaaaaaga cgaaaatcgt ttgcacgcag ggtccgtcca cagagaaacc gggcgtaatt 180

gatgcactga ttgccaatgg catgaactgc gcacgcttca atttctccca tggtgaccac 240

gaagaacatc ttggccgtat caatatggtt cgtgaagctg ccaagaaggc tggcaaggtt 300

atctctttaa tcctcgatac caaaggtccg gaaatgcgtc tgggcgagtt caaagatggc 360

aaagttatgc tcgaaaaggg caacaagttc actttgacct atgacgatga accgggtgat 420

gaaactcatg tttccgtaaa ccacaaaggt ctttacacgg aagttaagcc gggcgacacc 480

ctgctcctct ccgatggcct cgtagctctc aaagttgatg aaatcaaggg caaggatatc 540

gttacgacga ttcagaacag cggtaagatg agcacgcgca agcgcgtagc tgctccgggc 600

gtaccccttg gtctgcctcc tatctccgaa caggatgcta aggacatcat ctttggctgc 660

gaacaggata tggatttcgt agctgcttcc ttcatccagc gtccggatga tgttatcgcc 720

atccgcaagc tcatcgaaga gcacaatggc cacatggaaa ttctgccgaa gatcgaaaac 780

ctcgaaggtg ttaagaactt cgatgcaatc ctggaagttt ccgacggcat catggttgcc 840

cgtggtgacc tgggcgtaga agttccggca gaagatgtgc cccttattca gaaggaaatc 900

atccgcaagt gcaacgctgc tggcaagccg gttatcgttg ctacgcagat gctcgactcc 960

atggaacgca acccgcgtcc gacccgtgca gaagtttctg acgttggtaa cgccatcctc 1020

gatggtacgg atgccatcat gctgtccggc gaaacggctt ccggtgacta tccggtagaa 1080

gcagttgcca cgatgaaccg cattgcacag cgcatggaaa gctcccttga atacaaggaa 1140

ctctatgtag aacgtggtct gcagcacatg gaatcccgta cgcgtgctat cgctcatgct 1200

acggttcaga tggcttatga gctcgatgct ccggctatta tcacgccgac cgaatccggt 1260

tacacgacga aggtcgtttc caagtatcgt ccgaaggctg ctatcgtagc ttacacgccg 1320

agcgaaaaag ttctgcgtca gctgaacctg cgttggggcg tatatccggt actcggcacc 1380

cagtggagcg atgtggatga aatgatcagc aatgcaacgg ctgctgctgt taaggaagac 1440

ctcgtacagc gcggcgacct caccatcatc acctccggtg tgaagatgga atcccgtacg 1500

cgtgctatcg ctcatgctac ggacatctaa ggctgctgcc ccggctgctg ctaatctaga 1560

-continued

taatagtgat cccggccgct actaaagcct gatttgtctt gatagctgct cctgcctttg 1620

ggcaggggct tttttctgtc tgccattctt gaggatggcg gactctttcc cttttgctct 1680

acgcccatga atgcgatcgc agtctcccct gtccagcacg ttggagtgat tggtggtggc 1740

cagttagctt ggatgctggc accagcagcg caacagttgg ggatgtcgct gcacgttcaa 1800

acacccaatg atcacgaccc agcagtagcg atcgcggatc aaaccgtatt agcagcagtt 1860

gctgacgcgg ttctctcttc tgccgtta 1888

<210> SEQ ID NO 52
<211> LENGTH: 2188
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 52, Example 52: designer nirA-promoter-controlled Pyruvate-Decarboxylase DNA construct (2188 bp)

<400> SEQUENCE: 52

agaaaatctg gcaccacacc cttcttgcag aacatgcatg atttacaaaa agttgtagtt 60

tctgttacca attgcgaatc gagaactgcc taatctgccg agtatatgct cgagcatatg 120

gtatcaacct acccagaatc agaggttact ctaggaaggt acctctttga gcgactccac 180

caattgaaag tggacaccat tttcggcttg ccgggtgact tcaacctttc cttattggac 240

aaagtgtatg aagttccgga tatgaggtgg gctggaaatg ccaacgaatt gaatgctgcc 300

tatgctgccg atggttactc cagaataaag ggattgtctt gcttggtcac aacttttggt 360

gttggtgaat tgtctgcttt aaacggagtt ggtggtgcct atgctgaaca cgtaggactt 420

ctacatgtcg ttggagttcc atccatatcg tcacaggcta aacagttgtt gctccaccat 480

accttgggta atggtgactt cactgttttt cacagaatgt ccaatagcat ttctcaaact 540

acagcatttc tctcagatat ctctattgca ccaggtcaaa tagatagatg catcagagaa 600

gcatatgttc atcagagacc agtttatgtt ggtttaccgg caaatatggt tgatctcaag 660

gttccttcta gtctcttaga aactccaatt gatttgaaat tgaaacaaaa tgatcctgaa 720

gctcaggaag aagttgttga aacagtcctg aagttggtgt cccaagctac aaaccccatt 780

atcttggtag acgcttgtgc cctcagacac aattgcaaag aggaagtcaa acaattggtt 840

gatgccacta attttcaagt ctttacaact ccaatgggta aatctggtat ctccgaatct 900

catccaagat ttggcggtgt ctatgtcggg acaatgtcga gtcctcaagt caaaaaagcc 960

gttgaaaatg ccgatcttat actatctgtt ggttcgttgt tatcggactt caatacaggt 1020

tcattttcat actcctacaa gacgaagaat gttgttgaat tccactctga ctatatgaaa 1080

atcagacagg ccaccttccc aggagttcaa atgaaagaag ccttgcaaca gttgataaaa 1140

agggtctctt cttacatcaa tccaagctac attcctactc gagttcctaa aaggaaacag 1200

ccattgaaag ctccatcaga agctcctttg acccaagaat atttgtggtc taaagtatcc 1260

ggctggttta gagagggtga tattatcgta accgaaactg gtacatctgc tttcggaatt 1320

attcaatccc attttcccag caacactatc ggtatatccc aagtcttgtg gggctcaatt 1380

ggtttcacag taggtgcaac agttggtgct gccatggcag cccaggaaat cgaccctagc 1440

aggagagtaa ttttgttcgt cggtgatggt tcattgcagt tgacggttca ggaaatctct 1500

acgttgtgta aatgggattg taacaatact tatctttacg tgttgaacaa tgatggttac 1560

-continued

actatagaaa ggttgatcca cggcaaaagt gccagctaca acgatataca gccttggaac 1620

catttatcct tgcttcgctt attcaatgct aagaaatacc aaaatgtcag agtatcgact 1680

gctggagaat tggactcttt gttctctgat aagaaatttg cttctccaga taggataaga 1740

atgattgagg tgatgttatc gagattggat gcaccagcaa atcttgttgc tcaagcaaag 1800

ttgtctgaac gggtaaacct tgaaaattga ggctgctgcc ccggctgctg ctaatctaga 1860

taatagtgat cccggccgct actaaagcct gatttgtctt gatagctgct cctgcctttg 1920

ggcaggggct tttttctgtc tgccattctt gaggatggcg gactctttcc cttttgctct 1980

acgcccatga atgcgatcgc agtctcccct gtccagcacg ttggagtgat tggtggtggc 2040

cagttagctt ggatgctggc accagcagcg caacagttgg ggatgtcgct gcacgttcaa 2100

acacccaatg atcacgaccc agcagtagcg atcgcggatc aaaccgtatt agcagcagtt 2160

gctgacgcgg ttctctcttc tgccgtta 2188

<210> SEQ ID NO 53
<211> LENGTH: 1510
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 53, Example 53: designer nirA-promoter-controlled NAD(P)H-dependent Alcohol-Dehydrogenase DNA construct (1510 bp)

<400> SEQUENCE: 53

agaaaatctg gcaccacacc cttcttgcag aacatgcatg atttacaaaa agttgtagtt 60

tctgttacca attgcgaatc gagaactgcc taatctgccg agtatatgtt agctacctct 120

gtgccagaaa cccaaaaggg tgttattttc tatgagaatg gtggtaaatt ggaatacaag 180

gacattccag ttccaaagcc aaagccaaat gaaatcttga tcaacgtcaa gtactccggt 240

gtgtgtcata ccgatttgca cgcatggaag ggtgactggc cattgccaac caagttgcca 300

ttggtcggtg gtcacgaagg tgctggtgtc gttgttgcta tgggtgaaaa cgtcaagggc 360

tggaacattg gtgactttgc gggtatcaaa tggttgaacg gttcttgtat gtcctgtgaa 420

tactgtgaat tgtccaatga atccaactgt ccagatgctg acttgtctgg ttacacccac 480

gatggttctt tccaacaata ccgtaccgca gatgctgttc aagctgccag aattccaaag 540

ggtaccgatt tggctgaagt tgctccaacc ctatgtgccg gtgttactgt ttacaaggct 600

ttgaaaagtg ctaacttgaa ggctggtgac tgggttgcca tctctggtgc tgctggtggt 660

ctaggttctc tagctgtcca atacgccaag gccatgggtt acagagtcgt tggtatcgac 720

ggtggtgaag aaaagggtaa gttggtcaag caattgggtg gtgaagcctt tgttgatttc 780

accaaaacca aggacatggt tgctgaaatc caagaaatca ccaacggtgg tccacacggt 840

gtcattaacg tctctgtttc tgaagctgcc atgaacgctt ccactcaatt cgtcagacca 900

actggtactg tcgtattggt cggtttgcca gctggtgccg tcatcaagtc cgaagtcttc 960

tcccacgtcg ttaagtctat taacatcaag ggttcttacg tcggtaacag agctgacacc 1020

agagaagcta tcaacttctt cgctaacggt cacgtccact ctccaatcaa ggttgttggt 1080

ttgtccgaac taccaaaggt ttacgaattg atggaacaag gtaagatttt gggtagatac 1140

gttgttgaca cctccaacta gggctgctgc cccggctgct gctaatagtg atcccggccg 1200

ctactaaagc ctgatttgtc ttgatagctg ctcctgcctt tgggcagggg ctttttttctg 1260

tctgccattc ttgaggatgg cggactcttt ccctttttgct ctacgcccat gaatgcgatc 1320

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gcagtctccc ctgtccagca cgttggagtg attggtggtg gccagttagc ttggatgctg 1380

gcaccagcag cgcaacagtt ggggatgtcg ctgcacgttc aaacacccaa tgatcacgac 1440

ccagcagtag cgatcgcgga tcaaaccgta ttagcagcag ttgctgacgc ggttctctct 1500

tctgccgtta 1510

<210> SEQ ID NO 54
<211> LENGTH: 56
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 54, Example 54: designer selected Hyd1 transit peptide (amino acids sequence)

<400> SEQUENCE: 54

Met Ser Ala Leu Val Leu Lys Pro Cys Ala Ala Val Ser Ile Arg Gly
1 5 10 15

Ser Ser Cys Arg Ala Arg Gln Val Ala Pro Arg Ala Pro Leu Ala Ala
20 25 30

Ser Thr Val Arg Val Ala Leu Ala Thr Leu Glu Ala Pro Ala Arg Arg
35 40 45

Leu Gly Asn Val Ala Cys Ala Ala
50 55

<210> SEQ ID NO 55
<211> LENGTH: 45
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 55, Example 55: designer selected RbcS2 transit peptides (amino acids sequence)

<400> SEQUENCE: 55

Met Ala Ala Val Ile Ala Lys Ser Ser Val Ser Ala Ala Val Ala Arg
1 5 10 15

Pro Ala Arg Ser Ser Val Arg Pro Met Ala Ala Leu Lys Pro Ala Val
20 25 30

Lys Ala Ala Pro Val Ala Ala Pro Ala Gln Ala Asn Gln
35 40 45

<210> SEQ ID NO 56
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 56, Example 56: designer selected ferredoxin transit peptide (amino acids sequence)

<400> SEQUENCE: 56

Met Ala Met Ala Met Arg Ser
1 5

<210> SEQ ID NO 57
<211> LENGTH: 33
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 57, Example 57: designer selected CF0CF1 subunit-a transit peptide (amino acids sequence)

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<400> SEQUENCE: 57

Met Leu Ala Ala Lys Ser Ile Ala Gly Pro Arg Ala Phe Lys Ala Ser
1 5 10 15

Ala Val Arg Ala Ala Pro Lys Ala Gly Arg Arg Thr Val Val Val Met
20 25 30

Ala

<210> SEQ ID NO 58
<211> LENGTH: 1417
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 58, Exmaple 58: designer nirA-promoter-controlled NADPH-dependent Glyceraldehyde-3-Phosphate Dehydrogenase DNA construct (1417 bp)

<400> SEQUENCE: 58

agaaaatctg gcaccacacc tgacccccat cgagagactc cgaacgtggc aaatggaggg 60

accagagttg ttcagttcac aggtagataa tgtcgcgggt cttgatagtt agcaataaat 120

acagtttcag aatatctgta atacaaaaac tgtatcgaga caagaaaaaa gtagcaaaat 180

ttacaaatgt tcatgattca tctggctaaa ttggatgttc aactgaccca ttgaagacaa 240

gggcaacaac catgacttgc acttacagtt tcttttgatg tcaaaagtgc tccaatttgc 300

tcagcaacat ctacaactct atttgaataa ccccattcat tatcatacca agcaataact 360

tttactttat tccctgacat gaccattgtt gattttgcat caataatagc tgaatttgga 420

ttagtattaa aatcaacaga cactagtggt tgatgttcga cttctatgat accttctaaa 480

cctgcatttt caaaagcttg gtttacttct tctgcagtta cttctttttc taaatcaaca 540

actaaatcaa cgagcgatac attctttgtt ggtacacgta atgccatgcc gtgtaattta 600

ccttctaatt ctggtaatac ttcttttaaa gctttcgccg caccagtaga agtaggaata 660

atgctttcat tacatgaacg tgcacgtctt aaatctttat gtggattatc aatatttttt 720

tggtcatttg taatagcgtg aacagtagtc attaaaccat taactattcc aaactgatta 780

tttaaaactt ttgcaactgg accaatgcaa ttagtagtac atgaagcatt actaaaaatg 840

tcaaatgctt ctatatctaa ttggttatca tttacgcctt taactaacat ttgaacatgt 900

ccacctttg aaggaccagt taacaatact tttttggcac ctgctttaat atgtgcgatg 960

gctttatcac catgattaaa tttaccagtt gcatctatag caatatcgat atctaattct 1020

ttccatggca agttttcagg attgcgatca gcaaccaatt taatttttatg atcaccaact 1080

tgcaatccat tttcaatcgg ttcaactttt agattatatt ttccatgtgt tgtatcgtaa 1140

ttgattaaat gtgcaattgt ttcgggtgga taactagcat ttatcgctac tacatttaaa 1200

tttttatttt gtaatgcaat acgtaatacc attcttccaa ttctacccat accattaatt 1260

gcaatattcg ttgacattaa ggctgagatc ttcttcagtg cattgtagtt gaatgaaggg 1320

ttaggggggga aatgcccccc tatttttttgt ctagccatcc tgccacgttt gacagggtag 1380

caatttcgac acgatagggt tctctcttct gccgtta 1417

<210> SEQ ID NO 59
<211> LENGTH: 1387
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

-continued

<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 59, Exmaple 59: designer nirA-promoter-controlled NAD-dependent Glyceraldehyde-3-Phosphate Dehydrogenase DNA construct (1387 bp)

<400> SEQUENCE: 59

agaaaatctg gcaccacacc tgacccccat cgagagactc cgaacgtggc aaatggaggg 60

accagagttg ttcagttcac aggtagataa tgtcgcgggt cttgatagtt agcaataaat 120

acagtttcag aatatctgta atacaaaaac tgtatcgaga caagaaaaaa gtagcaaaat 180

ttacaaatgt tcatgattca tctggctaaa ttggatgttc aactgaccca ttgaagacaa 240

gggcaacaac catgcttaga gatgtgtgcg atcagatcca gaactttgtt ggagtagcca 300

gtttcgttgt cataccaaga aaccagtttc acgaagttgt cgttcagaga gataccggcg 360

tcggcatcaa acacggaggt gcatacttcg ccgttgaagt cggtagaaac gacggcttcg 420

tcggtgtagc ccagaacgcc tttcatttcg ccttcagaag cggccttcat cacgtcacag 480

atctgctgat aggtcgccgg cttggccagg cgagcagtca ggtcaacaac ggagacgttc 540

ggggtcggaa cgcggaaagc cataccggtc agtttgccgt tcagctccgg gatgaccttg 600

ccaacggcct tggctgcacc ggtagaggac gggatgatgt tctggctagc gccgcggccg 660

ccgcgccaat ctttcatgga cgggccgtcg acagttttct gggtcgcggt ggtagcgtga 720

acggtggtca tcagcgcttc aacgatgccg aagttgtcgt tcaggacttt agccagcgga 780

gccaggcagt tggtggtgca ggatgcgttg gaaacgatct cctggccagc gtagttcttg 840

tggtttacgc ccataacgaa catcggggta gcatctttag acgggccagt catgacgact 900

ttcttggcac cggcggcgat gtgcttacgc gcggtttcgt cggtcaggaa cagaccggtc 960

gcttcggcaa caacgtcaac gccgatttcg ttccacttca ggttagccgg atctctttca 1020

gcggtaacac ggatttttt accgttaacg atcaggtggc catctttcac ttcaacagtg 1080

ccgttgaaac gaccgtgagt agagtcgtac ttcagcatgt atgccatgta gttggcatcc 1140

agcagatcgt tgatgccaac gatttcgatg tcagaacgtt cctgagcagc acggaaaaca 1200

atacggccga tacggccaaa accgttgata cctactttga tagtcattaa ggctgagatc 1260

ttcttcagtg cattgtagtt gaatgaaggg ttaggggga aatgcccccc tatttttgt 1320

ctagccatcc tgccacgttt gacagggtag caatttcgac acgatagggt tctctcttct 1380

gccgtta 1387

<210> SEQ ID NO 60
<211> LENGTH: 1627
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 60, Exmaple 60: designer nirA-promoter-controlled phosphoglycerate mutase DNA construct (1627 bp)

<400> SEQUENCE: 60

agaaaatctg gcaccacacc tgacccccat cgagagactc cgaacgtggc aaatggaggg 60

accagagttg ttcagttcac aggtagataa tgtcgcgggt cttgatagtt agcaataaat 120

acagtttcag aatatctgta atacaaaaac tgtatcgaga caagaaaaaa gtagcaaaat 180

ttacaaatgt tcatgattca tctggctaaa ttggatgttc aactgaccca ttgaagacaa 240

gggcaacaac catgggcccc gaacttttgc agcttgcccg cgtgcgccag caggagcggc 300

agcacgtggg tgccgtgcag gtcgccgagc gcgccccctg ccgcctcgtc ctcggtgaag 360

-continued

cggcgggccg cgtcggcgcg caggttgggg ccgtagagca ggaagggcac cgggtgccag 420

gagtgcgcct tcatcacgct gggcgtggag tggtcgccgg tgatggcgat cacctcgggc 480

tccagcgcca gcagctcggg cagcagggcg tcgaaggcct cgatcttgtg caccttcgcg 540

tcgaagtcgc cgtcctcgcc ggtggagtcg gtcttcttga agtgcaggta gaagtagtcg 600

aaggcttccc agtgggcctt cagggccgcg agcttgcctt cgggggcgtc ggggtcctcg 660

cccacctcga cctccagcgc ggtcatcccc accagcgagg ccaccccgcg gtacatcggg 720

tagctggcga ccgccgcggg ggtgagcccg gtgatctcgc ccagggtggg ccagaccggg 780

cgcttggaga cgccgcgaag cagcaccccg ttgatcctgg gctcgtccgc gagcgcctgc 840

cgcgccagcg cgctgaactt gttgagcacg tcggccgtct tggcgctggg ctcgtcgctt 900

tcgtcgtgcg gacgggccgc gagcggcggc accccggtct tctgggggtc ggtgtcgtgg 960

acccggtcgc ccagccccac gccccgcagc accagcacga agcggtgctc cgactcggtg 1020

tggagctcga tcctgacgcc gtcgatctcg cggatgcgct ccctcagctt ggcgagcacc 1080

cgccggtttt cctcggtggg ggggcggccg gcgcggcggt cggcgatggt gccgtcgggg 1140

ttcaaggtgg cgaagttgcc gcgcaccgcg acgtcgtcgg gccccagctc gatgcccagc 1200

cccagcgccg agaggacgcc gcgcccgacc tcgtagcgga aggggtcgta gccgaagagg 1260

ctcaggtggc cgggcccgga gccgggcgcg aagccggggg ccaccagggt gactcgcccc 1320

aggttggcct tttcggccag ggcgtcgagg ttgggggtgc gggccgcggc cagctccgtg 1380

ggcccgcccg gctcgcgggg cagcccgccc accccgtcga gcacgacgaa gaggatcttg 1440

ctgggcgtgg tgcggctcag ttccttgagg tgggggagga ggtccattaa ggctgagatc 1500

ttcttcagtg cattgtagtt gaatgaaggg ttaggggggа aatgcccccc tatttttgt 1560

ctagccatcc tgccacgttt gacagggtag caatttcgac acgatagggt tctctcttct 1620

gccgtta 1627

<210> SEQ ID NO 61
<211> LENGTH: 1678
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 61, Exmaple 61: designer nirA-promoter-controlled Enolase DNA construct (1678 bp)

<400> SEQUENCE: 61

agaaaatctg gcaccacacc tgacccccat cgagagactc cgaacgtggc aaatggaggg 60

accagagttg ttcagttcac aggtagataa tgtcgcgggt cttgatagtt agcaataaat 120

acagtttcag aatatctgta atacaaaaac tgtatcgaga caagaaaaaa gtagcaaaat 180

ttacaaatgt tcatgattca tctggctaaa ttggatgttc aactgaccca ttgaagacaa 240

gggcaacaac catgtttttg taaattatag aaaaccccca acccacgata cagcccgata 300

tcgcttaatt cttcttctat ccgcaacagc tggttgtatt tcgctacccg gtcagtcctg 360

gccggagccc cggtctttat ctgccctacg ttggtcgcta ctaccaggtc agcgatgaag 420

gtgtcctccg tctccccgga acggtgggat actacacagg tgtaaccggc tcttttagcc 480

atttcaatcg tatccaaggt ctcagtgacc gtgcctatct gattcagttt gataagtatg 540

ctgttggcca caccctttt tattcctgtg gtaaaacgct ggggattggt tacgaaaata 600

-continued

tcatctccga cgatctgaat cttcttgccc agcttacggg tgagcttttt ccacccttcc 660

cagtcttctt cctgcagccc gtcttccagg gatatgatag gatacttacg cacaaggcca 720

tcgtaaaact cgaccacctc atcggcggtc agctcttggc cggtgctggc aaaaacgtat 780

ttcccgtcct tgaaaatctc attggcagca acatccagtc ccaggtaaat atccttcccc 840

ggcttgtacc ccgccgtttt aatagcctcc aaaattactt caatcgcggc ttcattcgaa 900

ggcaagttgg gagcaaatcc tccttcatcc ccgatggaag tagaaaaccc ttttttactc 960

aataccttct tcagggtatg gtagacctcc acccccatgc gcagggcctc ggcaaaagaa 1020

gtagctccta ccggtaggat caagaattct tgaatgtcca cattattatc cgcgtgcttg 1080

ccgccgttca agatgttcat ttgcgggatc ggcagttctt tggcgtttac gccgcccagg 1140

tactggtaaa gcggcatgga taggtaggaa gcagcagccc gcgccacagc catcgacacg 1200

cctaagatag cgttagctcc cagcttgccc ttgttgtcag tcccatcgag gtcaatcatc 1260

aaccggtcaa tccccacctg gtcgagcgca tccatcccca caacctccgg ggcgatgacc 1320

gtgttgacgt tatccaccgc attcagcacg cctttgccgc cgaaacgctc tgcgtcccca 1380

tcccgcagtt ccaccgcctc aaaagcacca gtggacgcgc cggaaggaac cgcagcccgt 1440

cccatggtcc catcttctaa aaggacctcg acctccaccg tcgggtttcc ccgcgaatcc 1500

agtatttctc tggcgtaaac ctcggtgata atactcacta aggctgagat cttcttcagt 1560

gcattgtagt tgaatgaagg gttaggggggg aaatgccccc ctatttttttg tctagccatc 1620

ctgccacgtt tgacagggta gcaatttcga cacgataggg ttctctcttc tgccgtta 1678

<210> SEQ ID NO 62
<211> LENGTH: 2137
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 62, Exmaple 62: designer nirA-promoter-controlled Pyruvate Kinase DNA construct (2137 bp)

<400> SEQUENCE: 62

agaaaatctg gcaccacacc tgacccccat cgagagactc cgaacgtggc aaatggaggg 60

accagagttg ttcagttcac aggtagataa tgtcgcgggt cttgatagtt agcaataaat 120

acagtttcag aatatctgta atacaaaaac tgtatcgaga caagaaaaaa gtagcaaaat 180

ttacaaatgt tcatgattca tctggctaaa ttggatgttc aactgaccca ttgaagacaa 240

gggcaacaac catgccgcac ttgggcttgg ccgcggtaga tttgtcccct agccgtatcc 300

atggttatgg tttctccgtc ttggatgaca cgggttgcct cggcggctcc aacgatgaca 360

ggaatatcca agttaatacc tactatggct gcatgagaag tcaggcctcc ctgttccgtg 420

ataatccccc cggccttttc caacaacggc atatagtcct tgtctgttcc gactgccacc 480

actatatctc ccggagcaaa cgagcccggt ttgcccggat ccagtatcac ccgcgcctta 540

ctggtaacgg cccggctacc tatacccgtt cccttaacca gcaccttgcc tactacttga 600

actctcagta gattggtagt cccagggatt ccaggagtac ctgcggttat gactaccagg 660

tcaccggggg agattagccc tcgcctgact gcggcatcca gggctgtttc tatcatctgg 720

tcagttccgt gggtttccgg gaccgtgagc gcgtataccc cccataccaa agttagcttg 780

cgtaccactt cgggtgaagg cgtagtagcc acgatcggag cccggggacg gtacttggcc 840

accattctcg ccgtatggcc cgattttgta gcagtaacaa tggccgaggc ccccaggtcg 900

-continued

gtagcggtag cacaggtggc ataactgatg gcatcggtca cggtacgcct gccttcgaat 960

cgtcttgccg ccagcatgtt ctcatagggc aaagccatct ccgtccgccg ggctattcgc 1020

gccatggttt ccaccgcaac taccggatat ttaccggctg cggtctctgc cgacagcata 1080

atggcgtctg ccccctcaaa tatggcatta gccacgtctg acgcttcggc ccgggtgggg 1140

cgcggcacgt ttaccatcga ttcgagcatc tgggtggcaa ttatcaccgg cttaccctga 1200

gcccggcatt tctcgattat aacctttgc accagaggta cttcttcggt aggtatttca 1260

acccccaggt ctccccgggc gaccatgacg ccatcagcaa cctttattat gtcatccagg 1320

ttgtccagcc cctcctggct ctcaatctta gcgattatat cgatgtcggc tccctttcc 1380

tctaatatgc gtctgatatc caaaacatca tcggccgtcc ttacgaacga ggcagcaatg 1440

aaatccatat tctgctggat gccgaagtta atgtcttcga tgtctttctg gctcaaaaaa 1500

ggcaggttgg ttctcacacc cggcaggttt atgcctttcc tttcaccgag tactcctccc 1560

gcaaccacct ggcagacgat gtcggtgtcg ttcgcctcta aaacagacag ctggatgacg 1620

ccgtcagcga tcaatatgca gtcacccgct tttacctgcg aaggtaactc atggtaactt 1680

atctggacct cgtcttcgtt accttcaacc ggacggttgg tgagaacgaa cttttgacca 1740

ggacgcagct ctatcttacc ttctttcaag ggcccggtcc tgatctccgg ccctttggta 1800

tcaagcatca accctacttc cgcattcagt tcccgcgcca cctcacgcac catgcggatg 1860

cggcgctcat gctcatcata agtgccgtgt gaaaaattca aacgggccac gttcatgccg 1920

ttggtgatca aagctcttag ccgctcataa tcatcggtgg aaggtcccag ggtacagatg 1980

attttggtct tccgcaataa ggctgagatc ttcttcagtg cattgtagtt gaatgaaggg 2040

ttaggggggga aatgcccccc tatttttttgt ctagccatcc tgccacgttt gacagggtag 2100

caatttcgac acgatagggt tctctcttct gccgtta 2137

<210> SEQ ID NO 63
<211> LENGTH: 2163
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 63, Example 63: designer nirA-promoter-controlled citramalate synthase DNA construct (2163 bp)

<400> SEQUENCE: 63

agaaaatctg gcaccacacc tgatctgcaa gagacgctca cgcgatacct ctgggcgtgc 60

aatcaccgca ttccccaacg cgctttgggc cacatgaccc ccatcgagag actccgaacg 120

tggcaaatgg agggaccaga gttgttcagt tcacaggtag ataatgtcgc gggtcttgat 180

agttagcaat aaatacagtt tcagaatatc tgtaatacaa aaactgtatc gagacaagaa 240

aaaagtagca aaatttacaa atgttcatga ttcatctggc taaattggat gttcaactga 300

cccattgaag acaagggcaa caaccatgga gcaggttttt atctacgaca ccaccttgag 360

ggatggctcg caggcagaag gtataaactt ttccgtagag gataagatgc gcatacttca 420

aaaactggac gaatttggag tgcattacat agagtgcgga tggcccggtg cgaacccaaa 480

agacactatt ctctttgaaa ggctgagaaa gataaaaact caaaatgcca aaatagtagc 540

ctttggtgca acaagaaaag ctggaaagaa ggcgcacgaa gataagcagg tggaaaacct 600

tttgaaatcg ggtgccaagg tgataaccgt atttggcaag agctgggact ttcatgtaac 660

-continued

gcatgccata gggaccacct tagaggaaaa cctggacatg gtttacgaga cggtaagcta 720

tcttaaaaag catgtggagg aggttatctt tgacgcagag cacttctttg acggatacag 780

gcacaacgaa agctatgctt ttaaggtatt ggaggcagct tttcaggcag gtgcggactg 840

gatagtcctc tgcgatacca acggtggcac ccttcccaat gaggtttatg agataaccaa 900

aaaggttgta caaaagtttc cacaggcacg cgtaggcata cacgctcaca acgattcaga 960

tactgctgtg gctaactctc ttatggcggt gcttgcaggt gcaaggcagg ttcacggcac 1020

tataaacggc ttgggggaaa gaacgggcaa tgctaatctg tgttccataa tacctaacct 1080

tcagctcaag ctgggcttta gtgtagtgcc ttcccaaaac ctcaaaaagc tcaccgagct 1140

tgctcacttt gtctccgaaa tctccaacac gccactgccc aaaaacatgc cttatgtagg 1200

ggagagtgct tttacccaca aagcaggcgt acacgcctct gcagttatga aaaggtcaga 1260

aacatacgaa cacatagacc cttctttggt aggaaacaga aggaaggtga cagtgtctga 1320

cctttctgga aggagtaata tactttacaa gctcagggaa atggggcttg aggtggatga 1380

taagtcccct gagcttatca aactccttga aaagataaag gaacttgaga aggaaggcta 1440

ccactttgaa gcagctgaag cttcttttga gcttctttgc aagaggcatt ttgggcttgt 1500

taaaaactat tttgaccttg atgcttacag ggtgctaata gccagaagga gtacagacct 1560

atctcctgtt tcggaagcca ccgtaagact ctatgtggaa gacataaagg agcatacagc 1620

agctcttggt aacggaccag tgagcgccct tgacagagcc ctcagaaaag ccttggaaga 1680

gttttatcca agccttaaag atgttcagct catagactac aaggtgagaa tagttaacga 1740

atcggagggt acatctgcca aagtgagggt gcttatagaa tctaccgatg gtagaagaaa 1800

gtggggaacg gtgggagttt cggaaaacat aatagaagcc tcttggatag ccttaactga 1860

tagcctcgta tataaactct taaaagacga agaagagggt ataatgtgat aaggctgaga 1920

tcttcttcag tgcattgtag ttgaatgaag ggttaggggg gaaatgcccc cctatttttt 1980

gtctagccat cctgccacgt ttgacagggt agcaatttcg acacgatagc gtgctgtact 2040

gttttttgct cgtcagggtt gggttttgtc atcgacaccc aaggattgga gtcggtgctc 2100

aataatcgcc agttgctgtt gggcagccgc caattgcgcc tgaggttctc tcttctgccg 2160

tta 2163

<210> SEQ ID NO 64
<211> LENGTH: 2878
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 64, Example 64: designer nirA-promoter-controlled 3-Isopropylmalate/(R)-2-Methylmalate Dehydratase DNA construct (2878 bp)

<400> SEQUENCE: 64

agaaaatctg gcaccacacc tgacccccat cgagagactc cgaacgtggc aaatggaggg 60

accagagttg ttcagttcac aggtagataa tgtcgcgggt cttgatagtt agcaataaat 120

acagtttcag aatatctgta atacaaaaac tgtatcgaga caagaaaaaa gtagcaaaat 180

ttacaaatgt tcatgattca tctggctaaa ttggatgttc aactgaccca ttgaagacaa 240

gggcaacaac catgtaccat gtctgctgtt gctatctcgc ccttgattgc tgatgctgta 300

acagtagccg ctgaagcaag atatacaaaa gaatctttat gtcctgcacg tcccttgaag 360

tttcgtgtac ctgtactgat aagagtctca ccctcaccga taacaccctg acagcttccc 420

-continued

cagcatacag agcagttagg attcataaca attgcacctg cgtccatgaa tatatcaagg 480

agtccctctt tcatagcctg aagatatacc gaacggcttg caggaactac aaggaatctt 540

accttaggag caacctttt ccctttgatg atcgctgcgc caactcttaa atcctcgatt 600

cgtccattgt tacatgaacc aagaaatgct tcatcaatct ttacaccaag tgattcctta 660

gccggaacta cattgtcaac aaaatgtggc tttgcaacaa ttggctgtat tgttgaaagg 720

tcaatatcat aaacctgctc aaatactgca tcatcatctg atgtaaagca tgcctttggc 780

tctctgccat gctccttaag ataatccatt gcaacatcat caacttccat gagtgcagtc 840

ttagcacctg cctctacaca aaggttacag attgatattc tgtctgccat tgaaaggctg 900

tgtaagcctt ctcctgcaaa ttccattgct ttatagttag caccgttagc gccaatcttt 960

ccaataatag agagtattaa atctcttgca tatactccat cgttaagctt tcccttaagg 1020

ttgaatctta atgttcccgg aaccattacc catgatgttc ctgtaaccat tgcatacaaa 1080

taatctgtac aaccaacacc tgtaccaaat gcacctaacg caccatatgc acaagtatgg 1140

ctgtctgctc caaatataag ctcacccggc actacatgat tttccatcat aacctgatga 1200

cacacaccct cgccctcgta gaacttaata tcattagcct tagcaaagtc tctcatcttc 1260

ttctgtgagg ctgctgtctt aggactgtct gatggaatat tgtggtctac aatccataca 1320

agcttatcct tgtcagcaat atgaggattc tttaacttct catacatacc aatagtaaga 1380

tgtgttgttc catcattact cataagtctg tcaagagtaa cagttgcaat atcaccagcc 1440

ttaacctgtg aaagacctgc tgcccttgcg ataatcttct ctgcaatagt catgccatgc 1500

tttgcctcat ctgcaggtac ggctgtactc tcagactctt ctttctcacc atcaagtgat 1560

gcaataagac caccctgatt aagaatagcc tgcatcttgg ctggaagctt agtacatgta 1620

taagtctttc cattaacagt tataattcca tcttctaatg aaagctcaca ttcatccccc 1680

gcattaactt cgtcatggag ttctttacat acaataacag gaagtcctat attaatagca 1740

ttacgataga atattcttgc aaatgatttg gcaatcactg ccttgacacc taatgcctta 1800

agtacgcttg gtgcctgctc tcttgatgaa ccacatccaa agttgtcatc tgcaacaacg 1860

aaatctcccg gctttacggc agaagcaaaa tcagagtcta atgattcaaa tgtatgactc 1920

ttcatctcat caattgtcgg aaacaaaaga tactgcgatg caataatctg atctgtatca 1980

acatctttat caaacttaaa tatcctaccc attgaccccc atcgagagac tccgaacgtg 2040

gcaaatggag ggaccagagt tgttcagttc acaggtagat aatgtcgcgg gtcttgatag 2100

ttagcaataa atacagtttc agaatatctg taatacaaaa actgtatcga gacaagaaaa 2160

aagtagcaaa atttacaaat gttcatgatt catctggcta aattggatgt tcaactgacc 2220

cattgaagac aagggcaaca accatggtca agaccgttaa gctttctcat tgccttaaca 2280

agtccgcctg cattaagtat atccacaaga ttatcaggaa gtgaagcaat aggatatgct 2340

tttccattgt gtgtaatctt tgcatttact tcaacatcaa tagtatcgcc ttccgtaact 2400

tcgtcgtgaa ggtctgcatt ctctataagg agaagtccgt tattaataga atttctgaag 2460

aatattcttg catatgattt ggcaataaca catttaatac ctaatgcctt aataacctca 2520

ggtgcctgct ctcttgatga accacaacca aagttctttc ctgcaacaat gatgtcgcct 2580

ggcttaatct gacctgcaag ttctggtctt aatggcgaaa atgcatatgg tttcatatct 2640

tctactgtct ttaatgcaag gtactctgta gggataatga tatctgtatc aatgtcatca 2700

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ccaagtaccc atactttacc gctaaatttc tcgttcatta aggctgagat cttcttcagt 2760

gcattgtagt tgaatgaagg gttaggggggg aaatgccccc ctatttttttg tctagccatc 2820

ctgccacgtt tgacagggta gcaatttcga cacgataggg ttctctcttc tgccgtta 2878

<210> SEQ ID NO 65
<211> LENGTH: 2380
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 65, Example 65: designer nirA-promoter-controlled 3-isopropylmalate dehydratase DNA construct (2380 bp)

<400> SEQUENCE: 65

agaaaatctg gcaccacacc tgacccccat cgagagactc cgaacgtggc aaatggaggg 60

accagagttg ttcagttcac aggtagataa tgtcgcgggt cttgatagtt agcaataaat 120

acagtttcag aatatctgta atacaaaaac tgtatcgaga caagaaaaaa gtagcaaaat 180

ttacaaatgt tcatgattca tctggctaaa ttggatgttc aactgaccca ttgaagacaa 240

gggcaacaac catgaatgaa tcttcttgga tctgtgatgt atccggttac cgcggtggct 300

gccgccgttg caggagaagc aaggtatatc tccgcattgg gattccccat ccttcccttg 360

aagtttctgt tctgcgtgga aagtaccctc tctccgtctc caagaacacc catgtggatt 420

ccaacacatg ggccgcaacc tggtggtata actgccgctc cgagttcaac aaatttcttg 480

attattccct tttcaagggc gtccatgtag accttccttg aagcggggcc gacgatcagc 540

ctcacatccg ggtgctttcc gtgtttctca agaattttca aagcgatctc aagatcctga 600

agtcttccgt tcgtacaggt tcctatgaac acttgatcta tctttatctt ttccttttca 660

acctcgctca cctttctcac gttgtccaca tagtgaggca aagagacgag tggttcgagt 720

gtgtcggcat ctatctctat ctctgtctcg taaaccgcgt ctggatctgc tttcaactct 780

ctgaagtcct cctctcttcc catcttttttc aggaactctc tggtcttctc atcagaaggc 840

atgagacctg ctttcgctcc cacttccacc gccatgttgg aaatggtgag tctgtcctcc 900

acattcatat tttcgataca gcttccatgg aactccaacg ctttgtaagt tgcgccgtcg 960

cttcccagaa ttctcgcgat ctcgagaatg atgtctttcg cgtaaactcc atcctgtaac 1020

ttcccgttca ccacaacctt gatcgtctca ggtactttga accagttctg tccaagcccg 1080

aagatgatcg caacatctgt ggaccccatt cccgttccga aagcaccgag cccaccggca 1140

gtgcaggtgt gcgaatccgc acctgctacc agatcgccgg gtttcacgta tttttccgcg 1200

aggatctggt gggatatccc gtctcccgca tcgaaaacct tgactcccat ctcttttcca 1260

aattctctca tcatcttctg cgaattcgaa agctctttcc tcgggctcgg agaagcgtga 1320

tcgatgaaga ggaaggcctt cgggaccttc acttctttga agccgagttc tctgaattcg 1380

tttatcatca gggggcctgt tccatcctgg gccatggcta tatccactct cgcgagtacg 1440

atttctccgg ctttcacgtc tcttccagta tgttcagaaa agatcttttc tgcgagtgtc 1500

ttacccattg acccccatcg agagactccg aacgtggcaa atggagggac cagagttgtt 1560

cagttcacag gtagataatg tcgcgggtct tgatagttag caataaatac agtttcagaa 1620

tatctgtaat acaaaaactg tatcgagaca agaaaaaagt agcaaaattt acaaatgttc 1680

atgattcatc tggctaaatt ggatgttcaa ctgacccatt gaagacaagg gcaacaacca 1740

tgaactcttg ggaaggaacc gtgctttttc agatagttca ctataccgtc ttctttcagt 1800

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atctcgagga gaaacttcgg aatcggagtg aatctgtatt cttttcctgt tgtgaggttc 1860

ttcaaaacac cgttttcgag atctatctca agttcgtctc cctggttgat ctcgtcgact 1920

tccttgagct ctatgactgg aagtcccaca ttgatggcgt ttcggtagaa gatccttgcg 1980

aaagacttcg ccacgataca ggaaacacca gcgatcttta tgatacgcgc agcgtgctct 2040

ctggaagaac caagtccgaa gttcttgcca gccacgatga tgtcaccttt ctgcaccttc 2100

ttcgcgaaat cctccatggc atcttccaag acgtgttttg cgagctcctc aagattgttc 2160

ctcagatgaa aataccttcc aggtgctata tggtcagtcg atatattgtc accgaatttc 2220

cagactcttc cccttatcat taaggctgag atcttcttca gtgcattgta gttgaatgaa 2280

gggttagggg ggaaatgccc ccctattttt tgtctagcca tcctgccacg tttgacaggg 2340

tagcaatttc gacacgatag ggttctctct tctgccgtta 2380

<210> SEQ ID NO 66
<211> LENGTH: 1456
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 66, Example 66: designer nirA-promoter-controlled 3-Isopropylmalate Dehydrogenase DNA construct (1456 bp)

<400> SEQUENCE: 66

agaaaatctg gcaccacacc tgacccccat cgagagactc cgaacgtggc aaatggaggg 60

accagagttg ttcagttcac aggtagataa tgtcgcgggt cttgatagtt agcaataaat 120

acagtttcag aatatctgta atacaaaaac tgtatcgaga caagaaaaaa gtagcaaaat 180

ttacaaatgt tcatgattca tctggctaaa ttggatgttc aactgaccca ttgaagacaa 240

gggcaacaac catgccatat ttcttcgagt tttttacata tgagatctcc catctgagag 300

gtcgaaaccg ccttttctgg atcctctgcg atgtctctgg ttctgtatcc ctcttctatc 360

accagctcaa ccgctctttc tatctttctt gcctcttcca ccattccaaa ggaatgctcg 420

agcatcatgg cgagagagag gatctgtgcg atcgggttgg cgatgttctt tccggctata 480

tcaggagcgg aacctcctgc cggctcgtag aggttcttat caccgaaaga cgcggacggc 540

agaagaccaa gagaaccagg aagtgccgca ctctcatccg agagaatgtc tccaaacatg 600

ttcgttgtga ggatcacatc gaactgcgat ggtttcagga tgagctgcat ggcagcgttg 660

tccacataca tgtgcgtcag ctccacatca gggtattctc tcgctacttc gttcacaact 720

ttcctccaca gcatggaact gtagaggacg ttcgctttgt caacggaggt gacctttttt 780

cttctgtttt ttgcgatttc aaaggcagtt ctcgcgatcc gttccacggt ttttctgtcg 840

tagatcatgg tgtcgaatcc cttttcttca tccaatcccc tcggctggcc gtagtaaact 900

ccgtaggaaa gttccctgac ggtcacaaga tcgaccccgg atccaatcac cttttctttc 960

aaaggagaga catgcacaag cgatctgtag acctttatcg gtcttatgtt tgcgtaaagg 1020

ttgagcatct tccttagggc aagaagcccc cctatttccg gcctcttctc cggaggaaga 1080

tcgtcccatt taggtcctcc gacgcttcca aggaagatcg cgtcggcttc cagacatatc 1140

ttttttgtct cttcaggaag gggttcaccg aatttgtcta tggcatcccc tccgatgtgt 1200

ccaaagactt tctcaaaggt tttccccgtt ttctttttcca ccacctcgag cactttaaga 1260

gcttccctta caacctcggg acctatgccg tctccaggca aaaccgctat cttcattaag 1320

-continued

gctgagatct tcttcagtgc attgtagttg aatgaagggt tagggggaa atgcccccct 1380

attttttgtc tagccatcct gccacgtttg acagggtagc aatttcgaca cgatagggtt 1440

ctctcttctg ccgtta 1456

<210> SEQ ID NO 67
<211> LENGTH: 1933
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 67, Example 67: designer nirA-promoter-controlled 2-Isopropylmalate Synthase DNA construct (1933 bp)

<400> SEQUENCE: 67

agaaaatctg gcaccacacc tgacccccat cgagagactc cgaacgtggc aaatggaggg 60

accagagttg ttcagttcac aggtagataa tgtcgcgggt cttgatagtt agcaataaat 120

acagtttcag aatatctgta atacaaaaac tgtatcgaga caagaaaaaa gtagcaaaat 180

ttacaaatgt tcatgattca tctggctaaa ttggatgttc aactgaccca ttgaagacaa 240

gggcaacaac catgctcagc acccccgttt tttctgagaa ggcctttagc gatgaggtac 300

ttgtttattg cgtttatgta agctatcgca gaggcttcca ctatgtccgt ggagacaccc 360

cttccactgt agagttcacc gtttattctc aacgtgagtt tgacctctcc ctgtgcgttc 420

tttccagttc caaccgcctg aattatgtac tcctcgagct tcggttgaat accgagcgct 480

ttgtctatag ccttgaagat agcatccact ggaccgtttc ctgcctctgc tgcttctttc 540

ttttcatctc caacctgaag cacgaccgcc gcggttggaa gcagcgtgtt tccggtgtgt 600

acatggaagt gaacgagctt gtaaccgttg atgggctccc tcaaaacttc cgagacgatc 660

gagaaaagat catcgtcgta aacctctttc tttctgtcgg cgagttctgt gaacttctcg 720

aacactttct ggaaggtctc ttcgtcgagt ttgatgccgt agctctccag cttctttctg 780

agggcgtgct ttccggagtg tcttccaagc acgagcgtct cggaagacct gccgatatcg 840

gatggtttca tgatctcgta ggtctccctg tgtttcagca caccatcctg gtgtataccc 900

gactcgtgaa ggaacacgtt ctctcccact atgggtttgt ttctggacgg gatgagcccc 960

gttatatgtg tgaggagcct ggaagcgggg tatatgagct ctgtctttat acccgtctcg 1020

tagggaagtt tgtctttcct caccttgagg atcatcacga actcttccag ggcacagttt 1080

cctgccctct ctccgatacc gttcagagtc acttcgacct gggtggctcc gttctgaacg 1140

gcagcgaggg agttcgccac agcgagtcca agatcgttgt gacagtgcac agaaagatcg 1200

acattctcta taccgggcac accctctctc aaggtcttta tgagttctcc aaactcatcg 1260

ggaagggcgt accccaccgt gtccggaaca ttgatcgttg tggctccggc ttcgatcgcc 1320

gtcttgtagg cttctatcaa aaagggaacc tccgttctcg aagcgtcttc cgccgagaac 1380

tccacaaggt cgaaaaactg ttttgcgtag ccgacgtatc ttctgatcct ctcgaggatt 1440

tcctctttct ccattctcag tttgtatttt ctgtgaatcg gagaggtcgc tatgaaaacg 1500

tgtatcatac gtttgtcttt tggtcgatcc ttgagagcct cgtacaccgc gtctatgtcc 1560

ttttcaacac accttgcgag tcccaccact atgggtttct gaacggcgct cgcaactctt 1620

tttacagctt caaactgcac gggagatgaa acgggaaacc cagcctcgat gagatcgaca 1680

ccgagatcct ctaacatgag tgccatttct acttttttcct caaccgacat cgaagcccct 1740

ggggattgct ctccatccct caacgttgta tcgaagatct taattctcct cattaaggct 1800

-continued

gagatcttct tcagtgcatt gtagttgaat gaagggttag gggggaaatg ccccccctatt 1860

ttttgtctag ccatcctgcc acgtttgaca gggtagcaat ttcgacacga tagggttctc 1920

tcttctgccg tta 1933

<210> SEQ ID NO 68
<211> LENGTH: 2632
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 68, Example 68: designer nirA-promoter-controlled Isopropylmalate Isomerase DNA construct (2632 bp)

<400> SEQUENCE: 68

agaaaatctg gcaccacacc tgacccccat cgagagactc cgaacgtggc aaatggaggg 60

accagagttg ttcagttcac aggtagataa tgtcgcgggt cttgatagtt agcaataaat 120

acagtttcag aatatctgta atacaaaaac tgtatcgaga caagaaaaaa gtagcaaaat 180

ttacaaatgt tcatgattca tctggctaaa ttggatgttc aactgaccca ttgaagacaa 240

gggcaacaac catgacagac cggctcggct tcaagctggc gcacatcgac aaaatgtccg 300

taaatcgcag ccgccgcggc catcaccggg ctgacgagat gcgtgcgcgc ccctttttcct 360

tgccgccctt caaagttgcg gttcgacgtt gacgcacagt gctcgccttc tgggatgatg 420

tccgggttca tgcccaaaca ggcgctgcag ccggagtcgc gccattcaaa accggcgtcg 480

atgaaaattt gtgccaaccc ttccgcttcg gcttgttttt tcacttgctg cgatccaggc 540

acgacgagcg cccgtacacc aggagccact ttttttccctt tcacgatgct cgccgccgcg 600

cgcaaatcgc tgaggcgtga gttggtgcac gaaccgatga agacgtgctg caccggaata 660

tccgtaatcg gcgtgcccgg cttgagcccc atgtactcaa gcgcccggcg caccgcgttt 720

tgctctgttt tgctttcaaa ttgctcggga tgcggcacga cgccatcgac ggaagtgctc 780

atcgcggggt tcgtccccca cgtcaccatc ggagcgatcg tcgacgcatc gatttcaatc 840

gttttatcgt attttgcccc ctcatcgctg gctaacgccc gccaccgttc caccgccttg 900

tcaaactcct cgccttttgg tgcatatttg cggccgcgca aataggcgaa cgtcgtttca 960

tccggactga tgaggccggc tctcgcccca gcttcaatcg acatgttgca aatcgtcatt 1020

cgctcttcca tcgacatgcg tcggatcgct tcgcctgtaa attcgataat ataaccggtg 1080

ccgacgccaa cgccatagcg gccgataatg gccaagatga cgtctttggc ggtcactcct 1140

ttgccgaggc ggccgttgat gcagatttgc agcgttttcg gcttatgctg ccaaagcgtt 1200

tgtgtagcca atacatgctc gacttcgctc gtgccgatgc caaacgccaa ggcgccaaac 1260

gccccgtgcg tcgacgtatg gctgtcgccg caaacgatcg ttttccccgg ctgggtcaac 1320

ccgagctctg ggccgatgac gtgaacgatt ccttgctctt cgctgtgtag gtcggcgagc 1380

ggaatgccga actcgcggca gttgcgctca agcgcagcga tttggttgcg cgccacttcg 1440

tcggtaatca caaatcggtt aacggttggc acgttatggt ccatcgtcgc aaaggtcaaa 1500

tccggccgcc gcaccttccg tccttttttgc cgcaaccctt caaacgcttg cggcgaggtc 1560

acttcatgca ctaagtgcaa atcgatgtac aataaatccg gtttgccctc ctcacggtag 1620

acgacgtggt tttcccaaat tttatcgatg atcgttttcg gcttcattga cccccatcga 1680

gagactccga acgtggcaaa tggagggacc agagttgttc agttcacagg tagataatgt 1740

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cgcgggtctt gatagttagc aataaataca gtttcagaat atctgtaata caaaaactgt 1800

atcgagacaa gaaaaaagta gcaaaattta caaatgttca tgattcatct ggctaaattg 1860

gatgttcaac tgacccattg aagacaaggg caacaaccat gcggccgtgg acaatgccgt 1920

cgttcgtagg cggcgatatg cgcttcgtac acaaacgtca aatcaatttc gtcccatcct 1980

tttagcaaca gctgttttcg atacgggtcg atgtcaaacg gacgcgaaaa tccttcatcg 2040

tcaaataccc gctgttcttc aagcgaaacc gtcagttcat agtctgcgcg ctcgctttgg 2100

cgcagcaagt agcggacatc ctctttatcc agccggatcg gcaacagtcc atttttaag 2160

cagttgttgt aaaaaatatc ggcaaacgat ggggcaatga ttacgcggaa tccgtaatct 2220

tgcagcgccc acggcgcatg ttcgcgcgat gagccgcaac cgaagttttc atcggcgact 2280

aaaatcgtcg ccccttcgtt ttccgggcgg ttgagctcaa actccggatt tggcgtgccg 2340

tcgctcaaat accgccaatc gtaaaagaga aactggccaa agccggtgcg ttcaatccgt 2400

ttcaaaaact gctttggaat gatttgatcg gtatcaatat tcgcccgatc gatgccggcg 2460

gtttttccgc gatggatcgt aaacggcttc attaaggctg agatcttctt cagtgcattg 2520

tagttgaatg aagggttagg ggggaaatgc ccccctattt tttgtctagc catcctgcca 2580

cgtttgacag ggtagcaatt tcgacacgat agggttctct cttctgccgt ta 2632

<210> SEQ ID NO 69
<211> LENGTH: 2035
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 69, Example 69: designer nirA-promoter-controlled 2-Keto Acid Decarboxylase DNA construct (2035 bp)

<400> SEQUENCE: 69

agaaaatctg gcaccacacc tgacccccat cgagagactc cgaacgtggc aaatggaggg 60

accagagttg ttcagttcac aggtagataa tgtcgcgggt cttgatagtt agcaataaat 120

acagtttcag aatatctgta atacaaaaac tgtatcgaga caagaaaaaa gtagcaaaat 180

ttacaaatgt tcatgattca tctggctaaa ttggatgttc aactgaccca ttgaagacaa 240

gggcaacaac catgtataca gtaggagatt acctgttaga ccgattacac gagttgggaa 300

ttgaagaaat ttttggagtt cctggtgact ataacttaca atttttagat caaattattt 360

cacgcgaaga tatgaaatgg attggaaatg ctaatgaatt aaatgcttct tatatggctg 420

atggttatgc tcgtactaaa aaagctgccg catttctcac cacatttgga gtcggcgaat 480

tgagtgcgat caatggactg gcaggaagtt atgccgaaaa tttaccagta gtagaaattg 540

ttggttcacc aacttcaaaa gtacaaaatg acggaaaatt tgtccatcat acactagcag 600

atggtgattt taaacacttt atgaagatgc atgaacctgt tacagcagcg cggactttac 660

tgacagcaga aaatgccaca tatgaaattg accgagtact ttctcaatta ctaaaagaaa 720

gaaaaccagt ctatattaac ttaccagtcg atgttgctgc agcaaaagca gagaagcctg 780

cattatcttt agaaaaagaa agctctacaa caaatacaac tgaacaagtg attttgagta 840

agattgaaga aagtttgaaa aatgcccaaa aaccagtagt gattgcagga cacgaagtaa 900

ttagttttgg tttagaaaaa acggtaactc agtttgtttc agaaacaaaa ctaccgatta 960

cgacactaaa ttttggtaaa agtgctgttg atgaatcttt gccctcattt ttaggaatat 1020

ataacgggaa actttcagaa atcagtctta aaaattttgt ggagtccgca gactttatcc 1080

-continued

taatgcttgg agtgaagctt acggactcct caacaggtgc attcacacat catttagatg 1140

aaaataaaat gatttcacta aacatagatg aaggaataat tttcaataaa gtggtagaag 1200

attttgattt tagagcagtg gtttcttctt tatcagaatt aaaaggaata gaatatgaag 1260

gacaatatat tgataagcaa tatgaagaat ttattccatc aagtgctccc ttatcacaag 1320

accgtctatg gcaggcagtt gaaagtttga ctcaaagcaa tgaaacaatc gttgctgaac 1380

aaggaacctc attttttgga gcttcaacaa ttttcttaaa atcaaatagt cgttttattg 1440

gacaaccttt atggggttct attggatata cttttccagc ggctttagga agccaaattg 1500

cggataaaga gagcagacac cttttattta ttggtgatgg ttcacttcaa cttaccgtac 1560

aagaattagg actatcaatc agagaaaaac tcaatccaat ttgttttatc ataaataatg 1620

atggttatac agttgaaaga gaaatccacg gacctactca aagttataac gacattccaa 1680

tgtggaatta ctcgaaatta ccagaaacat ttggagcaac agaagatcgt gtagtatcaa 1740

aaattgttag aacagagaat gaatttgtgt ctgtcatgaa agaagcccaa gcagatgtca 1800

atagaatgta ttggatagaa ctagttttgg aaaaagaaga tgcgccaaaa ttactgaaaa 1860

aaatgggtaa attatttgct gagcaaaata aatagtaagg ctgagatctt cttcagtgca 1920

ttgtagttga atgaagggtt agggggggaaa tgccccccta ttttttgtct agccatcctg 1980

ccacgtttga cagggtagca atttcgacac gatagggttc tctcttctgc cgtta 2035

<210> SEQ ID NO 70
<211> LENGTH: 1426
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 70, Example 70: designer nirA-promoter-controlled NAD-dependent Alcohol Dehydrogenase DNA construct (1426 bp)

<400> SEQUENCE: 70

agaaaatctg gcaccacacc tgacccccat cgagagactc cgaacgtggc aaatggaggg 60

accagagttg ttcagttcac aggtagataa tgtcgcgggt cttgatagtt agcaataaat 120

acagtttcag aatatctgta atacaaaaac tgtatcgaga caagaaaaaa gtagcaaaat 180

ttacaaatgt tcatgattca tctggctaaa ttggatgttc aactgaccca ttgaagacaa 240

gggcaacaac catggggtat caggactgcc ctgcctagaa cttcaccttt ctctagcctc 300

tcaagcacat cgtttatttc atctagcttg tggatatcaa cctctaccct gaccttaccc 360

tgaagggcta acgtgactag ctcatggagc tctacatagt ttcctactag gcttccttca 420

aaggatacct cagaggatat caccctgatc gtggggaatc taagctcacc cccatagcct 480

acgatgataa gcctccccat cctccctagc aggtatggtg tataatcgac tgtagcctga 540

gagcctacga agtccattgc aacgttaact cctctccccc tggtaagctc catgacctgc 600

tttacagggt ctcgtctagc gtcaaccacg tgatccgctc caagcctctc ggccagcttt 660

agtttttctt ccttaacgtc cagtgctatc accgtcgcgg gtgtcataac tttaagtagc 720

tgaactgcaa tatgacctaa tcctcccacg cccactatag cgacgtatgc gccgggatag 780

agggttcggg cggccttctt aacagcccta taagccgtta tcccagcgtc cgctagaggg 840

gccatttcaa caagtttctc cctgctaata tccttaggca gctttatcac agacctgtgc 900

gaggtcctca tgaactctgc aaatccacca tcgatattaa gtcctgggaa ctctaggttc 960

-continued

tcgcagtgca tatcctcacc agctctacag gctagacagg ttccatctgt gaccgccggg 1020

tgaagaatta ccgggtcccc cttctctaag ccttccactc cttcggcaac ttcttcaata 1080

tacccgacgt tctcatggcc taaagtgtag ggtagcttag gctgcaatag ctcatgccac 1140

attccctgga caaggtggag gtccgtatgg catacgccag cgcctgcaat ccttacaata 1200

acgtcaaatc taccttctag cctcggatag tcgacatcct ctatcctcaa cggcttgtta 1260

tactcgtgga gcctggcagc tttcaataag gctgagatct tcttcagtgc attgtagttg 1320

aatgaagggt taggggggaa atgccccccc atttttttgtc tagccatcct gccacgtttg 1380

acagggtagc aatttcgaca cgatagggtt ctctcttctg ccgtta 1426

<210> SEQ ID NO 71
<211> LENGTH: 1468
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 71, Example 71: designer nirA-promoter-controlled NADPH-dependent Alcohol Dehydrogenase DNA construct (1468 bp)

<400> SEQUENCE: 71

agaaaatctg gcaccacacc tgacccccat cgagagactc cgaacgtggc aaatggaggg 60

accagagttg ttcagttcac aggtagataa tgtcgcgggt cttgatagtt agcaataaat 120

acagtttcag aatatctgta atacaaaaac tgtatcgaga caagaaaaaa gtagcaaaat 180

ttacaaatgt tcatgattca tctggctaaa ttggatgttc aactgaccca ttgaagacaa 240

gggcaacaac catggcgtac ccagacacct ttgaaggatt tgccgtcact gacactgcaa 300

aatggtccac aaccaagaag atagaattca ccccaaaaag gttccaggaa catgatatcg 360

atgtcaagat ccatgcctgt ggtatctgcg ggagtgatgt tcacactgtt tgcgggggat 420

gggcaaaacc agaccttccc gtgatcccag gacatgagat cgttggtgag gttgttagag 480

tgggcccaaa agtgaaggga tttgaaattg ggcaaagagt tggtgttgga gctcaagttt 540

gggcctgtct agagtgcgac acatgcaagg ataacaacga aacgtactgt cctcaatggg 600

tggacactta caatgccact tatcctgatg gtgacaaggc atggggtggt tattcctctc 660

acatcagagt ccacgatcac tttgtattcc ctattcctga tgaacttcca actaatgctg 720

tggccccaat gttgtgcgct ggtatcacca cgtactctcc gttggtaaga aatggagctg 780

gtccaggaaa gaaggtgggt atcatcggaa ttggagggtt gggacatttt gccatcatgt 840

gggctagggc tcttggttgc gaagtgtaca cgttttctag aacacatagc aaggaagctg 900

atgctaagaa attgggaact gaccatttta ttgcgacgtg ggaggacaaa gactgggcca 960

agaagattgg cagaaagctg gactttatca tttcgtgtgg aaattcggcc acgaactttg 1020

atatggatgg ttacctcagt gtgctgaagg ttcatggtaa actcatttcc gtcggccttc 1080

cagaggagcc attcacgctg tctgctggaa gctttatcaa gaacggttgc tacttgggat 1140

cgtcccactt ggggaacaga caggagatgc ttgatatgct gaaacttgct gctgataagg 1200

gcattggttc ttggtatgag gagctcccaa tctctgagga agggctgaag gaaggactgg 1260

agagatgcca caacaatgac gttaagtata ggttcaccct gaccggttac gataaggcat 1320

tcaaatagta aggctgagat cttcttcagt gcattgtagt tgaatgaagg gttaggggggg 1380

aaatgccccc ctatttttttg tctagccatc ctgccacgtt tgacagggta gcaatttcga 1440

cacgataggg ttctctcttc tgccgtta 1468

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<210> SEQ ID NO 72
<211> LENGTH: 1555
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 72, Example 72: designer nirA-promoter-controlled NADH-dependent Butanol Dehydrogenase DNA construct (1555 bp)

<400> SEQUENCE: 72

agaaaatctg gcaccacacc tgacccccat cgagagactc cgaacgtggc aaatggaggg 60

accagagttg ttcagttcac aggtagataa tgtcgcgggt cttgatagtt agcaataaat 120

acagtttcag aatatctgta atacaaaaac tgtatcgaga caagaaaaaa gtagcaaaat 180

ttacaaatgt tcatgattca tctggctaaa ttggatgttc aactgaccca ttgaagacaa 240

gggcaacaac catgcaggga agcgcgcaaa atggcgagca catcatcgcg gttcaatgtt 300

ttgaaacggc cgaactcgcc aaacgccatc gctttatcgg ccatcagctc caagttttcc 360

tcgccgatgc catagtccgc aagccgcgac ggcgccccga ggctcgacca gaactcgcgc 420

agccgctcga tgccttcaag cgccacatcc cgctccgatt tgcccgccgg atcgacatca 480

aagacgcgca ccgcgagctg ggcgaaacgg ctgacatttt catcgagcac atgcttcatc 540

cagttcggga acaaaatcgc caatcccccg gcgtgcggga tgtcatacac ggcggaaacg 600

gcatgctcaa tattgtgcgt cgcccagtcg ccgcggacgc ccatttgcaa gaagccgttt 660

aaggcgatcg tgcccgagta catgatcgtc tcgcgcagct cgtagttttc caaatcgttg 720

atcagtttgg gcgccgtttc gatcacggtt ttcaacaccg cttcacacat ccggtcttgc 780

aatggcgtgt tcggcgtatg gtggaaatat tgctcaaaca catgcgacat catatcgaca 840

atgccgtaaa ccgtatggtc tttcggaacg gtcatcgtat acgtcggatc caaaatcgaa 900

aattgcggga acgtaaacgg gctgccccag ccgtattttt ctttcgtctc ccagtttgtg 960

atcaccgaac cagaattcat ctccgacccg gtcgccgcca gcgtcaagac gacgccaaac 1020

ggcagggcgc cggtgacggg cgcttttttc gtgataaact cccacggatc gccatcgaat 1080

ttcgccccgg cggcgatcgc tttcgtgcag tcgatgacgc tgccgccgcc aaccgccagc 1140

aaaaattcga cgccttcccg cttgcaaatg tccacccctt ttcttacggt cgagacgcgc 1200

gggttcggtt cgacgcctgg cagttcgatg acctcggcgc caatattccc caatatcttc 1260

atgacttcct catacaatcc gtttcgtttg atgctgccgc cgccatacac gagcagcact 1320

ttcttgccgt agcgcggcac ttcttctttg agacgttcga gctgcccttt tccgaaaatc 1380

agtttcgtcg ggttgcggaa aataaactct tgcattaagg ctgagatctt cttcagtgca 1440

ttgtagttga atgaagggtt agggggggaaa tgccccccta ttttttgtct agccatcctg 1500

ccacgtttga cagggtagca atttcgacac gatagggttc tctcttctgc cgtta 1555

<210> SEQ ID NO 73
<211> LENGTH: 1558
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 73, Example 73: designer nirA-promoter-controlled NADPH-dependent butanol dehydrogenase DNA construct (1558 bp)

<400> SEQUENCE: 73

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agaaaatctg gcaccacacc tgacccccat cgagagactc cgaacgtggc aaatggaggg 60

accagagttg ttcagttcac aggtagataa tgtcgcgggt cttgatagtt agcaataaat 120

acagtttcag aatatctgta atacaaaaac tgtatcgaga caagaaaaaa gtagcaaaat 180

ttacaaatgt tcatgattca tctggctaaa ttggatgttc aactgaccca ttgaagacaa 240

gggcaacaac catgaaaatc cacatcactg ccgtaatatg cacaagtata taatttttcc 300

atagtttcat cattaatctc ccttggattt gatcctgtgc atggatctaa aacagcatta 360

tgagctataa atttaagatt agctttaaat tcattctcat ctattccata ctctttcatt 420

gatgaaggta tatttaattc cttattaaac ttatttatta aatctattag gtcatctgtt 480

aattctcttt cactttctcc ctttaatcca atatgtcttg caatgttagc atatctattt 540

tcacaagctt ttctattata tttaattaca tatggcaaga agatagcatt agcacatcca 600

tgtggtatat ggaatacagc ccctacctta tgagccatag aatgtactat tcctaaaagg 660

gcattagaga aggccattcc tgctaaacat tgagcctcat gcatttctcc cctagcttcc 720

atatctccct tatatgaatt tactaagtgc atattaacca tttcaattgc ctttaaagct 780

aaaggatctg taaagtttga tcttaaactt gcagtataag cctcaatagc atgagttaag 840

gcatccattc ctgtgtgagc tactaacttc tctggcatag tttctgctaa gctaggatca 900

acaatagcta tatctggagt tatttcaaaa tctgctaaag gatatttaat cttagcctta 960

taatcagtta ttactgagaa ggcagttacc tctgtagcag ttccagaagt tgatggaata 1020

gctacaaact ttgcttttct tctaagctta ggtaatccaa aaggaacaat ggccttttca 1080

aaagtaaaat caggatactc gtagaaaatc cacatagcct ttgctgcatc aataggtgaa 1140

cctcctccta tggaaactat ccagtctgga ttaaattcct ccatttcctt tgcacccttc 1200

ataacagttt ctactgatgg atctggttct actccttcaa aaacctttgt ttccatatta 1260

gcttcctttа aataacttaa aaccttatct aaaaagccaa atcttttcat tgatccgcca 1320

ccaataacta taaaggcctt tttaccttct aaactcttta atacttctaa ggaatctttt 1380

ccatgatata tgtcccttgg taaagtaaat cttgccatta aggctgagat cttcttcagt 1440

gcattgtagt tgaatgaagg gttaggggggg aaatgccccc ctatttttтg tctagccatc 1500

ctgccacgtt tgacagggta gcaatttcga cacgataggg ttctctcttc tgccgtta 1558

<210> SEQ ID NO 74
<211> LENGTH: 3646
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 74, Example 74: designer nirA-promoter-controlled Phosphoenolpyruvate Carboxylase DNA construct (3646 bp)

<400> SEQUENCE: 74

agaaaatctg gcaccacacc tgacccccat cgagagactc cgaacgtggc aaatggaggg 60

accagagttg ttcagttcac aggtagataa tgtcgcgggt cttgatagtt agcaataaat 120

acagtttcag aatatctgta atacaaaaac tgtatcgaga caagaaaaaa gtagcaaaat 180

ttacaaatgt tcatgattca tctggctaaa ttggatgttc aactgaccca ttgaagacaa 240

gggcaacaac catggccggc gttccgcaag cccgccgcga tgcccaggat ggagagcagc 300

agcgcccgct ccagggccgg gcgctcgggg tcgccttccg gcgaggcccg gtaccgggcc 360

agcagctcca cctgcaggta gctgatgggg tcgacgtacg ggttgcgcaa ggccgtctgc 420

-continued

cgcgccagca cggggtggtg ggccagaagc ggcccgccga aggtctcctc caagagcgcc 480

cgggtccgca ccatggcctc ctcgagccgg gggaagaacc ggttcgccag gggcccgggc 540

accagccgca ggtactccct ggccacggcc aggtcggcct tggccagggc cagggccgcg 600

ccgtccagca ccgagcggaa gaagggccag cgggcaaaca tcgcctggcg aaggtcccgc 660

ggcaccgccg caagaccttc ggccagcccg taccagccgg gcagcagaag acgcacctgg 720

gtccaggcca tcacccaggg gatggcccgc agatcctgga cgcgccgggc ccggcccgtg 780

cgggccaccg ggcgggaagc gatcttcagg gcggcgatct cccggatcgg ggtgaagtgc 840

tcgaagaact cgaagaaccc gggctccgcc agcagctggc ggtaggcctc cgccgaccgg 900

gcggcggccc ggtccatggc ctcccgccag gccgccggga cgggggaacc gcccggggcg 960

agcccctggc gcccgccgcc cggcctgctc ggcgcggtcc cggccccgcc gggcgggccg 1020

ggttcctccg gcgaaagcac cgcctcttgg gcctgggcca gcgtgtcccg ggccgccgcc 1080

agaaggaagt ggtagaggag ctgctccagg ttgcgcaggg ccagctcggg gtgagcgtag 1140

cggtccgcca gcgcctctcc ctgctcggtg agccgcaggc ggcggcccac ggtgcccggc 1200

ggcaggctgg cgatggcgcg gccggcggtc cccccgccgc cccgggctgt ggacgtgccg 1260

cgaccgtgga agaaggacac cggcacgccc gccgcccggg ccaccgccgc gatgccctcc 1320

tgggcccggt agagggccca gttggccgcc aggtagcccg cgtccttgct ggagtcggag 1380

tagccgatca tcacctcgca gccgccgcgg ccgcgggcgt ggacgccgaa gacggggttc 1440

tgcagcagct gctccatggc gcggggcgcc gcctccaggt cggccagggt ctcgaacagg 1500

gggaccacgt caaagggcaa ggggtggccg gggcggtaca gccccacctc ccgcgccagg 1560

acgaacacct ccagcacgtc ggcggggccg cggcagccgc tgatgatgta agccccccgg 1620

tcctgccagg cccgcagagc atccagggcc acggccagct cgcggctgcg gggccggtag 1680

cccaccggcg ccagcggccg gggcgaagcc agctcccggg tcagcaccgc ctcccgcccg 1740

gcggcatcca gggccaggta ctcccctgcc gccatgaccc caccggcttc cagcagctcc 1800

gccaccgccc gcccgtgggc ctcggcatgc tcccgcaggt cgaggggcgc catggcctcg 1860

ccaaagacct gggcccgcca gcgcagggga cgcaccaggg tggccgccgc ctcgcccagc 1920

ccggcatccc gcagcccctc ttccacctgg aagagcaggc gatccagggc ggtggaaccg 1980

gcggcctccg gcccctcgcc ggccggcggt tccccggcgg tcccctttgg tggcgcggcc 2040

gcggcgggcc gggaaggccg ttcgccggct gggtccgctg gaacggcggg ccctccaggg 2100

atgccctccg ctgaagcggg cggccgggga ggcattgccg ctccctccgg cggagccgcc 2160

ggccggggag gcggtgccgt tgcctcgact gcagcgtccg gccggtgggg tacagccggt 2220

gcctcggctg gagccgccgc ccgggcgggc gtctcgctcc acacctcttc cggcaccgcc 2280

cttgccgccc agtgccgctg cagccggtag gcgaaccgcc ggtagggctc gccggggaac 2340

cggccggcgg ccgccggcgg caggggcgcc acggcctctg cgggcaagga gggcagggga 2400

ggcagggaag cccgttcttc cgccacggac agatcccgcg tcagggcggc caggcctccg 2460

gcgtactttc gggcgatctc ggcccgcgcg taggcctggg cccaggcggt gacctccggg 2520

gtcacaaagg ggttgccgtc ccggtcacca ccgatccagc tccggaaggc caggcgcggg 2580

ggaagaaccg gccgccgccc gtagcgggcg gccaccgccc cctcgagggc ctccatgagc 2640

cggggcaccg cctcccacag ggtggtgggc aggtagtaga ggccgccgcg gacctcgtcc 2700

-continued

tccacccggg gcggggccgg gcgcagctcg cgggtggtcc agagcagggt gacccgggcc 2760

accacctcgt ccaggtcccc ctcgccccgc tccagccggt ccagggcctg gttgagctgc 2820

agcaggtggt ggcgcagggt gcgccgccgc gtctcggtcg gatgggccgt gaaggtcagc 2880

tccagccggg ccgaggcgag gaggcgcacc acgtcgtcga attccatccc ttgggcctga 2940

agctgggtga ccagggccag cagcgactcg ggccggggcc ggtcgggcgt gctggcctgc 3000

tcgcgccggc ggttcacccg cacccggtgc cgctcctccg ccaggttgac cagatggaaa 3060

taggtcgaaa aggcccggat cagcccttcg gccgcggcca ccgaaagccc gccgatctcg 3120

gcccgcagcg cctgccgggc ggcgtcgtcc cccgggtgct gccggaggtg cttggtgtgg 3180

gcgcggatgt cctcttccag ttcgaacagg cgatcccccg agaggcggcg gatggcctcc 3240

cccagggccc gtcccaggag gtcgacctcc cgcttgagaa gggggtacag ctcctcttcc 3300

ggccgcccat ccggcggggg aacggatccc gccggggcag gcaacgcctc gccggacgag 3360

ccggccgccg cagggcggct cccctgcccg ccgccccggt cctggcggtc ctgaccgtcc 3420

ttgcggtccc ggccgtcctt caggtcccgg ctccccttcc ccgccgccga gccggccccct 3480

gccggccggt caccctcgcc gctcactaag gctgagatct tcttcagtgc attgtagttg 3540

aatgaagggt taggggggaa atgccccccct atttttttgtc tagccatcct gccacgtttg 3600

acagggtagc aatttcgaca cgatagggtt ctctcttctg ccgtta 3646

<210> SEQ ID NO 75
<211> LENGTH: 1591
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 75, Example 75: designer nirA-promoter-controlled Aspartate Aminotransferase DNA construct (1591 bp)

<400> SEQUENCE: 75

agaaaatctg gcaccacacc tgacccccat cgagagactc cgaacgtggc aaatggaggg 60

accagagttg ttcagttcac aggtagataa tgtcgcgggt cttgatagtt agcaataaat 120

acagtttcag aatatctgta atacaaaaac tgtatcgaga caagaaaaaa gtagcaaaat 180

ttacaaatgt tcatgattca tctggctaaa ttggatgttc aactgaccca ttgaagacaa 240

gggcaacaac catgagaatt tcggaaagat caaaaaaggc gccggcgagt cccataagaa 300

aattagtgcc atttgccgag gaagctgtaa aaaaaggtaa aaaaatctat tatttaaaca 360

taggtcaacc tgatatacca acaccttcaa tttattttca gtatgaggaa aaacacagac 420

cccagattgt agcttataca cactcagcag gtcttctgcc actgagggag gcttttacaa 480

aatattacgc cagattcgat atagatgttt tcccggatga aatcatcgtt accaatggtg 540

gaagtgaagc tgtcctgttc gctatgacag tcgtggcgga tccgggagat gaaatacttg 600

ttctggagcc gttctatgcc aattacgctg gatttgctgc tcaacttggt atcaatcttg 660

ttccagttag aactcgcccg gaggatggat atcaaatacc aaagatgggt gattttctgg 720

agaaaatcag tcacaggact aaagcaatca ttttttccaa tccctgcaat cctacggggg 780

ctgtttacga tgaaaaacaa cttgaagtta ttgctgaagt tgctttgaag agagatttgt 840

ttgtgatttc agacgaggtt tatagagaat tcacttttga tggttttagg gccatatcta 900

tgatgagttt ttctaatatt tctgacaaag tcatagttgt tgacagtatt tctaaaagat 960

atagtgcctg cggcgcgcgg attggtacat ttattaccaa gaataaagat atatatcaag 1020

-continued

cagctatgaa actggctcag gcgagactct gtcctgctat gacatctcaa tacggtacta 1080

ttggtcttct gacgcttgac gatttgtatt attcacaaat gagaaaagag tatgaaatga 1140

gaagagatgt tgtttacgaa gaacttcagc gcattgatgg agcagtcttc aagaaacctc 1200

acggggcttt ttatatttcg gtgaaacttc caatcgacaa ttctgaagat tttgtgaaat 1260

ttatgttgac ggagtatgag gttgaaggaa aaacgacaat ggtggcacct ctcagtggat 1320

tttatgtaac accatctacg gggatgagtg agatcagaat agcgtatgtt ctggaacgcg 1380

aacaactgag ggatgcagtt gcaattttga cttcaggttt gaaaacttac atagagagaa 1440

gaaataaata ataaggctga gatcttcttc agtgcattgt agttgaatga agggttaggg 1500

gggaaatgcc cccctatttt ttgtctagcc atcctgccac gtttgacagg gtagcaattt 1560

cgacacgata gggttctctc ttctgccgtt a 1591

<210> SEQ ID NO 76
<211> LENGTH: 1588
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 76, Example 76: designer nirA-promoter-controlled Aspartate Kinase DNA construct (1588 bp) SEQUENCE: 76

agaaaatctg gcaccacacc tgacccccat cgagagactc cgaacgtggc aaatggaggg 60

accagagttg ttcagttcac aggtagataa tgtcgcgggt cttgatagtt agcaataaat 120

acagtttcag aatatctgta atacaaaaac tgtatcgaga caagaaaaaa gtagcaaaat 180

ttacaaatgt tcatgattca tctggctaaa ttggatgttc aactgaccca ttgaagacaa 240

gggcaacaac catgtagtcc gaaaacttga cagagttctt tcaacaaatc ttctgcttta 300

tcttcatgta caaggcatga tatctttatt tcagaagttg ttatcatttc tggctctatg 360

tttttctttc tcaaaacttc aaaaaatttt gctgcaacac ctcgttgata tttcattcct 420

aaacctatta ttgatacctt agaaaacccc cctgtgatct taatttcaca atcaagatct 480

ctcattgcct tctgtacgtc aaccgagtta ctttcaacaa ttgtgaaaga tagattaatg 540

tctcctgagt tactcaccaa cgatatcata tcaacgttaa agccttttc agcgagttct 600

ctaaatacgt cggcggttgc tttagaattt ttcaagctat aaacgctgac ctttacctga 660

tttttctcta tcgtcgcgcc tgtaacaacg ggtcgctcaa gccattccgg aagttttccc 720

atcacccacg ttccctcctc atttgaaaac gaagaagcgc aataaattgg tacgctgtat 780

ttttttgcta tctcaacact tcgagaatgt agaaccctgg caccaagtgc ggagaattcc 840

aacatttcat cgtatgtaat ataagacagt ttttttgcct ggggaaagat cctgggatct 900

gttgtatata tgccagcgac gtcgctgtat atttcgcaga ttgttccaag ttttgcggca 960

atagcaacag cagaagtatc tgatcctcct cttccaagag ttgtcagttc atcgttttcg 1020

tttattccct gaaaccctgt aacaagtaaa acatcgttat gaaaagccag cgatcttaat 1080

tttcggtcat ctatatcttt tatccttgcc gaattaaaat cgctggttgt cagaatccga 1140

gcctgaaacg cattcaaaga tacagctttc atacctattc tgtcaaggta tatggatagc 1200

aaagcagcgg atatttgttc gccacaggat aacaacatat ccagttctct tggattgggt 1260

ttttcagaca gccttcttgc aagaaaaacc aatttgtctg ttgtttttcc cattgcagag 1320

acaacaacga ttaacttttt cccatttttt actgttttca ctattttctc ggtaattttt 1380

-continued

ttgattcttt ctatgctggc aagcgatgag ccaccatatt tttgtacaac aagtttcaga 1440

aaaatcacta aggctgagat cttcttcagt gcattgtagt tgaatgaagg gttaggggggg 1500

aaatgccccc ctatttttttg tctagccatc ctgccacgtt tgacagggta gcaatttcga 1560

cacgataggg ttctctcttc tgccgtta 1588

<210> SEQ ID NO 77
<211> LENGTH: 1411
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 77, Example 77: designer nirA-promoter-controlled Aspartate-Semialdehyde Dehydrogenase DNA construct (1411 bp)

<400> SEQUENCE: 77

agaaaatctg gcaccacacc tgacccccat cgagagactc cgaacgtggc aaatggaggg 60

accagagttg ttcagttcac aggtagataa tgtcgcgggt cttgatagtt agcaataaat 120

acagtttcag aatatctgta atacaaaaac tgtatcgaga caagaaaaaa gtagcaaaat 180

ttacaaatgt tcatgattca tctggctaaa ttggatgttc aactgaccca ttgaagacaa 240

gggcaacaac catgtcccct gaaaatatta taaatctctg cattgagaac tgcacacccg 300

gcagcccctc tgattgtatt atgaacaaga gcaacgaacc caaactgttt gttcgaatac 360

tgtttcaacc tgccaacact gacactcatt ccaccaccaa gatctctgtg aaacttcggc 420

tgcggagaat caactcctgt caaataaaaa acaggttttt caggtgcggt tggaagatac 480

attcctttaa gtggttgaaa atcttcaaaa gctctcacaa tttcacttaa agtggccttt 540

tcctgagttt tgatagttat agatagcata tgaccgtcaa caacggctac cctgttgcac 600

tgtgcgaaaa tatcgagatt cgccgggtat atttttccat ctttcaatct gccaagtatt 660

ttttttgatt cggtcatgat ttttttcttcc tcatttttta tgaacggcac aacattgtca 720

attatatcca tagatggtac accgggatat cccgcgccag agatagcctg cattgtgaca 780

acatttgcct cttctatacc gaatctatcc attatgggtt taagaaccat tgtaaaacct 840

atcgttgagc aattagggtt ggtgattatt tttccttttc tcttttgagt ttcggttatt 900

ttcaaatgat ccagattaac ttcagggata attagaggta catcctcgtc cattctatgg 960

cttgcggcat ttgagaaaac aatgtatcct gcgtttgcaa attcctcctc aatttcgcct 1020

gcaacatctg aaggcaaagc agaaaacaca taatcacaat ctatatcagg tgtgcatttt 1080

tttaaaacca tatctcctgc tttttcggct acaggaacat tcaagcgcca ttgaactgct 1140

tctctgtact tttttcccgc agaattatca gaagctgcca gagctgttat ctcaaaaaat 1200

ggatgatttg aaagcaattg aacaaatctc tgtccaacaa gccctgttgc accaagaata 1260

gctaccttca ttaaggctga gatcttcttc agtgcattgt agttgaatga agggttaggg 1320

gggaaatgcc cccctatttt ttgtctagcc atcctgccac gtttgacagg gtagcaattt 1380

cgacacgata gggttctctc ttctgccgtt a 1411

<210> SEQ ID NO 78
<211> LENGTH: 1684
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 78, Example 78: designer nirA-promoter-controlled Homoserine Dehydrogenase DNA construct (1684 bp)

-continued

<400> SEQUENCE: 78

agaaaatctg gcaccacacc tgacccccat cgagagactc cgaacgtggc aaatggaggg 60

accagagttg ttcagttcac aggtagataa tgtcgcgggt cttgatagtt agcaataaat 120

acagtttcag aatatctgta atacaaaaac tgtatcgaga caagaaaaaa gtagcaaaat 180

ttacaaatgt tcatgattca tctggctaaa ttggatgttc aactgaccca ttgaagacaa 240

gggcaacaac catgaacttt actatcttcg ccttccaccc ggatgacgtt gcaaatctct 300

gccactatac tcatttctcc caacaccatc agggcatctc gcaggtcaga ttcaggaact 360

ctatgggtca ctaagaccag ctgggcgaac tcctcgccgc ttgtcttctg cagcacggta 420

gctatgctca gctgatggct gccaaaaacc ccggcgatgg ccgccaatac cccagggcgg 480

tccttaacca gcatccgaat atagaacttg ctctccactt tgtcgatagg aataatctcc 540

ttggcttcaa aacaagtaca gcccagcatg ccggtggtac catgactgag gttatggcat 600

atctccatta tgtctcccac caccgcgcta gcagtgggca tctgccctgc ccctcttcca 660

aagaacatga cttctcccac cgcgtccccg ttcacgaata cggcgttgta aacccccttt 720

accgcggcca gagggtggtg cataggtatg aaagccgggt ggacccgggc ttgcacccgg 780

ccgtcgattt cctgcgcgat agccaggagc ttcaccacat agcccaattc ataaccgtac 840

ttgatatcta aagggcttaa acgggtaatt ccttcaacgt aaacgttttc gaacgtaacc 900

cggctgttga aggcgatcga agccaggatg gcaattttac gagcagcatc atagccttct 960

acgtctgaag taggatcagc ttcagcatac cccagttcct gcgcctcttt caaagccctc 1020

gaaaactcta ggccttcctc gctcatctta gtaaggatgt agttggttgt cccgttaaca 1080

atccccatta cttctttgat tcgattggca cctagcgaat gcttcaaagg ataaattaag 1140

gggatgcccc caccaacact ggcttcaaaa aagaagtcca ccttgttctc ttcagctgcg 1200

gccagcagtt cctgcccgtg gaccgctatt aaatctttat tggcagtcac cacgttcttg 1260

cctttgcgta acgcctgcaa aataaaggtt cgagccggtt cgatgcctcc tatgagttct 1320

acaacaacac ttatatggtc atcatccagt atgtctttga tatcggcgca aaggacgtct 1380

tcgcttaaac ctagactcaa aaccttctcc gggtcttttt cgaggattcg cttgatcgcg 1440

actccttgtc cggtacggag cgaaataaca tcccggtttg aggctaaaag cttgaccaca 1500

ccggatccaa ccgttccaca acccaagagg ccaatattaa ccactaaggc tgagatcttc 1560

ttcagtgcat tgtagttgaa tgaagggtta ggggggaaat gccccccctat tttttgtcta 1620

gccatcctgc cacgtttgac agggtagcaa tttcgacacg atagggttct ctcttctgcc 1680

gtta 1684

<210> SEQ ID NO 79
<211> LENGTH: 1237
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 79, Example 79: designer nirA-promoter-controlled Homoserine Kinase DNA construct (1237 bp)

<400> SEQUENCE: 79

agaaaatctg gcaccacacc tgacccccat cgagagactc cgaacgtggc aaatggaggg 60

accagagttg ttcagttcac aggtagataa tgtcgcgggt cttgatagtt agcaataaat 120

-continued

acagtttcag aatatctgta atacaaaaac tgtatcgaga caagaaaaaa gtagcaaaat 180

ttacaaatgt tcatgattca tctggctaaa ttggatgttc aactgaccca ttgaagacaa 240

gggcaacaac catgaaggtc ctggtaccgg ccacaacgac caatctcgga gcgggattcg 300

acgtctttgg actcgcgctg gatcttttca acgaagtgga gttttctttc gatacaaaag 360

agacaaccat agaaagtact ggaaaatacg cttcggattt gaaggaccac aatctgtttt 420

tcgaagtctt caggttcttt gagagaaaaa ccgggtacag agttccgcca gtcaggatca 480

agcagacatg caacatccct gtatcgagcg gtcttggatc gagcgccgct gtgatcgtcg 540

cggcactcca cattgcgaac gaaggaacgg gcagaaatct ttcacgggaa gatcttatga 600

aactcgctgt ggagctggaa ggacaccctg acaacgttgt acccgctttc acaggggggc 660

ttgtggtctg ttatcaaaac ggaagtcatc ttgattttga aaagttcgag atcgatcttt 720

ctctcacatt tttcgttcca aacttttcga tgtgcacgaa cgagatgaga aagatccttc 780

cggagaaggt ccctttcgaa gatgcggtct tcaacataaa gaattcatgc cagttccttg 840

caaagatcgc agctggaaag atcaaagagg ctctgaaata cgtgggagat cgacttcacc 900

agaactacag gataaacggc aataagaaga tgaaagagtt tgtggaagcc atcttatcaa 960

aaaatcccga gtactggttt gtgagcggat ccggtccttc tgtttgttcc aatataaatg 1020

actttgaagg gattccctat ctcaaggacg ttctgaagct gagggtgaac aacaggggga 1080

tgatagtttc agaatagtaa ggctgagatc ttcttcagtg cattgtagtt gaatgaaggg 1140

ttaggggggа aatgcccccc tatttttttgt ctagccatcc tgccacgttt gacagggtag 1200

caatttcgac acgatagggt tctctcttct gccgtta 1237

<210> SEQ ID NO 80
<211> LENGTH: 1438
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 80, Example 80: a designer nirA-promoter-controlled Threonine Synthase DNA construct (1438 bp)

<400> SEQUENCE: 80

agaaaatctg gcaccacacc tgacccccat cgagagactc cgaacgtggc aaatggaggg 60

accagagttg ttcagttcac aggtagataa tgtcgcgggt cttgatagtt agcaataaat 120

acagtttcag aatatctgta atacaaaaac tgtatcgaga caagaaaaaa gtagcaaaat 180

ttacaaatgt tcatgattca tctggctaaa ttggatgttc aactgaccca ttgaagacaa 240

gggcaacaac catgaaattg ggaatactcg aaaagtacag agaatttctt cccgtaacag 300

acaaaacccc catgctctct ttgaatgaag ggaacactcc tctcataccc ctcgtgaaca 360

tgagcaggga actcggaata aacatctacg taaaatacga aggggccaat ccgacggggt 420

ccttcaaaga cagaggaatg gtcgttgccg tcgcaaaggc actggaagaa ggctcgaaag 480

ccatcatgtg cgcttcaacg gggaacacct ccgcatccgc tgccgcgtac gccgcaaggg 540

caggaataaa ggcgatcgtt ctgataccag aagggaagat cgcactcgga aagctggctc 600

aggcgatgat atacggcgcc gtggtgcttc aggtgagagg gaatttcgac aagtgtctgg 660

aactggtcaa ggagatcaca tccaaatatc ccatcacact cgtgaacagt atcaatccct 720

acagactcga aggtcagaaa acggccgctt ttgagatagt cgacgagctc ggagatgcac 780

cggactacca cttcatcccc gtgggaaacg cgggcaacat ctccgcttac tggatgggat 840

-continued

acaaggagta ttatcagcat gggttctcca ccaaactgcc gaagatgatg ggattccagg 900

cggaaggggc cgcccccata gttcgcggtc atcccataga aaacccggag acggtcgcca 960

ctgcaataag gatcggtaac cccgcgaact gggaaaaagc ggtccgggca cgcgatgaat 1020

cgggtggaga catcgacatg gtgagcgacg aagaaatact gcgcgcacag agactcttgg 1080

ctcagaaaga agggatcttc tgtgagcccg catccgctgc atcgatagcg gggcttttga 1140

agaagcacag acagggaatc ttcaggggtg gagagatcgt tgtgtgtacc ctcacaggga 1200

acggtttgaa agatccgaac atcgtcatct cacagcttga acccccaagg atcatagaag 1260

gaagagtaga agagattctg gaggtactcg acatatgata aggctgagat cttcttcagt 1320

gcattgtagt tgaatgaagg gttaggggggg aaatgccccc ctatttttttg tctagccatc 1380

ctgccacgtt tgacagggta gcaatttcga cacgataggg ttctctcttc tgccgtta 1438

<210> SEQ ID NO 81
<211> LENGTH: 1600
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 81, Example 81: designer nirA-promoter-controlled Threonine Ammonia-Lyase DNA construct (1600 bp)

<400> SEQUENCE: 81

agaaaatctg gcaccacacc tgacccccat cgagagactc cgaacgtggc aaatggaggg 60

accagagttg ttcagttcac aggtagataa tgtcgcgggt cttgatagtt agcaataaat 120

acagtttcag aatatctgta atacaaaaac tgtatcgaga caagaaaaaa gtagcaaaat 180

ttacaaatgt tcatgattca tctggctaaa ttggatgttc aactgaccca ttgaagacaa 240

gggcaacaac catgttgaca ttagcagaca ttgaacaagc gcgagcgaaa atgaaaggca 300

tcgtccatca aacgccgctt gagcattcgc aaacgttcag ccggctgtct ggcaatgatg 360

tatatatgaa actcgaaaat ttgcaaaaaa cgggctcgtt taaagtaaga ggttcattca 420

ataaaattat gtcgctcacg gaagaagaga gggcgcgcgg cgtcatcgcc gcttcggccg 480

gcaaccacgc ccaaggggtc gcctatgcga gcggcatgct tcatattccg tgcacgatcg 540

tcatgccaaa aggcgcgccg ctcagcaaaa ttgaagcgac gaaaagctac ggggcggaag 600

tcgtgctgta cggcgatgtg tttgacgagt ctttggaata tgcgttagag ttgcagcgtg 660

aacgggggat gacgtttgtt catccgtttg acgacttggc ggtgatggcc ggccaaggga 720

cgatcggctt agagctgatc gagcagcttc ccgacgtcga tgtcgttctt tgtccagtcg 780

gcggcggcgg gttgcttgcg ggggtggcgc ttacgttaaa acagctgaag ccgtcggttg 840

aagtgtacgg cgttgagtca tcggcttgcc ccggcatgac ggcggccata cgccataaac 900

agcccgtctc cattgccgca tcgaatacga tcgccgatgg gattgccgtg aaaaagccgg 960

gcaatattac gtaccaatac attgagcaat acgtcgatgg cgttgtatgc gtggaagagg 1020

cggaaatttc gcggacgatg ctgtatgtgc tcgagcggaa caagctgttg atcgaagggg 1080

cggcagcttg tccgctggcg gcattgttgt atcaaaagct gccgtttcgc ggcaaaaaag 1140

tcgccgccat tttaagcggc ggcaacgtcg atgtgacgct catttcccgc atcatcgagc 1200

gggggctcgt cgaagccggg cgattcgtta cgtttacaac ggtcatctcc gacaagccgg 1260

gccagttgaa caagctgctg cgcattattg cggagcttga ggcaaacgtg atgtcgattc 1320

-continued

atcatcagcg catcggcgcc aaagtgctgc caggtcaggc ggaaattcac ttttcgctcg 1380

agacaaaaaa cgaagaccac attcagcaaa tctaccaagt gttgttgaaa gaaggctacg 1440

atgtacagtt ttaccgatga taaggctgag atcttcttca gtgcattgta gttgaatgaa 1500

gggttagggg ggaaatgccc ccctattttt tgtctagcca tcctgccacg tttgacaggg 1560

tagcaatttc gacacgatag ggttctctct tctgccgtta 1600

<210> SEQ ID NO 82
<211> LENGTH: 2107
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 82, Example 82: designer nirA-promoter-controlled Acetolactate Synthase DNA construct (2107 bp)

<400> SEQUENCE: 82

agaaaatctg gcaccacacc tgacccccat cgagagactc cgaacgtggc aaatggaggg 60

accagagttg ttcagttcac aggtagataa tgtcgcgggt cttgatagtt agcaataaat 120

acagtttcag aatatctgta atacaaaaac tgtatcgaga caagaaaaaa gtagcaaaat 180

ttacaaatgt tcatgattca tctggctaaa ttggatgttc aactgaccca ttgaagacaa 240

gggcaacaac catgttgaca aaagcaacaa aagaacaaaa atcccttgtg aaaaacagag 300

gggcggagct tgttgttgat tgcttagtgg agcaaggtgt cacacatgta tttggcattc 360

caggtgcaaa aattgatgcg gtatttgacg ctttacaaga taaaggacct gaaattatcg 420

ttgcccggca cgaacaaaac gcagcattca tggcccaagc agtcggccgt ttaactggaa 480

aaccgggagt cgtgttagtc acatcaggac cgggtgcctc taacttggca acaggcctgc 540

tgacagcgaa cactgaagga gaccctgtcg ttgcgcttgc tggaaacgtg atccgtgcag 600

atcgtttaaa acggacacat caatctttgg ataatgcggc gctattccag ccgattacaa 660

aatacagtgt agaagttcaa gatgtaaaaa atataccgga agctgttaca aatgcattta 720

ggatagcgtc agcagggcag gctggggccg cttttgtgag ctttccgcaa gatgttgtga 780

atgaagtcac aaatacgaaa aacgtgcgtg ctgttgcagc gccaaaactc ggtcctgcag 840

cagatgatgc aatcagtgcg gccatagcaa aaatccaaac agcaaaactt cctgtcgttt 900

tggtcggcat gaaaggcgga agaccggaag caattaaagc ggttcgcaag cttttgaaaa 960

aggttcagct tccatttgtt gaaacatatc aagctgccgg tacccttttct agagatttag 1020

aggatcaata ttttggccgt atcggtttgt tccgcaacca gcctggcgat ttactgctag 1080

agcaggcaga tgttgttctg acgatcggct atgacccgat tgaatatgat ccgaaattct 1140

ggaatatcaa tggagaccgg acaattatcc atttagacga gattatcgct gacattgatc 1200

atgcttacca gcctgatctt gaattgatcg gtgacattcc gtccacgatc aatcatatcg 1260

aacacgatgc tgtgaaagtg gaatttgcag agcgtgagca gaaaatcctt tctgatttaa 1320

aacaatatat gcatgaaggt gagcaggtgc ctgcagattg gaaatcagac agagcgcacc 1380

ctcttgaaat cgttaaagag ttgcgtaatg cagtcgatga tcatgttaca gtaacttgcg 1440

atatcggttc gcacgccatt tggatgtcac gttatttccg cagctacgag ccgttaacat 1500

taatgatcag taacggtatg caaacactcg gcgttgcgct tccttgggca atcggcgctt 1560

cattggtgaa accgggagaa aaagtggttt ctgtctctgg tgacggcggt ttcttattct 1620

cagcaatgga attagagaca gcagttcgac taaaagcacc aattgtacac attgtatgga 1680

-continued

acgacagcac atatgacatg gttgcattcc agcaattgaa aaaatataac cgtacatctg 1740

cggtcgattt cggaaatatc gatatcgtga aatatgcgga aagcttcgga gcaactggct 1800

tgcgcgtaga atcaccagac cagctggcag atgttctgcg tcaaggcatg aacgctgaag 1860

gtcctgtcat catcgatgtc ccggttgact acagtgataa cattaattta gcaagtgaca 1920

agcttccgaa agaattcggg gaactcatga aaacgaaagc tctctagtaa ggctgagatc 1980

ttcttcagtg cattgtagtt gaatgaaggg ttaggggga aatgcccccc tatttttgt 2040

ctagccatcc tgccacgttt gacagggtag caatttcgac acgatagggt tctctcttct 2100

gccgtta 2107

<210> SEQ ID NO 83
<211> LENGTH: 1405
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 83, Example 83: designer nirA-promoter-controlled Ketol-Acid Reductoisomerase DNA construct (1405 bp)

<400> SEQUENCE: 83

agaaaatctg gcaccacacc tgacccccat cgagagactc cgaacgtggc aaatggaggg 60

accagagttg ttcagttcac aggtagataa tgtcgcgggt cttgatagtt agcaataaat 120

acagtttcag aatatctgta atacaaaaac tgtatcgaga caagaaaaaa gtagcaaaat 180

ttacaaatgt tcatgattca tctggctaaa ttggatgttc aactgaccca ttgaagacaa 240

gggcaacaac catgttttac ctctttaagc caaggcatca tcgccctaag ttccttacct 300

acttttttcta tcaggtgctc ctgccctttc ctccgcaagg cactgaagac cggacggccc 360

acttggaatt cgagcaagag ctcccgggca aaagttccat cctggatggc agccaaaacc 420

tttttcatct cagccctggt gttttcgttt attatgcgcg gacctaccgt gaggtcgccg 480

tactcagcgg tatcactgac cgagtaccgc ataaggccga taccgccttc gtatataagg 540

tctactatga gcttaagctc gtgcaggcac tcgaaatagg ctatctccgg ctggtatcct 600

gcctctacca aggtatcaaa accggcttta ataagttcag tgaccccgcc acagagcaca 660

cattgttctc cgaataggtc ggtctcggtt tcttctttaa aagtagtagc gatgacacct 720

gcacgggtac agccgatacc tttagcatag gctaaccccg tttccaaggc tttccccgta 780

tggtcattat gtacggctat gagcccgggg actcccactc cttgcctgta catacgcctg 840

accagatgac caggactctt aggcgctacc atgaagacat cgacggaagg cggaggcaca 900

atttgcccga aatgtatgtt gaacccatga gaaaatccca acgcatcgcc ttcgttaagg 960

taaggttcga tcttttcccg gtaaaccttg gcctggatat catccggcac caaaatctgg 1020

attatctggg cagctcgggc cgcttcatct accggtaaag gcgtaagccc gtcggctaca 1080

acctgattcc actccgcagt ggtaaaatcg tcctccggct tacgcaaccc taccaccact 1140

tcgagaccac tgtcgtgaag gttctgggcc tgagcgtgtc cctggctgcc ataaccgatc 1200

acggcaatgg tcttgccttt aagcaggtca aggtttgcat cagcatcata atacatccta 1260

gccattaagg ctgagatctt cttcagtgca ttgtagttga atgaagggtt agggggggaaa 1320

tgccccccta ttttttgtct agccatcctg ccacgtttga cagggtagca atttcgacac 1380

gatagggttc tctcttctgc cgtta 1405

-continued

<210> SEQ ID NO 84
<211> LENGTH: 2056
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 84, Example 84: designer nirA-promoter-controlled Dihydroxy-Acid Dehydratase DNA construct (2056 bp)

<400> SEQUENCE: 84

agaaaatctg gcaccacacc tgacccccat cgagagactc cgaacgtggc aaatggaggg 60

accagagttg ttcagttcac aggtagataa tgtcgcgggt cttgatagtt agcaataaat 120

acagtttcag aatatctgta atacaaaaac tgtatcgaga caagaaaaaa gtagcaaaat 180

ttacaaatgt tcatgattca tctggctaaa ttggatgttc aactgaccca ttgaagacaa 240

gggcaacaac catggggctt cctgaagatt gccccccttgc tcgccgactg tacgaagaat 300

gcgtaccttc tcaggtaatc gctgtccact tctttcacca gaggcgtgaa ctctttcatt 360

cttctttcga actcttcgtc tgagatcaag agattcaggg ttctcttttc aaaatctatc 420

tcgatgaggt ccccgtcttt cacgatacct ataggaccgc cttctgccgc ttctggagaa 480

acgtgaccta tcacggcacc gtgcgatcca cccgagaacc taccgtctgt gatgagagcc 540

acgtcctccg caaggcccat ccccacgatg gcggaggtgg gtgagagcat ctctctcatc 600

ccgggaccgc ccttcggccc ttcgtagcgg atcacaacca catctccttt tttgatcttt 660

ccagatagaa tggcttttgt cgcctcttct ccgtcttcaa agacgacggc cgggccaacg 720

tggtgcatca tcttctcggg aacaccggag agtttggcaa ccgctccttc tggagcgagg 780

ttcccgaaga ggataccgag tccgccctct ttgtggtacg gattatcgaa gggcctgatc 840

acatcttcat tcaggatctt agcctctctg acgagatctc caatctttct caaatagatg 900

gtcatggcgt cttccttcaa aagaccattt tcctggagac gtttcatcac agcgtagata 960

ccaccagcat cgtcgagatc ctggatgtgg tacggaccaa cgggagagat gttgcagatg 1020

tgaggaatct tcctgctgag ttcgtcaaag agctttatat cgaaatctat tccaaaactc 1080

tcggctatcg ccttcaaatg cagaactgtg ttcgtggaac ctcccgttgc gaggtccacc 1140

atgacagcgt tcatgaaaga gtccagagtg acgatatccc ttggttttac atctcttttc 1200

acgagttcca caacgagcat ccccgcttct ttcgccattc tcaacctctt cgcgtggacg 1260

gccggtacag tcccattccc cctcggtgca attccgagag cttccgccag agagttcatc 1320

gtgttcgcgg tgaacaatcc agcacacgaa ccggcaccgg gacacgcgag gtcttctatc 1380

gctttgagcg tttcttcatc gacttttccc actttgtatc caccaaccgc ttcgaagacg 1440

gtgatgagat cgatgtctct gccgttgtag cgacctgcga gcatgggacc gccggatatc 1500

agaacggacg ggatgttcaa tcttcccatg gccatcatca tgccgggtgt gatcttgtcg 1560

cagttgggga cgaagaccaa accatcgaag gggaaaccgc ttgcaacgat ctctatggag 1620

tccgctatga gttccctcga gggcaaggaa aacttcatcc ccctgtgatc cattgctatt 1680

ccgtcacaga tcccgatcgt tggaaagacg aagggaactc ccccggccat tctcacaccg 1740

gctttcaccg cttcaacgac cttgtcaagg tggacatggc cgggaatgat ctcgttccac 1800

gaggacacta tgccgatgaa aggccttcgc atttcgtcgt ccgttattcc gagcgctttc 1860

aaaagtgatc tatggggagc cctttcgaga cctttcttta tcacatcact cctcattaag 1920

gctgagatct tcttcagtgc attgtagttg aatgaagggt taggggggaa atgccccct 1980

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atttttgtc tagccatcct gccacgtttg acagggtagc aatttcgaca cgatagggtt 2040

ctctcttctg ccgtta 2056

<210> SEQ ID NO 85
<211> LENGTH: 1360
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 85, Example 85: designer nirA-promoter-controlled 2-Methylbutyraldehyde Reductase DNA construct (1360 bp)

<400> SEQUENCE: 85

agaaaatctg gcaccacacc tgacccccat cgagagactc cgaacgtggc aaatggaggg 60

accagagttg ttcagttcac aggtagataa tgtcgcgggt cttgatagtt agcaataaat 120

acagtttcag aatatctgta atacaaaaac tgtatcgaga caagaaaaaa gtagcaaaat 180

ttacaaatgt tcatgattca tctggctaaa ttggatgttc aactgaccca ttgaagacaa 240

gggcaacaac catggcttct gtaaatgact actttgagaa cgccaagacg acgtacttta 300

ctttgagatc gggtgacaag atccccgctg ttggattggg tacttggcaa tcacccacca 360

acgagactaa agaggcagtc aagtacgctt tgcagcacgg ttaccgtcac atcgatgctg 420

ccgccattta tggtaacgaa gacgaggttg gtgacggtat caaggagagt ggaatccctc 480

gtgaccaaat ctgggtcaca tctaagctct ggtgcaatgc tcatgctccc gaggctgtcc 540

ccaaggcttt ggagaagacc ttgcgtgagc tgaaacttga ttaccttgac ctttacctca 600

tccactggcc tatttctttg aagaccggcg atgacttggt tcccaaggac aaggacggca 660

acaccatcac tgtcgaaatt cccctcgagg acacctggaa ggctatggag ggtcttgtga 720

agtccggcaa ggtgaagaac attggtattt ccaatttcaa caacgaagag ttggatcgta 780

ttttgaaggt tgccgagatt cctcctgccg tccaccaaat ggaaactcat ccttacttga 840

agcagacgga gttcattgag aagcacaaga agcttggcat tcacgtcacc gcttactcgc 900

ctttggccaa ccaaaatgct ctttacggca atgccgttcc caagttgatt gagcacaaga 960

ctcttgtcga cattgccaag accaagggtg agggcgtcac tggtgccaac attgctattt 1020

cttgggcagt caagcgcggt acttcggtta ttcctaagtc tgttcatgcc aacagaatta 1080

agagcaactt cctcgttgtt cccttgactg atgacgagat gaaggccatc gataacattg 1140

gtgtcagcaa gcgtttcaat tggagcaaag ttttctgcaa tgagaattgt ttctacggtc 1200

ttgaggatgg tcctcagtaa taaggctgag atcttcttca gtgcattgta gttgaatgaa 1260

gggttagggg ggaaatgccc ccctattttt tgtctagcca tcctgccacg tttgacaggg 1320

tagcaatttc gacacgatag ggttctctct tctgccgtta 1360

<210> SEQ ID NO 86
<211> LENGTH: 1420
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 86, Example 86: designer nirA-promoter-controlled 3-Methylbutanal Reductase DNA construct (1420 bp)

<400> SEQUENCE: 86

agaaaatctg gcaccacacc tgacccccat cgagagactc cgaacgtggc aaatggaggg 60

-continued

accagagttg ttcagttcac aggtagataa tgtcgcgggt cttgatagtt agcaataaat 120

acagtttcag aatatctgta atacaaaaac tgtatcgaga caagaaaaaa gtagcaaaat 180

ttacaaatgt tcatgattca tctggctaaa ttggatgttc aactgaccca ttgaagacaa 240

gggcaacaac catgtcagtt ttcgtttcag gtgctaacgg gttcattgcc caacacattg 300

tcgatctcct gttgaaggaa gactataagg tcatcggttc tgccagaagt caagaaaagg 360

ccgagaattt aacggaggcc tttggtaaca acccaaaatt ctccatggaa gttgtcccag 420

acatatctaa gctggacgca tttgaccatg ttttccaaaa gcacggcaag gatatcaaga 480

tagttctaca tacggcctct ccattctgct ttgatatcac tgacagtgaa cgcgatttat 540

taattcctgc tgtgaacggt gttaagggaa ttctccactc aattaaaaaa tacgccgctg 600

attctgtaga acgtgtagtt ctcacctctt cttatgcagc tgtgttcgat atggcaaaag 660

aaaacgataa gtctttaaca tttaacgaag aatcctggaa cccagctacc tgggagagtt 720

gccaaagtga cccagttaac gcctactgtg gttctaagaa gtttgctgaa aaagcagctt 780

gggaatttct agaggagaat agagactctg taaaattcga attaactgcc gttaacccag 840

tttacgtttt tggtccgcaa atgtttgaca aagatgtgaa aaaacacttg aacacatctt 900

gcgaactcgt caacagcttg atgcatttat caccagagga caagataccg gaactatttg 960

gtggatacat tgatgttcgt gatgttgcaa aggctcattt agttgccttc caaaagaggg 1020

aaacaattgg tcaaagacta atcgtatcgg aggccagatt tactatgcag gatgttctcg 1080

atatccttaa cgaagacttc cctgttctaa aaggcaatat tccagtgggg aaaccaggtt 1140

ctggtgctac ccataacacc cttggtgcta ctcttgataa taaaaagagt aagaaattgt 1200

taggtttcaa gttcaggaac ttgaaagaga ccattgacga cactgcctcc caaattttaa 1260

aatttgaggg cagaatataa taaggctgag atcttcttca gtgcattgta gttgaatgaa 1320

gggttagggg ggaaatgccc ccctattttt tgtctagcca tcctgccacg tttgacaggg 1380

tagcaatttc gacacgatag ggttctctct tctgccgtta 1420

<210> SEQ ID NO 87
<211> LENGTH: 1540
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 87, Example 87: designer nirA-promoter-controlled 3-Ketothiolase DNA construct (1540 bp)

<400> SEQUENCE: 87

agaaaatctg gcaccacacc tgacccccat cgagagactc cgaacgtggc aaatggaggg 60

accagagttg ttcagttcac aggtagataa tgtcgcgggt cttgatagtt agcaataaat 120

acagtttcag aatatctgta atacaaaaac tgtatcgaga caagaaaaaa gtagcaaaat 180

ttacaaatgt tcatgattca tctggctaaa ttggatgttc aactgaccca ttgaagacaa 240

gggcaacaac catgcgtgaa gcggtcattg tcgaagcggt caggacgccg gtcggcaagc 300

ggaacggcgt cttccgggac gttcatccgg tccatttggc cgcggtggtg ctcgatgaag 360

tcgtgcgccg ggccggcatg gacaaagggg cggtggaaga catcgtcatg ggctgcgtga 420

cgccggtcgc cgaacaaggg tacaacatcg gccggctggc ggcgcttgag gccggattcc 480

cgatcgaagt gccggcagtg caaatcaacc gaatgtgcgg ctcggggcag caggcgattc 540

atttcgccgc ccaggaaatc cgctccggcg atatggatgt cacgatcgcc gccggggtcg 600

-continued

aaagcatgac gaaagtgccg attttaagcg atggcaacga gcggacgatt ccgccgtcgc 660

tgcatgaaaa atacgaattc atccaccaag gcgtctcggc tgagcggatc gccaaaaaat 720

acggcctaac gcgcgaggag cttgacgcct acgcgtacga aagccatcaa cgcgccttgg 780

cggccttgcg cgaagggaag tttcgcgcgg aaatcgtccc ggtgaaaggg cttgaccgcg 840

atggccgcga aatccttgtc accgatgatg aagggccgcg ggccgacaca tcgccggaag 900

cgctcgccgc gctcaagccg gtgtttcaag aagacggtct catcaccgct ggcaatgcga 960

gccaaatgag cgacggggcg gccgctgtgc ttttgatgga acgggaggcg gcgaggcggt 1020

tcggactgaa gccgaaagcg cgcattgtcg cgcaaacggt cgtcggctcc gacccgacgt 1080

atatgctcga tggcgtcatt ccggcgacga ggcaagtgct gaaaaaagcc ggcctctcga 1140

tcgatgacat cgacctcatt gaaatcaacg aagcgttcgc cccggtcgtg ctcgcctggc 1200

aaaaagaaat cggcgctccg cttgagaagg tgaatgtcaa cggcggcgcc attgcgcttg 1260

gccatccgct cggcgccacc ggtgcgaagc tcatgacgtc gcttgttcat gaacttgaac 1320

ggcgcggcgg ccgctatggg ctattgacga tttgcatcgg ccacgggatg gcgacggcca 1380

cgatcatcga gcgggagtaa taaggctgag atcttcttca gtgcattgta gttgaatgaa 1440

gggttagggg ggaaatgccc ccctattttt tgtctagcca tcctgccacg tttgacaggg 1500

tagcaatttc gacacgatag ggttctctct tctgccgtta 1540

<210> SEQ ID NO 88
<211> LENGTH: 1231
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 88, Example 88: designer nirA-promoter-controlled 3-Hydroxyacyl-CoA Dehydrogenase DNA construct (1231 bp)

<400> SEQUENCE: 88

agaaaatctg gcaccacacc tgacccccat cgagagactc cgaacgtggc aaatggaggg 60

accagagttg ttcagttcac aggtagataa tgtcgcgggt cttgatagtt agcaataaat 120

acagtttcag aatatctgta atacaaaaac tgtatcgaga caagaaaaaa gtagcaaaat 180

ttacaaatgt tcatgattca tctggctaaa ttggatgttc aactgaccca ttgaagacaa 240

gggcaacaac catgatactt aaagaaacct tctccggtct tacgccccag cttccctgca 300

cggaccatct taaccaagag cgggcaagga cgatacttgt catcgccaaa ctcgcgatgc 360

aaagtctgca tgatagccaa acatatatct agcccaatca tgtctgctaa agcgagggga 420

cccataggat gccctgctcc gagcttcatg gaggtatcca cgtcctcggg gcttgcaacc 480

ccctccatga cggcatacat accttcgttc agcattggaa taagcaggcg gttgacaaca 540

aagccaggag cttcgttgat ctcaaccggg gtcttgccca gcttaattga aagatccttg 600

atggtattaa aagtttcctg gctagtagaa gccccttga taatctcgat aagcttcatt 660

gccggtaccg ggttgaagaa atgcatgcct attaccctgt ctgcccgctt ggttgctgct 720

cctatctcgg ttatgctcag agctgatgtg ttagaagcca ggatacattc aggcttgcag 780

atctcgtcca gttccttgaa aatcgctttt ttgatgtcca tattctcgat agcagcttca 840

attaccacat ccacatcttt ggccgcagcc atgtcgaccg taccgctaat cctggccatc 900

accgcgttct tgtcatctgc gctcatcttg ccctttttcga ccattttgct gagacccttg 960

-continued

tcgatgcctt ttataccatt gtcaacaaac tcttgtttaa tatcacgtac gattacttcg 1020

aacccagctt gagcagcgac ttgaacaatc ccagctccca tagtacctgc gcctaaaacc 1080

attattttca ttaaggctga gatcttcttc agtgcattgt agttgaatga agggttaggg 1140

gggaaatgcc cccctatttt ttgtctagcc atcctgccac gtttgacagg gtagcaattt 1200

cgacacgata gggttctctc ttctgccgtt a 1231

<210> SEQ ID NO 89
<211> LENGTH: 1162
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 89, Example 89: designer nirA-promoter-controlled Enoyl-CoA Dehydratase DNA construct (1162 bp)

<400> SEQUENCE: 89

agaaaatctg gcaccacacc tgacccccat cgagagactc cgaacgtggc aaatggaggg 60

accagagttg ttcagttcac aggtagataa tgtcgcgggt cttgatagtt agcaataaat 120

acagtttcag aatatctgta atacaaaaac tgtatcgaga caagaaaaaa gtagcaaaat 180

ttacaaatgt tcatgattca tctggctaaa ttggatgttc aactgaccca ttgaagacaa 240

gggcaacaac catgacggtt cgactggaat acgatggcgg gttcgcgcac ctgacgctca 300

gccgcccgca ggtcctgaat gcgctcagtt tcgagctgct cgccgagttg agccgggcgc 360

ttgccggcgt cgccgaatcc gatgcgcgcg ccctgatcgt cacgggcgag ggcgacaagg 420

cgttctgcgc cggcgcggac attcccgagc tgatgaatcg gccgctcatg caagagctcg 480

aaggggccgc gaaaggccag gcggtgttca gccggatcgc cgagctgaag attccgtctg 540

tcgccgtcat ccagggttat gccttcggcg gcgggctgga gcttgccctg gcatgcacat 600

tccgcgttgc cactgatcgc gcccgcatgg ggctgcccga ggtcaagctc ggcctgatcc 660

cgggttatgg cggaacgcag cgtctgccga ggctgatcgg cgaggggcgc gcactcgacc 720

tgatcatgtc cggccgcacg atagacggcg gggaagccga gcgaatcggc ctggtcaatc 780

gcatagacaa cgaggggacg cccctggaga tcggcaagcg gtttctggag ccttatctca 840

agcacagtct ctgcgccttg tattttgccc gcgaggccgt gcagagggga ggcggtgtcg 900

ccattgcgga tggcctgcgc atcgagcggg atctttccac gctggcttac cggagccagg 960

atgcggccga ggggctgcgc gcttttgtgg aaaaacggcc cgcgtctttc aaggactgct 1020

gataaggctg agatcttctt cagtgcattg tagttgaatg aagggttagg ggggaaatgc 1080

ccccctattt tttgtctagc catcctgcca cgtttgacag ggtagcaatt tcgacacgat 1140

agggttctct cttctgccgt ta 1162

<210> SEQ ID NO 90
<211> LENGTH: 1561
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 90, Example 90: designer nirA-promoter-controlled 2-Enoyl-CoA Reductase DNA construct (1561 bp)

<400> SEQUENCE: 90

agaaaatctg gcaccacacc tgacccccat cgagagactc cgaacgtggc aaatggaggg 60

accagagttg ttcagttcac aggtagataa tgtcgcgggt cttgatagtt agcaataaat 120

-continued

acagtttcag aatatctgta atacaaaaac tgtatcgaga caagaaaaaa gtagcaaaat 180

ttacaaatgt tcatgattca tctggctaaa ttggatgttc aactgaccca ttgaagacaa 240

gggcaacaac catggccggc gcgcagcagg atcttgccgc tgcgtccggg cttgtcgctg 300

gccgcggcgg ccttggcggc atcgtgcagg tcgaacaccg cttccaccgg cagcgccagg 360

ctgccatcga gcgcggcggt gagcagttcg ccgatcatgc ggcgcttgtc ctcggccttg 420

gtggcctgca tcaccttgct gccccagaag ccacgcacgg tggcctgctt gaagatcaca 480

tcgccgctgg atatctgcag cggctcgccg gtcatcgagc caaaggaaat cagctcgccg 540

ccttcggcca gcaaggccat cagctcaccc gctgcattgc cggccaccga atcgatggcg 600

cgcacgatgg gcgcatcgcc ggccagcgcg cgcaccttgt cctgccagcc tgcttgcgca 660

gtggagattg cgttgccgat gcccagcgct ttcagctcgt ccacgccggc gtcgcggcgc 720

accaggttga tcacgttgat gccgcgtgcg gcggcgagca tcgccaccgt cttgccgacc 780

gcaccgttgg cggtgttctg cacgatccag tcgccctgtt tcacctgcag gaattcgatc 840

agcatcagcg cgctcagcgg catggcgatc aactggcaac cacgctcgtc gtccaggcca 900

tccggcaacg gcaccacgcc ggaggcgtcg gcaaggaagt actcggccca ggcctcatgc 960

acaccggcgg cgaccacgcg ctggccaacc tgcaagccct cgacaccctc acccagcgca 1020

tcgatgacac ccgccgcttc gctgccgccg atggctggca gttccggctt gtagccgtaa 1080

ttgccgcgca cggtccacag gtcatggtta tggatcggcg cgcgccgcat cgcaacgcgc 1140

acctggccct tgcctggctg cggcgtgggg cgctcgccca gttcgagcac cttggccgga 1200

tcgccgaatt gggtatggat ggctgcgcgc atggaggtct cctgccgggc acgctcttgc 1260

tgcgacgcgc ccgatcgttg tgaaaggtgg cgcgatgcta tcggcagggc tgcaaggaag 1320

ggatgaagcg aacggaactg ctgtgtgaag ttgttggcgt gcgcgcgtag tgacgatgct 1380

ctgctgcagc gccggaggac tgcgtgcagg ccgaccctca ttaaggctga gatcttcttc 1440

agtgcattgt agttgaatga agggttaggg gggaaatgcc cccctatttt ttgtctagcc 1500

atcctgccac gtttgacagg gtagcaattt cgacacgata gggttctctc ttctgccgtt 1560

a 1561

<210> SEQ ID NO 91
<211> LENGTH: 1747
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 91, Example 91: designer nirA-promoter-controlled Acyl-CoA Reductase DNA construct (1747 bp)

<400> SEQUENCE: 91

agaaaatctg gcaccacacc tgacccccat cgagagactc cgaacgtggc aaatggaggg 60

accagagttg ttcagttcac aggtagataa tgtcgcgggt cttgatagtt agcaataaat 120

acagtttcag aatatctgta atacaaaaac tgtatcgaga caagaaaaaa gtagcaaaat 180

ttacaaatgt tcatgattca tctggctaaa ttggatgttc aactgaccca ttgaagacaa 240

gggcaacaac catgtagttg tctactaact acgtaagtca tttcctgcaa attgtgcatt 300

ccatcatgag aagttcctgg ataatgtgct ggcatttccc ctggcttagt gactatgctt 360

acaccaagta acgtcatttt ttcaataaat tcgtggtcgt caccactata ccccatagtt 420

-continued

tgaaggaatt gctttaaatt ttcttcaaca taatcatgta cttcatcttt attttcatat 480

gggcaaacaa atataagtct attaaagcat ctatcaatat ccttttttttc aggcattctg 540

ttgcttaaaa tcacagtata gtcggcatta cacgatgcaa acacctttgc cggtttctcc 600

tcatcaacac tatattttaa taaacaatac tgtcggtctt gtattgattt catagaactc 660

caaggactca gatatgcctt tgggaaaacc tctgtaagct ctttcaagct ttctgctaca 720

gtttctgcaa gaatattaat gtctattttt ttattggcaa ataccatcct aggagacaaa 780

caggcttttt gctcccaaca tatcacatca ctagcaatac cttttgcaat agtcttaata 840

tcttctactt tatctataac ttcaaaacta attttagcac catgcattat taaatgagaa 900

ttatattttg cacataactc tgccattatc cttcctgaat attctccacc ccaatgtata 960

acacaatcca tttctctcac gacagtctca tatatatcag aacattcact actaaagtat 1020

aaaacagata gtctatcttt tatacttgga tcaagctgta ccaaactttc atagaaagca 1080

tacgcaaaat atggttcatc agcagaaacc tttactaaat tacagttctt tgataataac 1140

cccataccta tacttgtcgg aacaactaca aatgcatttc cagaaatatt atgaaacatc 1200

acacctcttg gctgtctatg cacagctcca taacttgttg gaacccaatt atctagtata 1260

tcaatgttac caagttcttc tttaatgatt atctcaagat tttctcttaa aagcattctc 1320

atactatttt caagttcata tgttacaagt tcttcacttt gattcaatat gttagctaat 1380

ctttctatat gtactttgga gtatcctcta tcaagccaca atcttccaca cctatccaaa 1440

agatcaattg tatcctgcac tgatattgca tgactcttac ttttactttt tctaagtctt 1500

tttatttcct caattacctg atctctactt gagtaagtta attctaattc caggccattt 1560

atattcttta ttaaaacatt actttcacaa acagtttcgc tcttcattaa ggctgagatc 1620

ttcttcagtg cattgtagtt gaatgaaggg ttaggggga aatgcccccc tatttttgt 1680

ctagccatcc tgccacgttt gacagggtag caatttcgac acgatagggt tctctcttct 1740

gccgtta 1747

<210> SEQ ID NO 92
<211> LENGTH: 1450
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 92, Example 92: designer nirA-promoter-controlled Hexanol dehydronase DNA construct (1450 bp)

<400> SEQUENCE: 92

agaaaatctg gcaccacacc tgacccccat cgagagactc cgaacgtggc aaatggaggg 60

accagagttg ttcagttcac aggtagataa tgtcgcgggt cttgatagtt agcaataaat 120

acagtttcag aatatctgta atacaaaaac tgtatcgaga caagaaaaaa gtagcaaaat 180

ttacaaatgt tcatgattca tctggctaaa ttggatgttc aactgaccca ttgaagacaa 240

gggcaacaac catggaactc gacctcgacg gtcccggggt tggtgaagtg ctgatcaagt 300

acaccgccgc ggggttgtgc cattcggacc tgcacttgac cgacggggac ctaccgccgc 360

gctatccaat cgtcgggggg cacgaggggt caggcatcat cgaggacgtc ggacctgggg 420

tcaccaaggt caaaccaggc gatcacgttg tttgcagctt catcccgaac tgcggaacct 480

gtcggtactg cgccaccgga cgctccaacc tctgcgatat gggcgccacc atcctcgaag 540

ggtgcatgcc cgacggcagt taccggttcc acagtaacgg cctggatttc ggtgcgatgt 600

-continued

gcatgctcgg cacattctcc gaacgcgcaa ctatctccca gcattcggtg gtcaagatcg 660

acgactggct gccgctcgag accgcggtgg tcgtcggctg cggcgtgccg actggctggg 720

gcacctccgt ctatgccggc ggggttcgtt gcggtgacac caccgtcatc tatggcgtcg 780

gcggcctggg agtcaacgcc gtccaaggcg cggtgagtgc gggcgcgaag tacatcgtgg 840

tcgtcgatcc ggttgcgttc aaacgcgaca ccgcgctcaa gttcggcgcc acccacgcgt 900

tcgccgacgc cgccaccgcc gcggccaagg tcgacgaact gacctgggga cagggtgccg 960

atcaggcgct gatcctggtc ggcaccgtcg acgaggacgt ggtctcggcg gcgactgcgg 1020

tgatcggtaa gggaggcacc gtcgtgatca ccggactggc ggacccagca aagctcacgg 1080

tgcacgtttc gggaacggac ctgacgctta acgagaagac aatcaagggc acgttgttcg 1140

gctcgtccaa tccgcaatac gacatcgtac ggctgctccg tctctacgac gccggccagc 1200

taaaactcga cgatctgatc accacccgat acacgctcga ccaggtcaac cagggctacc 1260

aggatctgcg agacggcaag aacatccgcg gcgtgatcat ccacgcctga taaggctgag 1320

atcttcttca gtgcattgta gttgaatgaa gggttagggg ggaaatgccc ccctattttt 1380

tgtctagcca tcctgccacg tttgacaggg tagcaatttc gacacgatag ggttctctct 1440

tctgccgtta 1450

<210> SEQ ID NO 93
<211> LENGTH: 1074
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 93, Example 93: designer nirA-promoter-controlled Octanol Dehydrogenase DNA construct (1074 bp)

<400> SEQUENCE: 93

agaaaatctg gcaccacacc tgacccccat cgagagactc cgaacgtggc aaatggaggg 60

accagagttg ttcagttcac aggtagataa tgtcgcgggt cttgatagtt agcaataaat 120

acagtttcag aatatctgta atacaaaaac tgtatcgaga caagaaaaaa gtagcaaaat 180

ttacaaatgt tcatgattca tctggctaaa ttggatgttc aactgaccca ttgaagacaa 240

gggcaacaac catgttggga ggccaagaag ccgctggtga ttgaggacat tgaggtggcg 300

ccacctcagg cttggcaggt tcgcatcaag attacagcca ctggcgtttg ccacacggat 360

tctttttcgt tgagcggctc tgatcctgag ggtctctttc ccgtggtcct tggccatgag 420

ggcgccggca tcgtggagag cgttggcgag ggcgtaacca actttaaggc cggcgatcat 480

gtcattgccc tctacatacc ccagtgcaat gagtgcaaat tctgcaagag cggcaagaca 540

aatctctgcc agaagattcg cctcacccag ggcgctggtg tcatgcccaa tggatcctcc 600

cgcttgtcgt gcaagggtca gcagctgttc catttcatgg gcacctcaac tttcgccgag 660

tacgcggtgg tggccgacat atcggtgacc aaaatcaacg agtcggctcc attggagaag 720

gtgtgccttc tgggctgtgg catttccacg ggctatggtg ccgccttgaa caccttttagg 780

tggaacctgg cagcacttgc gccgtctggg gtctgggtgc tgttggactg gcagtgggtc 840

tgggctgcaa gaaggctggc gccgccaagg tctacggcat cgacatcaat ccctccaaat 900

tcgagctggc caggaagttc ggcttcaccg actttaaggc tgagatcttc ttcagtgcat 960

tgtagttgaa tgaagggtta gggggggaaat gccccccctat tttttgtcta gccatcctgc 1020

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cacgtttgac agggtagcaa tttcgacacg atagggttct ctcttctgcc gtta 1074

<210> SEQ ID NO 94
<211> LENGTH: 1096
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 94, Example 94: designer nirA-promoter-controlled Short Chain Alcohol Dehydrogenase DNA construct (1096 bp)

<400> SEQUENCE: 94

agaaaatctg gcaccacacc tgacccccat cgagagactc cgaacgtggc aaatggaggg 60

accagagttg ttcagttcac aggtagataa tgtcgcgggt cttgatagtt agcaataaat 120

acagtttcag aatatctgta atacaaaaac tgtatcgaga caagaaaaaa gtagcaaaat 180

ttacaaatgt tcatgattca tctggctaaa ttggatgttc aactgaccca ttgaagacaa 240

gggcaacaac catgaaggtt gccgtaatta ctggggcatc ccgtggaatc ggggaagcta 300

tagcaaaggc ccttgctgaa gatggatatt cccttgcctt aggggctaga agtgttgata 360

ggttagagaa gattgccaag gaactcagcg aaaaacatgg ggtggaggta ttttacgact 420

acctcgatgt atcaaaacca gaaagcgttg aagagtttgc aaggaaaacg ctagctcact 480

ttggagatgt ggacgttgtt gtggccaatg cggggcttgg ttactttggt aggcttgaag 540

agcttacaga agagcagttc cacgaaatga ttgaagtaaa ccttttggga gtttggagaa 600

caataaaagc tttcttaaac tccttaaagc ggactggagg agtggctatt gttgttactt 660

cagatgtttc tgcaaggcta cttccatacg gtggaggtta tgtggcaact aaatgggctg 720

caagagcatt ggtaaggacc ttccagattg agaatccaga tgtgaggttc ttcgagctaa 780

gacctggagc agtagataca tattttggag ggagcaaagc tgggaagcca aaggagcaag 840

ggtatttaaa acctgaggaa gttgctgagg cagtaaaata cctcctaaga cttccaaagg 900

atgttagggt tgaggaatta atgttgcgct caatttatca aaaacctgag tattgataag 960

gctgagatct tcttcagtgc attgtagttg aatgaagggt taggggggaa atgccccct 1020

atttttgtc tagccatcct gccacgtttg acagggtagc aatttcgaca cgatagggtt 1080

ctctcttctg ccgtta 1096

<210> SEQ ID NO 95
<211> LENGTH: 1438
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 95, Example 95: designer Synechococcus sp. strain PCC 7942 nirA-promoter-controlled NADPH-dependent Glyceraldehyde-3-Phosphate-Dehydrogenase DNA construct (1438 bp)

<400> SEQUENCE: 95

agaaaatctg gcaccacacc cttcttgcag aacatgcatg atttacaaaa agttgtagtt 60

tctgttacca attgcgaatc gagaactgcc taatctgccg agtatatgat gtcaacgaat 120

attgcaatta atggaatggg tagaattgga agaatggtgc taagaatagc actaaagaat 180

gaagcattga atgtagttgc catcaatgct agctatcctc ctgaaacaat tgcacattta 240

attaattatg acacaacaca tgggagatac gataaaagag tagaacctat tgaaagtgga 300

attcgagtgg aaggccatga tattaaatta gtgtctgata gaaacccaga aaatttaccc 360

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tggaaagatt tagaaataga tatcgtcatt gaagcgaccg gtaaatttaa ccatggtgat 420

aaagctaagg cacatattca agcaggagct aaaaaagtgt tattgacagg accatcaaaa 480

ggcggaaaag tacagatggt ggttaaaggt gttaacgatc aagacttaga tacagataca 540

tatgacatat ttagtaatgc gtcgtgtact acgaattgta tcggaccagt tgcaaaagtt 600

ttaaatgata gttttggcat tgaaaatggc ttaatgacaa cggtacatgc aattacaaat 660

gatcaaaata atatagataa tccgcataaa gatttgagaa gagcgcgttc ttgtggggaa 720

agtattatac caacatcaac aggtgctgct aaagcattaa aagaagttat gccagaattg 780

aatggcaaac tacatggcat agcacttcgt gtgccaactc aaaatgtatc attagttgat 840

ttagtcattg atttaaaaca aaaagtgaca gtagatgaag ttaatcatgc atttagagat 900

gcaaacttac aaggaattat tgatgttgaa gaggcccctc tagtttctaa ggactataat 960

acaaatcctc attcagcagt tatagatgct aaaaatacaa tggtcatggg agataataag 1020

gttaaagtta tagcctggta tgataacgaa tggggatatt ctaatagagt agttgaggta 1080

gcaaatcaac ttggagaact aattaaataa taatagtgat cccggccgct actaaagcct 1140

gatttgtctt gatagctgct cctgcctttg ggcaggggct tttttctgtc tgccattctt 1200

gaggatggcg gactctttcc cttttgctct acgcccatga atgcgatcgc agtctcccct 1260

gtccagcacg ttggagtgat tggtggtggc cagttagctt ggatgctggc accagcagcg 1320

caacagttgg ggatgtcgct gcacgttcaa acacccaatg atcacgaccc agcagtagcg 1380

atcgcggatc aaaccgtatt agcagcagtt gctgacgcgg ttctctcttc tgccgtta 1438

<210> SEQ ID NO 96
<211> LENGTH: 1447
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 96, Example 96: designer Synechococcus sp. strain PCC 7942 nirA-promoter-controlled NAD-dependent Glyceraldehyde-3-Phosphate-Dehydrogenase DNA construct (1447 bp)

<400> SEQUENCE: 96

agaaaatctg gcaccacacc cttcttgcag aacatgcatg atttacaaaa agttgtagtt 60

tctgttacca attgcgaatc gagaactgcc taatctgccg agtatatgat ggcagtaaaa 120

gtagcaatta atggttttgg tagaattggt cgtttagcat tcagaagaat tcaagaagta 180

gaaggtcttg aagttgtagc agtaaacgac ttaacagatg acgacatgtt agcgcattta 240

ttaaaatatg acactatgca aggtcgtttc acaggtgaag tagaggtagt tgatggtggt 300

ttccgcgtaa atggtaaaga agttaaatca ttcagtgaac cagatgcaag caaattacct 360

tggaaagact taaatatcga tgtagtgtta gaatgtactg gtttctacac tgataaagat 420

aaagcacaag ctcatattga agcaggcgct aaaaaagtat taatctcagc accagctact 480

ggtgacttaa aaacaatcgt attcaacact aaccaccaag agttagacgg ttctgaaaca 540

gttgtttcag gtgcttcatg tactacaaac tcattagcac cagttgctaa agttttaaac 600

gatgactttg gtttagttga aggtttaatg actacaattc acgcttacac aggtgatcaa 660

aatacacaag acgcacctca cagaaaaggt gacaaacgtc gtgctcgtgc agcggcagaa 720

aacatcatcc ctaactcaac aggtgctgct aaagctatcg gtaaagttat tcctgaaatc 780

gatggtaaat tagatggtgg tgcacaacgt gttcctgtag ctacaggttc attaactgaa 840

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ttaacagtag tattagaaaa acaagacgta acagttgaac aagttaacga agctatgaaa    900

aatgcttcaa acgaatcatt cggttacact gaagacgaaa tcgtttcttc agacgttgta    960

ggtatgactt acggttcatt attcgacgct acacaaactc gtgtaatgtc agttggcgac   1020

cgtcaattag ttaaagttgc agcttggtat gataacgaaa tgtcatatac tgcacaatta   1080

gttcgtacat tagcatactt agctgaactt tctaaataat aatagtgatc ccggccgcta   1140

ctaaagcctg atttgtcttg atagctgctc ctgcctttgg gcaggggctt ttttctgtct   1200

gccattcttg aggatggcgg actctttccc ttttgctcta cgcccatgaa tgcgatcgca   1260

gtctcccctg tccagcacgt tggagtgatt ggtggtggcc agttagcttg gatgctggca   1320

ccagcagcgc aacagttggg gatgtcgctg cacgttcaaa cacccaatga tcacgaccca   1380

gcagtagcga tcgcggatca aaccgtatta gcagcagttg ctgacgcggt tctctcttct   1440

gccgtta                                                            1447
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<210> SEQ ID NO 97
<211> LENGTH: 2080
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 97, Example 97: designer Synechococcus sp. strain PCC 7942 nirA-promoter-controlled 2-Keto Acid Decarboxylase DNA construct (2080 bp)

<400> SEQUENCE: 97

```
agaaaatctg gcaccacacc cttcttgcag aacatgcatg atttacaaaa agttgtagtt     60

tctgttacca attgcgaatc gagaactgcc taatctgccg agtatatgat gtatacagta    120

ggagattacc tgttagaccg attacacgag ttgggaattg aagaaatttt tggagttcct    180

ggtgactata acttacaatt tttagatcaa attatttcac gcgaagatat gaaatggatt    240

ggaaatgcta atgaattaaa tgcttcttat atggctgatg gttatgctcg tactaaaaaa    300

gctgccgcat ttctcaccac atttggagtc ggcgaattga gtgcgatcaa tggactggca    360

ggaagttatg ccgaaaattt accagtagta gaaattgttg gttcaccaac ttcaaaagta    420

caaaatgacg gaaaatttgt ccatcataca ctagcagatg gtgattttaa acactttatg    480

aagatgcatg aacctgttac agcagcgcgg actttactga cagcagaaaa tgccacatat    540

gaaattgacc gagtactttc tcaattacta aaagaaagaa aaccagtcta tattaactta    600

ccagtcgatg ttgctgcagc aaaagcagag aagcctgcat tatctttaga aaaagaaagc    660

tctacaacaa atacaactga acaagtgatt ttgagtaaga ttgaagaaag tttgaaaaat    720

gcccaaaaac cagtagtgat tgcaggacac gaagtaatta gttttggttt agaaaaaacg    780

gtaactcagt ttgtttcaga aacaaaacta ccgattacga cactaaattt tggtaaaagt    840

gctgttgatg aatctttgcc ctcatttta ggaatatata acgggaaact ttcagaaatc    900

agtcttaaaa attttgtgga gtccgcagac tttatcctaa tgcttggagt gaagcttacg    960

gactcctcaa caggtgcatt cacacatcat ttagatgaaa ataaaatgat ttcactaaac   1020

atagatgaag gaataatttt caataaagtg gtagaagatt ttgattttag agcagtggtt   1080

tcttctttat cagaattaaa aggaatagaa tatgaaggac aatatattga taagcaatat   1140

gaagaattta ttccatcaag tgctcccta tcacaagacc gtctatggca ggcagttgaa   1200

agtttgactc aaagcaatga aacaatcgtt gctgaacaag gaacctcatt ttttggagct   1260

tcaacaattt tcttaaaatc aaatagtcgt tttattggac aacctttatg gggttctatt   1320
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ggatatactt ttccagcggc tttaggaagc caaattgcgg ataaagagag cagacacctt 1380

ttatttattg gtgatggttc acttcaactt accgtacaag aattaggact atcaatcaga 1440

gaaaaactca atccaatttg ttttatcata aataatgatg gttatacagt tgaaagagaa 1500

atccacggac ctactcaaag ttataacgac attccaatgt ggaattactc gaaattacca 1560

gaaacatttg gagcaacaga agatcgtgta gtatcaaaaa ttgttagaac agagaatgaa 1620

tttgtgtctg tcatgaaaga agcccaagca gatgtcaata gaatgtattg gatagaacta 1680

gttttggaaa aagaagatgc gccaaaatta ctgaaaaaaa tgggtaaatt atttgctgag 1740

caaaataaat agtaatagtg atcccggccg ctactaaagc ctgatttgtc ttgatagctg 1800

ctcctgcctt tgggcagggg ctttttttctg tctgccattc ttgaggatgg cggactcttt 1860

ccctttgct ctacgcccat gaatgcgatc gcagtctccc ctgtccagca cgttggagtg 1920

attggtggtg gccagttagc ttggatgctg gcaccagcag cgcaacagtt ggggatgtcg 1980

ctgcacgttc aaacacccaa tgatcacgac ccagcagtag cgatcgcgga tcaaaccgta 2040

ttagcagcag ttgctgacgc ggttctctct tctgccgtta 2080

<210> SEQ ID NO 98
<211> LENGTH: 1603
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 98, Example 98: designer Synechococcus sp. strain PCC 7942 nirA-promoter-controlled NADH-dependent Butanol Dehydrogenase DNA construct (1603 bp)

<400> SEQUENCE: 98

agaaaatctg gcaccacacc cttcttgcag aacatgcatg atttacaaaa agttgtagtt 60

tctgttacca attgcgaatc gagaactgcc taatctgccg agtatatgat gtcaagattt 120

acactaccaa gagatattta tttcggagaa aacactttag aaactttaaa aactttaaaa 180

ggtaagaaag ctataattgt tgttggagga ggatcaatga aaaaatttgg tttccttcaa 240

aaagttgaag aatatctaaa agaagcagga atggaaataa aattaataga aggtgttgaa 300

ccagatccat cagttgaaac cgttatgaaa ggtgcagaaa tcatgagaga ttttgagcct 360

gattggatag tatccatagg tggaggatca ccaatagatg ctgctaaagc tatgtggata 420

ttctatgaat acccagaatt tacttttgag caagctgttg ttccttttgg aataccagat 480

ttaagacaaa aagctaaatt tgttgctata ccatctacaa gtggaacagc tacagaagtt 540

actgcttttt cagttataac tgattacaaa gctaagataa aatatccttt agctgatttt 600

aatttaacac cagatgtagc tattatagat ccagctcttg ctcaaacaat gcctgcaaaa 660

ttaacagctc atacaggtat ggatgcttta actcatgcaa tagaagctta tgtagcagga 720

ttaagatcat atttctcaga tcctcttgca atgcaagcta tagttatgac aaaagataat 780

ttaataaaat cctatgaagg agataaagaa gcaagagatg aaatgcatat agctcaatgt 840

ttagcaggaa tggcattctc aaatgcgcta cttggaatta ctcatagtat ggcacataag 900

acaggagcag tattccacat tcctcatggt tgtgcaaatg ctatattcct tccttatgta 960

atagatttta ataagaaaac atgtaaagat agatatgcaa ctatagctaa aactttaggt 1020

ttagcaggaa atactgatga tgaattagta gatgcattaa cttctatgat acaagaaatg 1080

aataagaaaa tggatatacc actaaactta aaagaatatg gagtaacaga agaagatttt 1140

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aatgaaaact tagatttcat agcacataat gcagtgttag atgcatgtac tggatcaaat 1200

ccaagaccta taactgaaga agaaatgaaa aaagtattca aatgcacatt tactggagag 1260

aaagttaatt tttaataata gtgatcccgg ccgctactaa agcctgattt gtcttgatag 1320

ctgctcctgc ctttgggcag gggctttttt ctgtctgcca ttcttgagga tggcggactc 1380

tttccctttt gctctacgcc catgaatgcg atcgcagtct cccctgtcca gcacgttgga 1440

gtgattggtg gtggccagtt agcttggatg ctggcaccag cagcgcaaca gttggggatg 1500

tcgctgcacg ttcaaacacc caatgatcac gacccagcag tagcgatcgc ggatcaaacc 1560

gtattagcag cagttgctga cgcggttctc tcttctgccg tta 1603

<210> SEQ ID NO 99
<211> LENGTH: 1654
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 99, Example 99: designer Synechococcus sp. strain PCC 7942 nirA-promoter-controlled NADPH-dependent Butanol Dehydrogenase DNA construct (1654 bp)

<400> SEQUENCE: 99

agaaaatctg gcaccacacc cttcttgcag aacatgcatg atttacaaaa agttgtagtt 60

tctgttacca attgcgaatc gagaactgcc taatctgccg agtatatgct agaaatcaac 120

ttctgtatcg taataacagc acttaagcag tttttccatt tcttctacgc ttggctgtct 180

tgggttagaa cctgtgcagg catcgcctat ggcattaact gcaatgtcat gtaacctctc 240

caggaataca ttttcaggca caaatccctg tgcaaccgga tagctgtctg caccgtaatt 300

tttaatgcag tgcggtatat taagttcatc attcatctta cggagataac cgattaatga 360

agctaccttt tcatcaaggt ctgctccgcc aagtcccatg aaatcagcaa tttcaccata 420

acgcttctta gcctgttcat cctttgcgtt aaatgcaatt accttaggga gatacattgc 480

attcgcagca ccgtgaatga tgtgtgcgcc gtaatcggca aatgccgcac ctgttttatg 540

cgccattgaa tgtacaatac caagaagtgc attagaaaat gccattcctg cgagacattg 600

tgcattatgc attgaatctc ttttttccat atcaccgtta tatgaaccga caaggtctct 660

ttgaatcatt ttaattgcat ggagtgccaa tgggtctgta aaatcacaat ttgcggtgga 720

tacatatgcc tcgatagcat gtgtcattgc atccatacct gtatgtgcca ccaatttttg 780

tggcatggtc tctgccagtt cagggtctac tattgcaaca tcaggtgtta tttcaaaatc 840

ggctattgga tattttattc ctttttcata atctgtaata attgaaaaag cagttacctc 900

ggtagcggtt cctgaagtag aagatattgc acaaaaatgt gctttttttac gaagtgaagg 960

tatgccaaat actttacaca tatcctcaaa ggtaatatca ggatattcat atttaatcca 1020

cattgcttta gccgcatcaa tcggagaacc tccgcctatt gcaacaatcc agtcaggttc 1080

aaactctgac atcgctttgg caccttttcat aacggtttcc accgaagggt caggttcaat 1140

tccttcaaaa agtctgactt ccataccggc ttccttaaga tactgttctg ccctgtcaag 1200

gaaaccaaaa cgtttcattg aacctccgcc aacacaaatc atggcttttt tgccttgaaa 1260

tgtcttaagt gcctctaatg caccctttcc atgatacaaa tctcttggta acgtaaatct 1320

tgccattaat agtgatcccg gccgctacta aagcctgatt tgtcttgata gctgctcctg 1380

cctttgggca ggggcttttt tctgtctgcc attcttgagg atggcggact ctttcccttt 1440

-continued

tgctctacgc ccatgaatgc gatcgcagtc tcccctgtcc agcacgttgg agtgattggt 1500

ggtggccagt tagcttggat gctggcacca gcagcgcaac agttggggat gtcgctgcac 1560

gttcaaacac ccaatgatca cgacccagca gtagcgatcg cggatcaaac cgtattagca 1620

gcagttgctg acgcggttct ctcttctgcc gtta 1654

<210> SEQ ID NO 100
<211> LENGTH: 1440
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 100, Example 100: designer Synechocystis sp. PCC 6803 nirA-promoter-controlled NAD-dependent Glyceraldehyde-3-Phosphate Dehydrogenase DNA construct (1440 bp)

<400> SEQUENCE: 100

atggtagtta aagttggtat taacggtttc ggtcgtatcg gacgtcttgc attccgccgt 60

attcaaaata tcgaaggtgt tgaagtaact cgtatcaacg accttacaga tccaaatatg 120

cttgcacact tgttgaaata cgatacaact caaggtcgtt ttgatggaac agttgaagtt 180

aaagaaggtg gatttgaagt aaacggaaac ttcattaaag tttctgctga acgtgatcca 240

gaaaacatcg actgggcaac tgatggggtt gaaatcgttc ttgaagcaac tggtttcttt 300

gctaaaaaag aagcagctga aaaacactta catgctaacg gtgctaaaaa agttgttatc 360

acagctcctg gtggaaacga tgttaaaaca gttgttttca acactaacca cgacattctt 420

gacggtactg aaacagttat ctcaggtgct tcatgtacta caaactgttt agctcctatg 480

gctaaagctc ttcacgatgc attcggtatt caaaaaggtc ttatgactac aatccacgct 540

tacactggtg accaaatgat ccttgacgga ccacaccgtg gtggtgacct tcgtcgtgca 600

cgcgctggtg ctgcaaatat cgttcctaac tcaactggtg ctgctaaagc tatcggtctt 660

gttatcccag aacttaacgg taaacttgac ggtgctgcac aacgtgttcc tgttccaact 720

ggatcagtaa ctgagttggt tgtaactctt gacaaaaacg tttctgttga cgaaatcaac 780

gctgctatga aagctgcttc aaacgatagc ttcggttaca ctgaagatcc aatcgtttct 840

tcagatatcg taggcgtatc atacggttca ttgtttgacg caactcaaac taaagtaatg 900

gaagttgacg gatcccaatt ggttaaagtt gtatcatggt atgacaacga aatgtcttac 960

actgctcaac ttgtacgtac tcttgagtac ttcgcaaaaa ttgctaaata atagtaatga 1020

gttacagttt tggcaattac taaaaaactg acttcaattc aatgttagcc cgctcccgcg 1080

ggtttttttgt tgctttttca cagtgactat aggtaatcag caacacaata cggccctgtt 1140

ctttggacag tttttgtata atgttgaccg catcctgacc ggatttttta tctaagtggg 1200

gaattgtcaa ttgtcaatta aagctaagtt ctactaatgt tttagaaggc attgtcgatt 1260

gaaaataagg gttgaatgga gaaaattttg agcctttgtc aaagataaaa atttatttca 1320

acagtttttt aactagccga accagagaat gacccagtgg cgctgacttt gctcccgagt 1380

ttttgttaga aattaccctc aagaagtaat ctaataataa ggttctctct tctgccgtta 1440

<210> SEQ ID NO 101
<211> LENGTH: 2182
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 101, Example

-continued

101: designer Synechocystis sp. PCC 6803 nirA-promoter-controlled 2-Keto Acid Decarboxylase dehydrogenase DNA construct (2182 bp)

<400> SEQUENCE: 101

agaaaatctg gcaccacacc ctaaatgcgt aaactgcata tgccttggct gagtgtaatt 60

tacgttacaa attttaacga aacgggaacc ctatattgat ctctacatga tgtatacagt 120

aggagattac ctgttagacc gattacacga gttgggaatt gaagaaattt ttggagttcc 180

tggtgactat aacttacaat ttttagatca aattatttca cgcgaagata tgaaatggat 240

tggaaatgct aatgaattaa atgcttctta tatggctgat ggttatgctc gtactaaaaa 300

agctgccgca tttctcacca catttggagt cggcgaattg agtgcgatca atggactggc 360

aggaagttat gccgaaaatt taccagtagt agaaattgtt ggttcaccaa cttcaaaagt 420

acaaaatgac ggaaaatttg tccatcatac actagcagat ggtgatttta aacactttat 480

gaagatgcat gaacctgtta cagcagcgcg gactttactg acagcagaaa atgccacata 540

tgaaattgac cgagtacttt ctcaattact aaaagaaaga aaaccagtct atattaactt 600

accagtcgat gttgctgcag caaaagcaga gaagcctgca ttatctttag aaaaagaaag 660

ctctacaaca aatacaactg aacaagtgat tttgagtaag attgaagaaa gtttgaaaaa 720

tgcccaaaaa ccagtagtga ttgcaggaca cgaagtaatt agttttggtt tagaaaaaac 780

ggtaactcag tttgtttcag aaacaaaact accgattacg acactaaatt ttggtaaaag 840

tgctgttgat gaatctttgc cctcattttt aggaatatat aacgggaaac tttcagaaat 900

cagtcttaaa aattttgtgg agtccgcaga ctttatccta atgcttggag tgaagcttac 960

ggactcctca acaggtgcat tcacacatca tttagatgaa aataaaatga tttcactaaa 1020

catagatgaa ggaataattt tcaataaagt ggtagaagat tttgatttta gagcagtggt 1080

ttcttcttta tcagaattaa aaggaataga atatgaagga caatatattg ataagcaata 1140

tgaagaattt attccatcaa gtgctccctt atcacaagac cgtctatggc aggcagttga 1200

aagtttgact caaagcaatg aaacaatcgt tgctgaacaa ggaacctcat tttttggagc 1260

ttcaacaatt ttcttaaaat caaatagtcg ttttattgga caacctttat ggggttctat 1320

tggatatact tttccagcgg ctttaggaag ccaaattgcg gataaagaga gcagacacct 1380

tttatttatt ggtgatggtt cacttcaact taccgtacaa gaattaggac tatcaatcag 1440

agaaaaactc aatccaattt gttttatcat aaataatgat ggttatacag ttgaaagaga 1500

aatccacgga cctactcaaa gttataacga cattccaatg tggaattact cgaaattacc 1560

agaaacattt ggagcaacag aagatcgtgt agtatcaaaa attgttagaa cagagaatga 1620

atttgtgtct gtcatgaaag aagcccaagc agatgtcaat agaatgtatt ggatagaact 1680

agttttggaa aaagaagatg cgccaaaatt actgaaaaaa atgggtaaat tatttgctga 1740

gcaaaataaa tagtagtaat gagttacagt tttggcaatt actaaaaaac tgacttcaat 1800

tcaatgttag cccgctcccg cgggtttttt gttgcttttt cacagtgact ataggtaatc 1860

agcaacacaa tacggccctg ttctttggac agtttttgta taatgttgac cgcatcctga 1920

ccggattttt tatctaagtg gggaattgtc aattgtcaat taaagctaag ttctactaat 1980

gttttagaag gcattgtcga ttgaaaataa gggttgaatg gagaaaattt tgagcctttg 2040

tcaaagataa aaatttattt caacagtttt ttaactagcc gaaccagaga atgacccagt 2100

ggcgctgact ttgctcccga gtttttgtta gaaattaccc tcaagaagta atctaataat 2160

-continued

aaggttctct cttctgccgt ta 2182

<210> SEQ ID NO 102
<211> LENGTH: 1705
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 102, Example 102: designer Synechocystis sp. PCC 6803 nirA-promoter-controlled NADH-dependent Butanol Dehydrogenase DNA construct (1705 bp)

<400> SEQUENCE: 102

agaaaatctg gcaccacacc ctaaatgcgt aaactgcata tgccttggct gagtgtaatt 60

tacgttacaa attttaacga aacgggaacc ctatattgat ctctacatga tgtcaagatt 120

tacactacca agagatattt atttcggaga aaacacttta gaaactttaa aaactttaaa 180

aggtaagaaa gctataattg ttgttggagg aggatcaatg aaaaaatttg gtttccttca 240

aaaagttgaa gaatatctaa aagaagcagg aatggaaata aaattaatag aaggtgttga 300

accagatcca tcagttgaaa ccgttatgaa aggtgcagaa atcatgagag attttgagcc 360

tgattggata gtatccatag gtggaggatc accaatagat gctgctaaag ctatgtggat 420

attctatgaa tacccagaat ttacttttga gcaagctgtt gttccttttg gaataccaga 480

tttaagacaa aaagctaaat ttgttgctat accatctaca agtggaacag ctacagaagt 540

tactgctttt tcagttataa ctgattacaa agctaagata aaatatcctt tagctgattt 600

taatttaaca ccagatgtag ctattataga tccagctctt gctcaaacaa tgcctgcaaa 660

attaacagct catacaggta tggatgcttt aactcatgca atagaagctt atgtagcagg 720

attaagatca tatttctcag atcctcttgc aatgcaagct atagttatga caaaagataa 780

tttaataaaa tcctatgaag gagataaaga agcaagagat gaaatgcata tagctcaatg 840

tttagcagga atggcattct caaatgcgct acttggaatt actcatagta tggcacataa 900

gacaggagca gtattccaca ttcctcatgg ttgtgcaaat gctatattcc ttccttatgt 960

aatagatttt aataagaaaa catgtaaaga tagatatgca actatagcta aaactttagg 1020

tttagcagga aatactgatg atgaattagt agatgcatta acttctatga tacaagaaat 1080

gaataagaaa atggatatac cactaaactt aaaagaatat ggagtaacag aagaagattt 1140

taatgaaaac ttagatttca tagcacataa tgcagtgtta gatgcatgta ctggatcaaa 1200

tccaagacct ataactgaag aagaaatgaa aaaagtattc aaatgcacat ttactggaga 1260

gaaagttaat ttttaatagt aatgagttac agttttggca attactaaaa aactgacttc 1320

aattcaatgt tagcccgctc ccgcgggttt tttgttgctt tttcacagtg actataggta 1380

atcagcaaca caatacggcc ctgttctttg gacagttttt gtataatgtt gaccgcatcc 1440

tgaccggatt ttttatctaa gtggggaatt gtcaattgtc aattaaagct aagttctact 1500

aatgttttag aaggcattgt cgattgaaaa taagggttga atggagaaaa ttttgagcct 1560

ttgtcaaaga taaaaattta tttcaacagt tttttaacta gccgaaccag agaatgaccc 1620

agtggcgctg actttgctcc cgagtttttg ttagaaatta ccctcaagaa gtaatctaat 1680

aataaggttc tctcttctgc cgtta 1705

<210> SEQ ID NO 103
<211> LENGTH: 1756
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 103, Example 103: designer Synechocystis sp. PCC 6803 nirA-promoter-controlled NADPH-dependent Butanol Dehydrogenase DNA construct (1756 bp)

<400> SEQUENCE: 103

agaaaatctg gcaccacacc ctaaatgcgt aaactgcata tgccttggct gagtgtaatt 60

tacgttacaa attttaacga aacgggaacc ctatattgat ctctacatgc tagaaatcaa 120

cttctgtatc gtaataacag cacttaagca gtttttccat ttcttctacg cttggctgtc 180

ttgggttaga acctgtgcag gcatcgccta tggcattaac tgcaatgtca tgtaacctct 240

ccaggaatac attttcaggc acaaatccct gtgcaaccgg atagctgtct gcaccgtaat 300

ttttaatgca gtgcggtata ttaagttcat cattcatctt acggagataa ccgattaatg 360

aagctacctt ttcatcaagg tctgctccgc caagtcccat gaaatcagca atttcaccat 420

aacgcttctt agcctgttca tcctttgcgt taaatgcaat taccttaggg agatacattg 480

cattcgcagc accgtgaatg atgtgtgcgc cgtaatcggc aaatgccgca cctgttttat 540

gcgccattga atgtacaata ccaagaagtg cattagaaaa tgccattcct gcgagacatt 600

gtgcattatg cattgaatct ctttttttcca tatcaccgtt atatgaaccg acaaggtctc 660

tttgaatcat tttaattgca tggagtgcca atgggtctgt aaaatcacaa tttgcggtgg 720

atacatatgc ctcgatagca tgtgtcattg catccatacc tgtatgtgcc accaattttt 780

gtggcatggt ctctgccagt tcagggtcta ctattgcaac atcaggtgtt atttcaaaat 840

cggctattgg atattttatt ccttttttcat aatctgtaat aattgaaaaa gcagttacct 900

cggtagcggt tcctgaagta gaagatattg cacaaaaatg tgctttttta cgaagtgaag 960

gtatgccaaa tactttacac atatcctcaa aggtaatatc aggatattca tatttaatcc 1020

acattgcttt agccgcatca atcggagaac ctccgcctat tgcaacaatc cagtcaggtt 1080

caaactctga catcgctttg gcacctttca taacggtttc caccgaaggg tcaggttcaa 1140

ttccttcaaa aagtctgact tccataccgg cttccttaag atactgttct gccctgtcaa 1200

ggaaaccaaa acgtttcatt gaacctccgc caacacaaat catggctttt ttgccttgaa 1260

atgtcttaag tgcctctaat gcacccttttc catgatacaa atctcttggt aacgtaaatc 1320

ttgccattag taatgagtta cagttttggc aattactaaa aaactgactt caattcaatg 1380

ttagcccgct cccgcgggtt ttttgttgct ttttcacagt gactataggt aatcagcaac 1440

acaatacggc cctgttcttt ggacagtttt tgtataatgt tgaccgcatc ctgaccggat 1500

tttttatcta agtggggaat tgtcaattgt caattaaagc taagttctac taatgtttta 1560

gaaggcattg tcgattgaaa ataagggttg aatggagaaa attttgagcc tttgtcaaag 1620

ataaaaattt atttcaacag ttttttaact agccgaacca gagaatgacc cagtggcgct 1680

gactttgctc ccgagttttt gttagaaatt accctcaaga agtaatctaa taataaggtt 1740

ctctcttctg ccgtta 1756

<210> SEQ ID NO 104
<211> LENGTH: 1655
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 104, Example 104: designer Anabaena PCC 7120 hox-promoter-controlled NAD-dependent Glyceraldehyde-3-Phosphate Dehydrogenase DNA construct (1655 bp)

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<400> SEQUENCE: 104

agaaaatctg gcaccacacc gcagaaatat aggggctagg agttgagggt actctggttc 60

gtcaagcatt tgggatgatt tcccctcaca agttcctcaa attattctcc tataaacaat 120

agatataagg tcaaaacttg agttatgagt gctgagtaaa aaattactct ccacgcctca 180

gaggtagata tgatggtagt taaagttggt attaacggtt tcggtcgtat cggacgtctt 240

gcattccgcc gtattcaaaa tatcgaaggt gttgaagtaa ctcgtatcaa cgaccttaca 300

gatccaaata tgcttgcaca cttgttgaaa tacgatacaa ctcaaggtcg ttttgatgga 360

acagttgaag ttaaagaagg tggatttgaa gtaaacggaa acttcattaa agtttctgct 420

gaacgtgatc cagaaaacat cgactgggca actgatgggg ttgaaatcgt tcttgaagca 480

actggtttct ttgctaaaaa agaagcagct gaaaaacact tacatgctaa cggtgctaaa 540

aaagttgtta tcacagctcc tggtggaaac gatgttaaaa cagttgtttt caacactaac 600

cacgacattc ttgacggtac tgaaacagtt atctcaggtg cttcatgtac tacaaactgt 660

ttagctccta tggctaaagc tcttcacgat gcattcggta ttcaaaaagg tcttatgact 720

acaatccacg cttacactgg tgaccaaatg atccttgacg gaccacaccg tggtggtgac 780

cttcgtcgtg cacgcgctgg tgctgcaaat atcgttccta actcaactgg tgctgctaaa 840

gctatcggtc ttgttatccc agaacttaac ggtaaacttg acggtgctgc acaacgtgtt 900

cctgttccaa ctggatcagt aactgagttg gttgtaactc ttgacaaaaa cgtttctgtt 960

gacgaaatca acgctgctat gaaagctgct tcaaacgata gcttcggtta cactgaagat 1020

ccaatcgttt cttcagatat cgtaggcgta tcatacggtt cattgtttga cgcaactcaa 1080

actaaagtaa tggaagttga cggatcccaa ttggttaaag ttgtatcatg gtatgacaac 1140

gaaatgtctt acactgctca acttgtacgt actcttgagt acttcgcaaa aattgctaaa 1200

taatgaagta agtaggaagc agggagcagg ggaaagaaaa ttgacaactg tacaagatta 1260

atcgcgtctc tgagcaatga ccaaatacat ctacctccac ggttttcttc cagcccccta 1320

tctgcgaaag cacaagatat tagcaagcgt ttcgcccaaa ttcacataca gctaacaatc 1380

cctgatctca atgctggtga attttctcag ttaacaatca cgcgccaaat tcaacaagtt 1440

gccgcaattt tccctgataa ttctgaacca ataacgctga taggttctag tttaggcggt 1500

ttaactgctg cttatctagg acagcgatat ttacaagtac aacgcttagt tttattagcg 1560

ccagtttggt tttttatccc attggttgcc caaaatgggt gaagaagctg tcacaagttg 1620

gcaacaaacg atataggttc tctcttctgc cgtta 1655

<210> SEQ ID NO 105
<211> LENGTH: 2303
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 105, Example 105: designer Anabaena PCC 7120 hox-promoter-controlled Acetolactate Synthase DNA construct (2303 bp)

<400> SEQUENCE: 105

agaaaatctg gcaccacacc gcagaaatat aggggctagg agttgagggt actctggttc 60

gtcaagcatt tgggatgatt tcccctcaca agttcctcaa attattctcc tataaacaat 120

agatataagg tcaaaacttg agttatgagt gctgagtaaa aaattactct ccacgcctca 180

-continued

gaggtagata tgctaagggg tgcagctgag ctccccaaga cgttggttaa agcgcagatt 240

ttcactatag tccacaggga catcaatgag agtgggaaca ttctgtgcca aggcggtttt 300

gagggttggg ataaagtcag tggtctcctc aatgcgatag cctttgagtc ccatgctttc 360

ggctaacttg acaaaatcgg gattactaaa gtggacatag gcagattcac caaagtagcg 420

ctgctgcttc cactcaatga gaccatagcc gccgtcatta aagatgatgg tggtaaagtt 480

tgtccccata cgcagggcag tttccagttc ttggaaattc atcatgaagc caccatcccc 540

cgtgactgcc accacatgcc gctgcggata gactaatttg gcggccattg cccccggtac 600

cgcaatcccc attgccgcaa agccattgga aatcaagcag gtgttggggc gatcgcagtg 660

gtagtgacga gcaatccaca ttttatgggc acccacatca gaaataacaa tgtcctcggg 720

ccccatgact tggcgcaggt catagattag cttttggggc ttaaccggaa aactctcatc 780

ctgggcatat tggtaatagt ccgccacaat ctcctgacgc agttgcacgg catagggggt 840

gggcttatct tggcgatcgg cccgcttaag aatttcatag agggagtcag aaatatcgcc 900

gacaacctca acgacaggga tatagctgct gtcaatttcc gcaggagtgg ccgcaatatg 960

gataatcggc aagcggccct cggggttcca gctttttggg gaatactcaa ttaagtcata 1020

gccaacggca atcactaagt cagcatgatc aaagccgcag ctaatgtaat cccgctgttg 1080

gagccccacg gtccacagag caaggggggtg ttgataggga atgacccctt tgcccatgaa 1140

ggtattggcc acggggatat tcagcttttc ggcaaaatgg gtgagggcag cggcagcatg 1200

ggcgcgaatg gcgccattcc ccactaggat caggggggttc tcggcagcat tgatgagttc 1260

agcggcctta agaatactct ggaaagaggc ataggttttt tcgggggagc tgggcttaag 1320

gggagcgccc tcggcttcca tggcggcaat gttttcaggc acatcaatgt gaacggcgcc 1380

cggcttctca ttctgggcaa ttttaaaggc cttgcggaca atttctgggg taatactagg 1440

gcggacaatc tgggcattcc atttggttac ggggctaaac atggccacca agtccaaata 1500

ttggtgggac tcgatgtgca tgcgatccgt ccccacttgc cctgtaatcg ccaccagggg 1560

agcgccgtcg aggttggcat cggcaacacc ggtcattaaa ttcgtggccc cggggccgag 1620

ggtagaaaga cagacccctg ctttgccggt gaggcgacca tagacatcgg ccataaaggc 1680

cgccccctgt tcgtggcggg tggttataaa ttgaatccga gagcgatgga gggcatggag 1740

gacatctaga ttctcttccc ccggcaaacc aaaaatatat tcaacgcctt cattttcaag 1800

gcattttacg agtaattcgg cggtattcat aggatgggcg atcgcaggca ctgaagtaag 1860

taggaagcag ggagcagggg aaagaaaatt gacaactgta caagattaat cgcgtctctg 1920

agcaatgacc aaatacatct acctccacgg ttttcttcca gccccctatc tgcgaaagca 1980

caagatatta gcaagcgttt cgcccaaatt cacatacagc taacaatccc tgatctcaat 2040

gctggtgaat tttctcagtt aacaatcacg cgccaaattc aacaagttgc cgcaattttc 2100

cctgataatt ctgaaccaat aacgctgata ggttctagtt taggcggttt aactgctgct 2160

tatctaggac agcgatattt acaagtacaa cgcttagttt tattagcgcc agtttggttt 2220

tttatcccat tggttgccca aaatgggtga agaagctgtc acaagttggc aacaaacgat 2280

ataggttctc tcttctgccg tta 2303

<210> SEQ ID NO 106
<211> LENGTH: 1661
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 106, Example 106: designer Anabaena PCC 7120 hox-promoter-controlled Ketol-Acid Reductoisomerase DNA construct (1661 bp)

<400> SEQUENCE: 106

agaaaatctg gcaccacacc gcagaaatat aggggctagg agttgagggt actctggttc 60

gtcaagcatt tgggatgatt tcccctcaca agttcctcaa attattctcc tataaacaat 120

agatataagg tcaaaacttg agttatgagt gctgagtaaa aaattactct ccacgcctca 180

gaggtagata tgttaatttt tatccttatc cactatcttt ccttttccaa gccagctcat 240

catacttcta agtttagatc ccacctgctc gatgggatgg ttttcatcag ccctggtgag 300

ggcattaaat actggtctgc cagctttatt ttccagcatc cattcttttg caaattctcc 360

tgattgtatc tgtcttaaaa cttccctcat gttgtcttta acctggggat ctattaccac 420

aggccccctt gtgaggtcac catattgggc tgtgttgctt atggaatatc tcatgttgga 480

gataccacct tcatagagaa gatccactat cagttttacc tcatgcatac attcaaaata 540

agccatttct ggagcgtagc cagcctccac caatgtttca aaaccatatt taataagctg 600

tgtcaaacca ccacataaaa ccgcctgctc accgaaaaga tctgtttctg tttcctcttt 660

gaagtttgtt tcaagcacac ctgctctggc tccaccaatg gcagctgcgt atgacaaagc 720

cacctctctt gaatcaccgg aatagtcttg atgcacagcg atgaggcatg gtactccgcc 780

acccttttgta tattctgctc ttacaagatg ccctggccct ttaggtgcaa tcattataac 840

gtttacgttt ttaggaggca ctatctgtcc aaaatggatg ttgaaaccgt gggcaaatgc 900

aagatatgtc ccctctttta tataaggggc aatctgctct ctgtaaagat ccccctgtat 960

ctcatcagga acgagtatca tgatgaggtc tgcccatttt gtggcctctg atatctccat 1020

aactttaagc ccggagcttt ccgcttttttt ccaggaatca ccacccttttc ttagggcaac 1080

ggcaacgtca acaccactat ctttgaggtt attagaatgt ccataaccct gacttccgta 1140

accaactatg gccacctttt tctttttaat caattctaaa tttgcatcct tttcgtagta 1200

tactttcatt gaagtaagta ggaagcaggg agcaggggaa agaaaattga caactgtaca 1260

agattaatcg cgtctctgag caatgaccaa atacatctac ctccacggtt ttcttccagc 1320

cccctatctg cgaaagcaca agatattagc aagcgtttcg cccaaattca catacagcta 1380

acaatccctg atctcaatgc tggtgaattt tctcagttaa caatcacgcg ccaaattcaa 1440

caagttgccg caattttccc tgataattct gaaccaataa cgctgatagg ttctagttta 1500

ggcggtttaa ctgctgctta tctaggacag cgatatttac aagtacaacg cttagtttta 1560

ttagcgccag tttggttttt tatcccattg gttgcccaaa atgggtgaag aagctgtcac 1620

aagttggcaa caaacgatat aggttctctc ttctgccgtt a 1661

<210> SEQ ID NO 107
<211> LENGTH: 2324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 107, Example 107: designer Anabaena PCC 7120 hox-promoter-controlled Dihydroxy-Acid Dehydratase DNA construct (2324 bp)

<400> SEQUENCE: 107

agaaaatctg gcaccacacc gcagaaatat aggggctagg agttgagggt actctggttc 60

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gtcaagcatt tgggatgatt tcccctcaca agttcctcaa attattctcc tataaacaat 120

agatataagg tcaaaacttg agttatgagt gctgagtaaa aaattactct ccacgcctca 180

gaggtagata tgttataaat ccgttataca tccaaaagat gctgatgata ccagcttgct 240

atacttcctt aagcttccac tcacatttcg ctcgggcttt ataggagttt gctcctttcg 300

tttttcccat tcctcttcct ccatcaatac actaattgaa ttttccactg catctattct 360

gatgcggtcg ccattttcta cataagctaa tgcgccatta tcaaaagctt cgggtgaaat 420

gtgtcccact acaaaaccgt gagttcctcc tgagaacctt ccatctgtaa tgagggctac 480

tttctttccc aaacctgctc ccattatagc agcagttggc tttaacattt cgggcattcc 540

aggacctcct tttggccctt catatcgaat caccactaca tcaccttctt ttatctcgcc 600

tctggcaata ccatcattgg ccagaaattc accatcataa actctagcag ttccttcgaa 660

tatctctcct tcctttccgg tgattttagc aacagctcct ccaggtgcta aattgccttt 720

caatattcgc aaatgacctg agcttttgat tggatttttc acagagtgaa tgatgtcttg 780

cttttcgcct aaaccctgaa catctttata attttcagct aaagttttac ctgttatggt 840

catgcaatcg ccatgaagaa gtccttcccc caacatcatt ttcatcactg caggaatccc 900

gccattttga tgaagatctt ccatcaagta tttaccagaa ggctttaagt cggctagata 960

aggagtttcg gcactgattc gagcgaaatc ttccaatgtt aaatcgattt caaaagcatt 1020

ggcaacagct aataaatgta aaactgcatt ggtcgatcct cccaaaactg taatcaaccg 1080

tatggcgttt tcaaatgatt ttttagtgac gatatcccgt ggcttcaaat cattttcaat 1140

caatttttta atggctaaac cagcctctgc acattctttc cttttctcag cactttgagc 1200

gggattggaa gcaccataag gcaagcataa tcctaaggct tcaatagcgg atgccatcgt 1260

attggcagtg tacattcctc cacaggctcc aggacctggg catgcatttg ccactactcc 1320

cttaaaatct tcttcagaaa tagtgttggc ttgcttctta cctaaagctt caaaagcaga 1380

aaccacatct aatttttctc cattatggca acctggagca atggttcctc cataaattat 1440

gagtgaaggt cgattcaatc tgcccatagc cagtaaggcg cctggcatat ttttatcgca 1500

tcccgtaata gcaatcatgg catcgtaagc ttgcgcattc actaccgttt ccatggaatc 1560

ggctatgata tcgcgggaag gcaatgaata gcgcattccg ttggtaccca tagaaatacc 1620

atcgcttact ccaatagtat tgaaaatcaa ccctacccac tcataagatt tgatgctttt 1680

cttgacctct acagccaaat cattcaaatg catattacat ggattgccct caaaaccagt 1740

gcttgcaata cctatttgtg gtttttccaa atcttcatca gacaaaccaa tggcatgcaa 1800

catggcttga gcggcaggtt gtgtaggatc ttgtgtaact gctttactat atggatttaa 1860

ttccttcgcc attgaagtaa gtaggaagca gggagcaggg gaaagaaaat tgacaactgt 1920

acaagattaa tcgcgtctct gagcaatgac caaatacatc tacctccacg gttttcttcc 1980

agccccctat ctgcgaaagc acaagatatt agcaagcgtt tcgcccaaat tcacatacag 2040

ctaacaatcc ctgatctcaa tgctggtgaa ttttctcagt taacaatcac gcgccaaatt 2100

caacaagttg ccgcaatttt ccctgataat tctgaaccaa taacgctgat aggttctagt 2160

ttaggcggtt taactgctgc ttatctagga cagcgatatt tacaagtaca acgcttagtt 2220

ttattagcgc cagtttggtt ttttatccca ttggttgccc aaaatgggtg aagaagctgt 2280

cacaagttgg caacaaacga tataggttct ctcttctgcc gtta 2324

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<210> SEQ ID NO 108
<211> LENGTH: 2288
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 108, Example 108: designer Anabaena PCC 7120 hox-promoter-controlled branched-chain alpha-Ketoacid Decarboxylase DNA construct (2288 bp)

<400> SEQUENCE: 108

agaaaatctg gcaccacacc gcagaaatat aggggctagg agttgagggt actctggttc 60

gtcaagcatt tgggatgatt tcccctcaca agttcctcaa attattctcc tataaacaat 120

agatataagg tcaaaacttg agttatgagt gctgagtaaa aaattactct ccacgcctca 180

gaggtagata tgatgtatac agtaggagat tacctgttag accgattaca cgagttggga 240

attgaagaaa tttttggagt tcctggtgac tataacttac aatttttaga tcaaattatt 300

tcacgcgaag atatgaaatg gattggaaat gctaatgaat taaatgcttc ttatatggct 360

gatggttatg ctcgtactaa aaaagctgcc gcatttctca ccacatttgg agtcggcgaa 420

ttgagtgcga tcaatggact ggcaggaagt tatgccgaaa atttaccagt agtagaaatt 480

gttggttcac caacttcaaa agtacaaaat gacggaaaat ttgtccatca tacactagca 540

gatggtgatt ttaaacactt tatgaagatg catgaacctg ttacagcagc gcggacttta 600

ctgacagcag aaaatgccac atatgaaatt gaccgagtac tttctcaatt actaaaagaa 660

agaaaaccag tctatattaa cttaccagtc gatgttgctg cagcaaaagc agagaagcct 720

gcattatctt tagaaaaaga aagctctaca acaaatacaa ctgaacaagt gattttgagt 780

aagattgaag aaagtttgaa aaatgcccaa aaaccagtag tgattgcagg acacgaagta 840

attagttttg gtttagaaaa aacggtaact cagtttgttt cagaaacaaa actaccgatt 900

acgacactaa attttggtaa aagtgctgtt gatgaatctt tgccctcatt tttaggaata 960

tataacggga aactttcaga aatcagtctt aaaaattttg tggagtccgc agactttatc 1020

ctaatgcttg gagtgaagct tacggactcc tcaacaggtg cattcacaca tcatttagat 1080

gaaaataaaa tgatttcact aaacatagat gaaggaataa ttttcaataa agtggtagaa 1140

gattttgatt ttagagcagt ggtttcttct ttatcagaat taaaaggaat agaatatgaa 1200

ggacaatata ttgataagca atatgaagaa tttattccat caagtgctcc cttatcacaa 1260

gaccgtctat ggcaggcagt tgaaagtttg actcaaagca atgaaacaat cgttgctgaa 1320

caaggaacct catttttgg agcttcaaca attttcttaa aatcaaatag tcgttttatt 1380

ggacaacctt tatggggttc tattggatat acttttccag cggctttagg aagccaaatt 1440

gcggataaag agagcagaca ccttttattt attggtgatg gttcacttca acttaccgta 1500

caagaattag gactatcaat cagagaaaaa ctcaatccaa tttgttttat cataaataat 1560

gatggttata cagttgaaag agaaatccac ggacctactc aaagttataa cgacattcca 1620

atgtggaatt actcgaaatt accagaaaca tttggagcaa cagaagatcg tgtagtatca 1680

aaaattgtta gaacagagaa tgaatttgtg tctgtcatga aagaagccca agcagatgtc 1740

aatagaatgt attggataga actagttttg gaaaaagaag atgcgccaaa attactgaaa 1800

aaaatgggta aattatttgc tgagcaaaat aaatagtgaa gtaagtagga agcagggagc 1860

aggggaaaga aaattgacaa ctgtacaaga ttaatcgcgt ctctgagcaa tgaccaaata 1920

catctacctc cacggttttc ttccagcccc ctatctgcga aagcacaaga tattagcaag 1980

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cgtttcgccc aaattcacat acagctaaca atccctgatc tcaatgctgg tgaattttct 2040

cagttaacaa tcacgcgcca aattcaacaa gttgccgcaa ttttccctga taattctgaa 2100

ccaataacgc tgataggttc tagtttaggc ggtttaactg ctgcttatct aggacagcga 2160

tatttacaag tacaacgctt agttttatta gcgccagttt ggtttttat cccattggtt 2220

gcccaaaatg ggtgaagaag ctgtcacaag ttggcaacaa acgatatagg ttctctcttc 2280

tgccgtta 2288

<210> SEQ ID NO 109
<211> LENGTH: 1613
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 109, Example 109: designer Anabaena PCC 7120 hox-promoter-controlled 2-Methylbutyraldehyde Reductase DNA construct (1613 bp)

<400> SEQUENCE: 109

agaaaatctg gcaccacacc gcagaaatat aggggctagg agttgagggt actctggttc 60

gtcaagcatt tgggatgatt tcccctcaca agttcctcaa attattctcc tataaacaat 120

agatataagg tcaaaacttg agttatgagt gctgagtaaa aaattactct ccacgcctca 180

gaggtagata tgatggcttc tgtaaatgac tactttgaga acgccaagac gacgtacttt 240

actttgagat cgggtgacaa gatccccgct gttggattgg gtacttggca atcacccacc 300

aacgagacta aagaggcagt caagtacgct ttgcagcacg gttaccgtca catcgatgct 360

gccgccattt atggtaacga agacgaggtt ggtgacggta tcaaggagag tggaatccct 420

cgtgaccaaa tctgggtcac atctaagctc tggtgcaatg ctcatgctcc cgaggctgtc 480

cccaaggctt tggagaagac cttgcgtgag ctgaaacttg attaccttga cctttacctc 540

atccactggc ctatttcttt gaagaccggc gatgacttgg ttcccaagga caaggacggc 600

aacaccatca ctgtcgaaat tcccctcgag gacacctgga aggctatgga gggtcttgtg 660

aagtccggca aggtgaagaa cattggtatt tccaatttca acaacgaaga gttggatcgt 720

attttgaagg ttgccgagat tcctcctgcc gtccaccaaa tggaaactca tccttacttg 780

aagcagacgg agttcattga gaagcacaag aagcttggca ttcacgtcac cgcttactcg 840

cctttggcca accaaaatgc tctttacggc aatgccgttc ccaagttgat tgagcacaag 900

actcttgtcg acattgccaa gaccaagggt gagggcgtca ctggtgccaa cattgctatt 960

tcttgggcag tcaagcgcgg tacttcggtt attcctaagt ctgttcatgc caacagaatt 1020

aagagcaact tcctcgttgt tcccttgact gatgacgaga tgaaggccat cgataacatt 1080

ggtgtcagca agcgtttcaa ttggagcaaa gttttctgca atgagaattg tttctacggt 1140

cttgaggatg gtcctcagta atgaagtaag taggaagcag ggagcagggg aaagaaaatt 1200

gacaactgta caagattaat cgcgtctctg agcaatgacc aaatacatct acctccacgg 1260

ttttcttcca gccccctatc tgcgaaagca caagatatta gcaagcgttt cgcccaaatt 1320

cacatacagc taacaatccc tgatctcaat gctggtgaat tttctcagtt aacaatcacg 1380

cgccaaattc aacaagttgc cgcaattttc cctgataatt ctgaaccaat aacgctgata 1440

ggttctagtt taggcggttt aactgctgct tatctaggac agcgatattt acaagtacaa 1500

cgcttagttt tattagcgcc agtttggttt tttatcccat tggttgccca aaatgggtga 1560

agaagctgtc acaagttggc aacaaacgat ataggttctc tcttctgccg tta 1613

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<210> SEQ ID NO 110
<211> LENGTH: 1300
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 110, Example 110: designer Prochlorococcus marinus MIT9313 groE-promoter-controlled NAD-dependent Glyceraldehyde-3-Phosphate Dehydrogenase DNA construct (1300 bp)

<400> SEQUENCE: 110

agaaaatctg gcaccacacc ccctttcaga gcggcgcaac attaccactg catggcgaga 60

tcttctcagg gttcggtgac ccgcacaggt atccactagt cggcacagca tcaacacaca 120

tagggttggc actcaatggc cacgagtgct actcatgtta tgccaagccg actttacgaa 180

ccaattccgc ggtgcgcgtg gcgtaaccca tttcgttgtc ataccaagtg tagattttca 240

ccattcgctt accaaccacc atggtggaga gcgcatccac aattgttgaa cgttgatcgc 300

cttggtaatc aatcgacacc agtggacgct cttcaaaacc cagaatgcct ttaagctcgt 360

tttctgaggc ttgttttaac agctgattga tctcttccac cgtcgtatca cgctgcacat 420

caaaaatgat gtcggttaac gaggcattcg ccaacggtac acgtacggcg tgtccatcaa 480

tcttgccttt cagatccggg aaaatttcga taatcgcttt agcagagccg gtggttgtgg 540

ggatgaggct cataccgcaa gcacgtgcac ggcgtaaatc tttatgcggt gcatccaaaa 600

tggtttgcgt attggttagg ttatggatgg tagtaaaaga ggcttgtgcg atacccagtt 660

tttcatggat tactttcacc actggagcaa tacagttagt ggtacaagaa gcggcagtga 720

caatgcgatg ttgctccgga ttgaagatgt gatcgttcac cccgaccacg atattggcga 780

tcccctcttc tttgacaggc gctgaaacga cgacgcgttt tactccttgt gccaaatact 840

ggttcaagaa ttcgccttta cggtgcttac ccgtagcctc aatcaccaca tcacagcccg 900

accaatccac tgcatcaatc gatttttctt gtgttgtgcg aatgcgtttg ccgttgatca 960

ggatagcatc cgcttcactg cccacagcat gatgccaacg accttgtacc gaatcgaact 1020

ccaaaaggtg cgctaatgtt gcagcatcac ccgccacatc gttgatctgt acaaactcaa 1080

tctcaggcca atcaaacgaa gctcttaaag ccaaacgccc aatacgacca aatccattaa 1140

ttccgacttt aattgccatt gatttagttt cggtgtctat ctcttaatag cctcgattta 1200

ttttcggggc tattaatcaa ctctcagagg cgacaagctt cttcttccct tacgacgttt 1260

ttattggttg gacatggcaa ggttctctct tctgccgtta 1300

<210> SEQ ID NO 111
<211> LENGTH: 1498
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 111, Example 111: designer Prochlorococcus marinus MIT9313 groE-promoter-controlled Phosphoglycerate Mutase DNA construct (1498 bp)

<400> SEQUENCE: 111

agaaaatctg gcaccacacc ccctttcaga gcggcgcaac attaccactg catggcgaga 60

tcttctcagg gttcggtgac ccgcacaggt atccactagt cggcacagca tcaacacaca 120

tagggttggc actcaatggc cacgagtgct actcatgaaa tatgtaatct tacttggcga 180

cggcatggcc gacgaaaaaa ttgccgaact ggacggcaaa acgcctcttc aatacgccag 240

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cacacccaat atggacaggc tggcggcagg cggggaaacc ggcatggtac ataccgtccc 300

ggatggattt ccgcctggca gcgatgtagc caacctctcg gtaatggggt acaatccgcg 360

ggaatattat accgggcgtt ctccgctgga agcggtaagc atgggggttg aactttcaga 420

tgacgatgta gccttccgct gcaacctggt taccctgtca gaagaagagg tatatgaaaa 480

caagattatg gtggattaca gctcggacga aattaccacc tctgaatcgc atgaactgat 540

cagggaagtc gccaaccgcc tgggcagtaa agagttgcgc ttttacccgg gtttcggatt 600

tagacacctt cttgtatgga aaacagggcc tgttggcggg aagctaacac caccccacga 660

tatctcgggg cgtaccattg ccccatacct ccccaaaggc gagggtagcg acactttaaa 720

gcggttaatg aaagaaagca acaggttcct gccagagcac ccggttaacc aaaaaagggt 780

aagggccggt cttaggcctg ccacttccat ctggttctgg ggacagggaa agaaaccctc 840

gataccgaag ttctacgaca aatacggggt aaccggctct gttatctctg ccgtggacct 900

gattaagggg attggcatct gtgccggctt cgatatagtt aaggtggagg gtgtaacggg 960

caccatccat accaacttcc gggggaaagt gcaggccgcc ctggaagaac tgaaaaaggg 1020

aaaggacctg gtctacattc acgttgaggc tccggacgca gcaagccaca ggggtgaaac 1080

tgttaccaaa gttaaagcta ttgaaatggt ggacaacatg ctgggccagc ttttaaacaa 1140

actggacgaa ttcggcatgt acaaaataat gctcttgccc gatcatccaa ccccgctcag 1200

cactaaaacc cactctaaca gccctgtccc ctttgttatc tatgccaagg ggcggaaaaa 1260

taaaagcgcc gcttcttttg acgaagaaac ggcggcaaaa agcggacttg ttttccgggc 1320

gggccatgag ttaatggatt actttatccg cagctaatga tttagtttcg gtgtctatct 1380

cttaatagcc tcgatttatt ttcggggcta ttaatcaact ctcagaggcg acaagcttct 1440

tcttccctta cgacgttttt attggttgga catggcaagg ttctctcttc tgccgtta 1498

<210> SEQ ID NO 112
<211> LENGTH: 1588
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 112, Example 112: designer Prochlorococcus marinus MIT9313 groE-promoter-controlled Enolase DNA construct (1588 bp)

<400> SEQUENCE: 112

agaaaatctg gcaccacacc ccctttcaga gcggcgcaac attaccactg catggcgaga 60

tcttctcagg gttcggtgac ccgcacaggt atccactagt cggcacagca tcaacacaca 120

tagggttggc actcaatggc cacgagtgct actcatggtg tacgtggaaa tcgtggatgt 180

aagagcaaga gaggtcctgg attcgagagg aaatcccacc gttgaagcgg aagtcgtgct 240

tgaagacgga acaatgggaa gagccatcgt gccctctggt gcctccactg gaaaattcga 300

agccctggaa atcagagaca aagacaagaa gagatacctc gggaagggtg ttctgaaggc 360

cgtagagaac gtgaacgaaa ccatagctcc cgcgctgatt ggaatgaacg cattcgacca 420

gccactcgtt gacaagacac tgatagaact ggatggcaca gagaacaaat ctaaactggg 480

tgccaacgct atactcgccg tttctatggc agttgccaga gcggcggcga attacctcgg 540

attgcccctc tacaaatacc ttggaggagt caacgcaaag gttctgccag taccttttgat 600

gaacgtgatc aacggtggac agcacgcaga caacaatctt gaccttcagg aattcatgat 660

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cgttcccgcc ggatttgaca gcttcagaga agctttgagg gcaggagcgg aaatattcca    720

cacgttgaaa aagatactcc acgaagccgg tcacgtgaca gcagtaggag acgagggtgg    780

attcgcaccc aatctgtctt ccaacgaaga agccataaag gttctgattg aagccataga    840

gaaagctggc tacaagcccg gagaagaagt cttcatagct cttgattgcg cagcatcttc    900

cttctacgat gaggaaaagg gagtttacta cgtcgatggt gaagaaaaat ccagcgaagt    960

tctcatggga tactacgaag aactggtggc gaagtacccc atcatatcca tcgaagatcc   1020

gttcgcggag gaagactggg atgcatttgt ggaattcaca aagagagtag gaaacaaggt   1080

tcagatcgtt ggagatgacc tttacgtgac caacgtgaaa agactttcca aaggaataga   1140

actcaaagcg accaactcca tactcatcaa actcaatcag ataggcaccg tcacggaaac   1200

tctcgacgcg gtggagatgg cacagaagaa caacatgaca gccatcattt cccacagatc   1260

tggagagagt gaagacacgt tcattgcgga tctcgctgtg gcaacgaacg ctggtttcat   1320

caagacaggt tccctctcca gaagcgaaag gatagccaag tacaaccagc ttttgagaat   1380

cgaggaagaa ctcggaaaag tggcagaatt cagaggtttg aaatctttct actctataaa   1440

gagataatga tttagtttcg gtgtctatct cttaatagcc tcgatttatt ttcggggcta   1500

ttaatcaact ctcagaggcg acaagcttct tcttccctta cgacgttttt attggttgga   1560

catggcaagg ttctctcttc tgccgtta                                      1588


<210> SEQ ID NO 113
<211> LENGTH: 1717
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 113, Example
      113: designer Prochlorococcus marinus MIT9313 groE-promoter-
      controlled Pyruvate Kinase DNA construct (1717 bp)

<400> SEQUENCE: 113

agaaaatctg gcaccacacc ccctttcaga gcggcgcaac attaccactg catggcgaga     60

tcttctcagg gttcggtgac ccgcacaggt atccactagt cggcacagca tcaacacaca    120

tagggttggc actcaatggc cacgagtgct actcatgatg agaaaaacca agcttatatg    180

ttcgatagga cctaaaaccg agaaaccaga gaaaataaag gaattgctaa aaagaggggt    240

aaatgctttt aggataagcg cagttcatta cacgatggaa aaaatcacag agctggtaga    300

gctaatcaaa gatattagat atgaactcaa aatgcctgtt tccatcattc ttgatttacc    360

aggttgcaaa ctccggacgg gagatcagaa agaagaaatc atcgaactta gacaaggtga    420

aaaagtgact gtaacaagcg aaaaaacttt ttcttctcgg gatactataa gcataaattt    480

ttccggacca tttcagggtg taaaaaccgg cgatttaatc ctcgtagatg atggaaaaat    540

acaactcaga gtggaaagaa tttctccaaa aaaagtagaa tgcgtcgtgg agataggagg    600

aattttgaag aaaaacagtg gcgtcaattt tcccaattct gatctacctg tcgaagtacc    660

aacagaagaa gatattaaga tcatagctga aactgtcaat atgggactgg actattactg    720

tgtatcattt gcaagaaacg caaaagatgt tcaaaaaatc aaaaaacatc ttgaatcttt    780

cgattcaagt gcgaaaattc ttacgaaaat agaaacaaaa aaatccatag aaacgctgga    840

agatatatgt cgcgtgagcg atggaataat cgtagcaaga ggagatttag cggtggagac    900

atctctgata gatttgccga tattgcaaaa aaagataata aataccgcat caaattataa    960

aatacctgtg atcgtcgcaa ccgaaatact caattctatg atcaacagtt catcaccaac   1020
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aagggttgaa ataatggatg ttgcaaacat agttttagat ggagcagatg ctatactgct 1080

aacctctgaa acagctgtgg ggaactttcc gatcgaaaca gttgaaaaaa ttaatgagat 1140

tgttgaaaat gttgagaact acctacccga aatcaatgct cattttaaag aacgcaggtt 1200

tgaaaaaatc gaagatccat ctgaagctat tgcaaggagt agttactaca tttctgaaga 1260

aataaatgcc aaagctataa taatatcaac agcttctgga agcactgcaa gaagggtggc 1320

ctatttcaag ccacttcgtc ctatcatagc tacgacccca gatgaaaaca cctttcatca 1380

gttgtctatt gtttgggggа tagttccgat gctaattcca gaagtccatt ccacagatat 1440

aatgatccac gtggccgtcg agaaggttaa agctgtcgga tatgttcaaa attccgacat 1500

tgtggttgtt acttctggtg ctccgtgtgg tattgttgga acaactaaca tgctcaaagt 1560

tcacatagtt gagtagtgat ttagtttcgg tgtctatctc ttaatagcct cgatttattt 1620

tcggggctat taatcaactc tcagaggcga caagcttctt cttcccttac gacgttttta 1680

ttggttggac atggcaaggt tctctcttct gccgtta 1717

<210> SEQ ID NO 114
<211> LENGTH: 2017
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 114, Example 114: designer Prochlorococcus marinus MIT9313 groE-promoter-controlled Acetolactate Synthase DNA construct (2017 bp)

<400> SEQUENCE: 114

agaaaatctg gcaccacacc ccctttcaga gcggcgcaac attaccactg catggcgaga 60

tcttctcagg gttcggtgac ccgcacaggt atccactagt cggcacagca tcaacacaca 120

tagggttggc actcaatggc cacgagtgct actcatgtca agattgctta gaggcttctt 180

tattaaaatg ttcctcaaat ttttttggaa aacgctgatc ggccaaatga atgttgtcgc 240

tgtaatcgac cggaatatca atgacaacag gcccctctgc atcaagacca gctttaagca 300

cctctgccaa ttcgtcaggt gaattgaccc ttaaaccttt tgcaccaaag ctttcagcat 360

attttacaat atcgattccg ccgaagtcga ctccggacgt ccgcttgtat ttcatctcct 420

gctggaacgc aaccatatcg tatgtgctgt cattccagac aatgtgaacg atcggcgctt 480

ttaatctgac cgctgtctca agctccatcg cggagaacag gaagcccccg tccccggaaa 540

cagacacgac tttctgtccc ggattgacca gcgttgctgc aatcgcccac ggcaaagcca 600

ccccaagcgt ctgcatgccg ttggaaatca gcagtccatg cggacggtag gtgcggaaat 660

atctagacat ccaaatcgca tgggagccga tgtcgcaagt caccgttatg tcatcgctca 720

gcagttcacg caaatcgcga acgatttgca gcggatgaac aagatcagtt tttgtttctt 780

taggaggttc gctttgctcc tccagtgctt tcttcaagta atcaaggaca ggtgcaaagg 840

actcgtcgat ggaaaccggc agagaatcat gttcaatatg gtttaacgtc tctgcgatat 900

cgccgatcaa ctcgatttcg ggctgatagt catgatcgat atcggcttgt atttcgtcaa 960

gatgaatcac gcttcgttcg ccttttccat tccaaaagac cggatcgtat tcaatcggat 1020

catagccgac cgtcaaaacg acatccgctt tttccaatag catgtctccg ggctgattgc 1080

ggaatagtcc gatccggccg aagtactggt cttccaaatc gtgagacagc gtacccgctg 1140

cttggtatgt ttcaacaaac ggcagtttca ctttccttag cagacgccga accgcttcaa 1200

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tcgcttcagg tcttccgcct ttcatcccga caagcacgac aggaaggttc gcattgtgaa 1260

ttttggcgat ggccgcgctg atttgttcgt ccgaagccgc gcccagcttc ggcgccggca 1320

tggttttcac cggcttggca gttgccggac cggccgtaac gtcctgcgga aagctgagaa 1380

acgctgcgcc agcctgtcca gaagccgccg ctctgaatgc attggttaca gcctcaggta 1440

tgttgttcgc atcttccact tctgcgctat atttcgtaat cggctgaaac aacgccgcat 1500

tatccatcga ttgatgagtt tttttgagac gatccgctct ttttacagca cccgccaggg 1560

caacaaccgg atctccttct gtattggctg ttacaagacc ggtcgctaaa ttagacgctc 1620

ccggacctga agtcaccagg caaacaccgg gctttccagt caatcgtccg actgccgccg 1680

ccataaatgc tgcattctgc tcgtgacggc aaacgatcaa ttcaggcccc ttgtctttca 1740

atacgtcaaa caccgcatcg attttcgctc ccggaatacc gaaaacatga gtgacacctt 1800

gctgaatgag actatccacc acaagctctg ctcctcttac agtaagagtt tcatttttag 1860

cggctacatt attcaatgat ttagtttcgg tgtctatctc ttaatagcct cgatttattt 1920

tcggggctat taatcaactc tcagaggcga caagcttctt cttcccttac gacgttttta 1980

ttggttggac atggcaaggt tctctcttct gccgtta 2017

<210> SEQ ID NO 115
<211> LENGTH: 1588
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 115, Example 115: designer Prochlorococcus marinus MIT9313 groE-promoter-controlled Ketol-Acid Reductoisomerase DNA construct (1588 bp)

<400> SEQUENCE: 115

agaaaatctg gcaccacacc ccctttcaga gcggcgcaac attaccactg catggcgaga 60

tcttctcagg gttcggtgac ccgcacaggt atccactagt cggcacagca tcaacacaca 120

tagggttggc actcaatggc cacgagtgct actcatgtca ctcctcatcc acgttcctct 180

ccttgagcca aggcatcatt tttctgagtt cttttcctac tttttctatg agatgctctg 240

attctttctt tctcatggtg tagaagtagg gtcttcccgc ctgattttcg agtatccagt 300

ccttggcgaa ctttcccgtc tgaatgtcct tgagcatctg cttcatgttc tccctcactt 360

cttttgtaac gatcttttcc tgactgatgt agtcaccgta ctccgcggtg ttgctgacgg 420

agtatctcat gaaagagaga ccaccctcgt agatgaggtc aacgatgagc ttgagctcat 480

tgagacactc aaagtaagct atttccggtt gataacccgc ctccacaaga gtttcgaaac 540

cagcttttat gagagccgtt actccaccac agaggaccgc ctgctctcca aacaaatccg 600

tttccgtctc ttccttgaag gtcgtctcta tcacacccgc ccttgtcaca ccgatacctt 660

tggcataagc gagcgctata tctttggctt taccggtgta gtcctgatag accgctacga 720

gagccggcac accccttcct tcgacgtatt ctcttctcac gatgtgacca gggctcttcg 780

gagcgatcat cgtcacatcc acgttcttcg gaggtatgat ctggtgatag tggatgttga 840

acccgtgggc gaacatcagc atcttaccct cggtgaggtg tttttctatg tatttttgt 900

agatctccgg ctggttctca tctgggatga gcatcatgat gatgtcggcc tcttttgccg 960

cttcttctat tgctttcacg gtgagaccct gttcctccgc cttcttccag ctcttgcttc 1020

cctctctcaa tccgaccaca acgttgagac cgctgtcttt cagattcaac gcgtgcgcat 1080

gcccctgact tccgtaccct atgatcgcga tctttttgtc cctgatcagt tcgagatccg 1140

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cgtctttgtc ataataaatc actgccattg atttagtttc ggtgtctatc tcttaatagc 1200

ctcgatttat tttcggggct attaatcaac tctcagaggc gacaagcttc ttcttccctt 1260

acgacgtttt tattggttgg acatggcaaa acaatccagt cgagagctag cgcttgaacg 1320

ccgtaaggcc ctgagtaatt caggtaagaa atcaaccaca ttaaatggat caagtcctaa 1380

tcgcatccgt actgcctctg atgcacgtct aaccaggact gatcaatctt tcgttaaggc 1440

tgggaaagaa tctgtgcagc taaccgctcc taagagagag caactagata cgtcttttgt 1500

tgcttctaga gaatcatccg gagcttcgcg ccgtcaagtg aaaacgatcc gaaattcaag 1560

cagagaatgg ttctctcttc tgccgtta 1588

<210> SEQ ID NO 116
<211> LENGTH: 1960
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 116, Example 116: designer Prochlorococcus marinus MIT9313 groE-promoter-controlled Dihydroxy-Acid Dehydratase DNA construct (1960 bp)

<400> SEQUENCE: 116

agaaaatctg gcaccacacc ccctttcaga gcggcgcaac attaccactg catggcgaga 60

tcttctcagg gttcggtgac ccgcacaggt atccactagt cggcacagca tcaacacaca 120

tagggttggc actcaatggc cacgagtgct actcatgcta atctttcaag atagcgcctg 180

tactggcgga ttgcaccatt tttgaatatc ttttcatata gcctgagttt atcttgggtt 240

ccggaactcg ccactgcgtt ctcctggcag caagttcctc gtcgctaagt cgtacactaa 300

ggctgtggtt cggtatatca atgacgatta tgtctccgtc ctgaataaga gcaatattgc 360

ccccttgtgc cgcctcggga gatacgtgcc ctatagaagc tccccgggta gcaccagaaa 420

aacggccatc ggttataagg gctacgtcct tgtctagccc catccccgct atagcagaag 480

taggcgtgag catttccctc atccctggcc ctccgcgcgg cccttcatac cggattacga 540

cgacttctcc tttttcaatc ttgcctccta gaatggctgc aacagcttct tcttccgagt 600

cgaaaacccg tgctttaccc tcgtgataga gcatgtccgg gtcaactgcc cccttcttca 660

ccaccgcgcc ctcctcggcc aggttaccga acagtatagc caacccccccg gtagtactgt 720

gcggattctc tatactacgg atgacctcgt ggtccttcac agggtagtca ttgataacct 780

ccccaaccgt cttaccagta accgtcaggc actggcggtt taccagccct gccttgtcta 840

actcgttgaa aatggcctga actccacccg cagcgtacaa gtcttctata aaatggttgc 900

cggcaggttc gattttacat aggtgaggag tggtatcgct gatatggttt atcaggttca 960

agtccagctt aacgccggct tcgtgagcga tagccataag atgcaaaacc gtattggtag 1020

aacaacctat tgccatgtcc aggcgtaagg cattgatgaa agcctcttgg gtcatgatat 1080

cccggggctt tatgtccctt tcccatagct ccatcacttt catgcccgcc tgtttggcta 1140

gacggattcg ttcagagtgt accgccggta tagttccgtt cccgggtaag cccattccta 1200

ccgcttccgt caggcagttc atggaattag cggtaaacat accggcacag ctgccacaac 1260

ccgggcaagc tacatcttca agctccgcta agtccgaaag cgacatctta cctgcgctga 1320

ccgcgcctac cccttcaaag accgtgttga ggctgacctt gcgcccccgg aaattgccag 1380

ccaacatcgg ccctccgctg acaaacatac aaggaagatt gaggcgagcg gccgccatca 1440

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gcatcccagg gatgattttg tcgcagttag gtataaaaac cagggcatcg aaaggatgag 1500

ccatagccat tatctcaata gaatcggcaa tcagttcccg gctggccaga gagtatttca 1560

taccgatatg gttcatggca ataccatcgc ataccctat agtagaaaac tctataggag 1620

tgccccttt catcctcacc ccggctttga ccgcctcggc tatacggtct agatgaatat 1680

gccctggaat aatctcgttg gccgagttga ctataccgac taagggtctc tccaactcct 1740

catcggtcaa tcctaaagct ttaaacagtg aacggtgagg tgctttttct agacccttt 1800

tcgccaggtc acttctcatt gatttagttt cggtgtctat ctcttaatag cctcgattta 1860

ttttcggggc tattaatcaa ctctcagagg cgacaagctt cttcttccct tacgacgttt 1920

ttattggttg gacatggcaa ggttctctct tctgccgtta 1960

<210> SEQ ID NO 117
<211> LENGTH: 1945
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 117, Example 117: designer Prochlorococcus marinus MIT9313 groE-promoter-controlled 2-Keto Acid Decarboxylase DNA construct (1945 bp)

<400> SEQUENCE: 117

agaaaatctg gcaccacacc ccctttcaga gcggcgcaac attaccactg catggcgaga 60

tcttctcagg gttcggtgac ccgcacaggt atccactagt cggcacagca tcaacacaca 120

tagggttggc actcaatggc cacgagtgct actcatgtta tgatttattt tgttcagcaa 180

atagtttacc catttttttc agtacttttg gtgcatcttc ttttgccaaa actaactcaa 240

tccagtacat tctatttgga tctgcttgag cttctttcat gacagacaca aattcatttt 300

cagttctaac gattttcgag actactcgtt cttctgttgc tccaaatgat tctggtaatt 360

ttgagtaatt ccacattgga atatcattgt agctttgatt tggtccatga atttctcttt 420

cgactgtata accatcatta ttgataataa agcaaattgg attaattttt tctctgattg 480

ctaatcctaa ttcttgcact gtaagttgaa gtgaaccatc accaataaat aaaaggtgtc 540

tgctttcttt atctgcaatt tggcttccta atgctgctgg gaatgtatat ccaattgatc 600

cccataaggg ttgaccaata aaatgactct ttggttttaa gaaaattgat gaagcgccaa 660

agaatgatgt cccttgttca gcaacgattg tttcattgct ttgagttagg ttttcaactg 720

cttgccatag gcggtcttgt gataaaagcg catttgatgg aacaaagtct tcttgctttt 780

tatcgatata ttttcctttg tattctattc cgcttaggtc taagagagag gagatgaggg 840

attcaaaatc aaaattttgg atgctttcgt taaatatttt tccttcgtct atgttcagtg 900

aaatcatttt attttcattt aaatgatggg taaatgctcc tgttgaagag tctgtgagtt 960

taactccaag catcaggatg aagtcggctg attccacgaa ttctttaaga ttaggctctg 1020

agagtttacc attatagatt cctaaaaatg aagggagagt ttcatcaact gaacttttc 1080

caaagtttaa tgtcgtaata gggagttttg tctttgaaat aaattgagtg actgtatttt 1140

ctaagccaaa gctaattatt tcatgtcctg taatcacgat tggttttttg gcatttttca 1200

agctttcttg aattttattc aaaatctctt ggtcacttgt atttgaagtt ggattttctt 1260

ttttcaaagg gagtgagggt ttctctgctt ttgcagcagc aacatcaact ggtaagttga 1320

tatagacagg ttttctttct tttagtagtg cagaaagtac tcggtcaatt tcaacggttg 1380

cattttctgc tgtcagtaaa gttcgagctg ctgtaacagg ttcgtgcatt ttcataaagt 1440

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gtttaaaatc accgtcagcc agcgtatgat gaacaaattt tccttcattt tggacttttg 1500

atgtaggtga tcccactatt tctactactg gtaaattttc ggcgtaactt cctgctaatc 1560

cattaactgc actcaattca cctactccaa aggttgtaag aaatgcggca gctttttag 1620

tacgagcata gccatcagcc atataagaag catttaattc attagcattt ccgacccatt 1680

tcatatcctt gcgggaaata atttgatcta aaaattgtaa gttatagtct ccagggactc 1740

caaaaatttc ttcaattcct aactcgtgta atcggtctaa taggtaatct cctactgtat 1800

acattgattt agtttcggtg tctatctctt aatagcctcg atttattttc ggggctatta 1860

atcaactctc agaggcgaca agcttcttct tcccttacga cgtttttatt ggttggacat 1920

ggcaaggttc tctcttctgc cgtta 1945

<210> SEQ ID NO 118
<211> LENGTH: 1138
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 118, Example 118: designer Prochlorococcus marinus MIT9313 nirA-promoter-controlled Alcohol Dehydrogenase DNA construct (1138 bp)

<400> SEQUENCE: 118

agaaaatctg gcaccacacc cctctagttg ccaacatcag ccgggttcag aatgtacaca 60

aagacaccaa ttcttgaatt tcacacaaat gctcagtttt gttcaatctg ataccgccaa 120

taccctcttc catcaggctt aatgactcca ttcgcaactt acccttgctt caataatggc 180

agggcctaaa aaccatggct atcgaatgcg cgaataaaat ttaaacaaca tgatcacttc 240

ttttcaagtt taatttcaac aaaatttcat gttgtcaccg gtggagcgaa tgggatcggc 300

aaggcgatcg ctagagcaat tcgcaaaaca gggagcgaac gtcgtgatca tcgaccgcga 360

tattcaaaac ggtgaagcgt tcgccgcgca attgcaatcg gacgggttcg aggcgatctt 420

tgtggcggcg gatgtgcgga aggtggacga tattgaacgg tttgtacaag aagctgccgg 480

ccgcttcggc cgcattgact atttgatcaa caatgctggc gtctcacgct ggaagtcgcc 540

gtatgagctg acggttgagg agtgggatga cgtgctgtca acgaatttgc gcagcgcttt 600

ttttgcttct cgagaagcag ctaaatatat gcgccgcaat gcaaaaggcg gagcaatcgt 660

caacattgcc tcgacaaggg cgctcatgtc cgagccgaat tccgaggcgt acgctgcatc 720

gaaaggcggc cttgtcgctt tgacccatgc gctggcggtg tcgtttgcgg atgatcgcat 780

tcgcgtcaat tgcatcagcc ccggttggat tgaaacgggc gattatgggc aactgcgaga 840

cattgaccac cggcagcacc cggccggccg cgtcggcaaa ccggatgata tcgcccgcgc 900

ttgtctgtat ttatgcgatg aggaaaacga ttttatcacc ggggtaaatt tggtcatcga 960

cgggggaatg accaggaaaa tgatttatat tgagtagtga tttagtttcg gtgtctatct 1020

cttaatagcc tcgatttatt ttcggggcta ttaatcaact ctcagaggcg acaagcttct 1080

tcttccctta cgacgttttt attggttgga catggcaagg ttctctcttc tgccgtta 1138

<210> SEQ ID NO 119
<211> LENGTH: 1816
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 119, Example 119: designer Prochlorococcus marinus MIT9313 groE-promoter-

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controlled 2-Isopropylmalate Synthase DNA construct (1816 bp)

<400> SEQUENCE: 119

agaaaatctg gcaccacacc ccctttcaga gcggcgcaac attaccactg catggcgaga 60

tcttctcagg gttcggtgac ccgcacaggt atccactagt cggcacagca tcaacacaca 120

tagggttggc actcaatggc cacgagtgct actcatggtg agccagcgcg tttatatttt 180

tgacaccact ttgagggacg gcgagcagtc gcccggcgta agcctgaacg taggcgagaa 240

ggtgcaaatt gccaggcagt tagccaagct cggggtggac ataattgagg ccggctttcc 300

gattacctcg ccgggggact ttaaagccgt aagcgaaatt gcccggcagg tgaagggcgt 360

tacggtggcc gccctggcca gggccaactt ccaggatatc gaccgggcct gggaggccgt 420

gcgccacgcc gagcagccgc ggattcatac ctttattgcc acttccgaca ttcatttaaa 480

atacaagctg cgcatgagcc gggaggaagt cctggatgcg gcggtggcgg cggtaaagcg 540

cgccagggcc tacaccggcg atgtggagtt ttcggcggag gacgcctccc gctccgacct 600

ggacttcctc tgccgggtgc tggccgcggc cattgaggcg ggggctaccg taataaatat 660

accggatacg gtcggttatg ccgttcctga ggaatggggg aaatttatca atactattta 720

tcataaagtt cccggaattg aaaaggtcat tgtcagcgtg cactgccaca acgacctggg 780

catggccgtg gccaactccc ttgctgccgt aatgaacggc gccaggcagg tggaaggggc 840

catcaacggc attggcgagc gggcgggaaa cgctgccatc gaagagatgg taatggccct 900

ttatacccgt aaagatcagt acaaccttta caccaacatc aaaaccgagg aaatttacag 960

gaccagcaag ctggtgagcg ccctgacggg catgaaggtg cagccgaaca aggccgtggt 1020

gggcaaaaac gcctttgccc acgaggccgg cattcaccag gacggggtgc tgaaggagcg 1080

caccacctac gagataatga acccggccat ggtagggatc agcaagagca acctggtgct 1140

gggcaagcat tccgggcggc atgcattccg ccaccggctg gaggaaatgg gctacaatct 1200

ttcggacgaa gagctgaaca gcgcctttga gcgcttcaaa aagctggccg acaagaagat 1260

ggagattacc gacgaagacc tggaagccat tatagaagaa gaaatgcgcc ttgtgccgca 1320

cacctacacc cttgagtacc tgcatatttc cagcggcacc acggtggtgc ctaccgccac 1380

ggtgggctta aagcgggacg ggcagcttat ggaagaggcg gcctgcggca acggcccggt 1440

ggacgccatc tgcaaggcaa ttgataaaat aacggggctt aactgcacca tgacgagctg 1500

gggaatcaac gccgtcactg cgggcaagga cgcccttggc gacgtcagcc tgaaggtgac 1560

cgccgacggc gagaaggttt acgttgggcg cggaatcagc accgatgtgc tggaggccag 1620

cgccaaagct tacgtcaacg cggtcaacaa actcatctgg gattcgcaga aataatgatt 1680

tagtttcggt gtctatctct taatagcctc gatttatttt cggggctatt aatcaactct 1740

cagaggcgac aagcttcttc ttcccttacg acgtttttat tggttggaca tggcaaggtt 1800

ctctcttctg ccgtta 1816

<210> SEQ ID NO 120
<211> LENGTH: 2199
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 120, Example 120: designer Prochlorococcus marinus MIT9313 groE-promoter-controlled 3-Isopropylmalate Dehydratase DNA construct (2199 bp)

<400> SEQUENCE: 120

-continued

agaaaatctg gcaccacacc ccctttcaga gcggcgcaac attaccactg catggcgaga 60

tcttctcagg gttcggtgac ccgcacaggt atccactagt cggcacagca tcaacacaca 120

tagggttggc actcaatggc cacgagtgct actcatgatg gccatgacca taaccgaaaa 180

aattctggcc gatcacgccg gcaaaaagca ggttgagccc ggcgaactga tcagcgtaaa 240

ggttgatctg gtgctgggca acgacataac ggcgccggtg gcgattaaag agtttgagaa 300

aataggggtg gcggaagtct ttgaccggga gcgggtggcc ctggtcccgg atcactttac 360

ccctaacaag gacattaagt cggcggaaca gtctaaaatt ctaagggagt tttccaaaaa 420

gcacaacctt gccaactatt tcgaggtggg ccgggccggc attgagcact gccttctgcc 480

cgaggaaggg ctggtaggcc ccggcgacct ggttatcggc gccgactcgc acacctgcac 540

ctacggcgcc ctgggggcct tctccacggg cgtgggcagc accgacctgg cggctgccat 600

ggcgctgggg gaaacctggc tgaaagtgcc ggagtcaatc aaattcgaat atgacgggga 660

aatgcagccc tgggtaggcg gcaaggacat gatcctgcac acaatcgggg atatcggggt 720

ggacggggcc ctttacaagg ctatggagtt taccggcccg gccgttgaaa aactttccat 780

ggacgggcgc tttaccatgt gcaacatggc cgtagaggcc gggggtaaga acggcattat 840

tgctccggac gaaacaaccc gggtctatgt cgagggccgc tgcaagcgac cctatcgttt 900

ttatcggagc gacccggacg ccaaatacga aaagatctac cgctacgacg cggcgcagat 960

cgaaccgcag gtggcctttc cccacctgcc cgaaaactcc cggccggtca gcgaggcagg 1020

caacattgaa atcgatcagg ttgttatcgg ctcctgcacc aacggccgga tggaggacct 1080

gcgggaggcc gccagggtgc tgaagggcag aaaagtgcat aaaaacgtcc gccttattat 1140

ttttccggga acgccgaaaa tttacctgca ggccttgcgg gaggggctga tcgaaacttt 1200

tgtcgaagct ggcggagtcg tgagcacgcc cacctgcggg ccctgcctgg gcggccactc 1260

gggcattctg gccaggggag agcgctgcgt tgccaccacc aaccgcaact ttgtaggcag 1320

gatggggcat cctgaaagcg aagtgtacct gtccaacccg gcagttgccg cggcttcggc 1380

cgtgctgggc cggataggcg gtccatggga ggtggattga ccctttcaga gcggcgcaac 1440

attaccactg catggcgaga tcttctcagg gttcggtgac ccgcacaggt atccactagt 1500

cggcacagca tcaacacaca tagggttggc actcaatggc cacgagtgct actcatgatg 1560

gaaattaaag ggaaagtgtg gaagttcggc ccggatatcg atacagacgc cattataccg 1620

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attttcgagt ctcccgaagc cgccgggggc attggccagg gcgacgaggt ggcggtggac 1920

gcggctgccg gcattataac cgacctgacc accggcaaga cctaccgggc ggcgccggtt 1980

ccgcctttca tgcggcagat cattgccgcc ggagggctga tcaattacgt ggccgggaag 2040

gtgagaggca atgcataatg atttagtttc ggtgtctatc tcttaatagc ctcgatttat 2100

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tattggttgg acatggcaag gttctctctt ctgccgtta 2199

<210> SEQ ID NO 121

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<211> LENGTH: 1378
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 121, Example 121: designer Prochlorococcus marinus MIT9313 groE-promoter-controlled 3-Isopropylmalate Dehydrogenase DNA construct (1378 bp)

<400> SEQUENCE: 121

agaaaatctg gcaccacacc ccctttcaga gcggcgcaac attaccactg catggcgaga 60

tcttctcagg gttcggtgac ccgcacaggt atccactagt cggcacagca tcaacacaca 120

tagggttggc actcaatggc cacgagtgct actcatgcta cacctcgacc tcctcaactt 180

ttctcgctac taaatcaccc atttccctgg tgttaaccag cttctgatcc ggctccgtaa 240

tgtccggcgt ccggtagcct tcggccagaa cttcgcggac cgcctgctca accgccaaag 300

cctcttgttc caaatcgaac gaatacctca gcatcatggc agccgacagt atcgtagcca 360

acgggtttgc tttcccctgc ccggcgatat cgggagctga cccgtgagaa ggctcataca 420

ttcctacttt cccgccaata gaggcagaag gtagcattcc caaagatccg gtcagcatag 480

aggcttcgtc ggtcaatata tctccaaaca tgttttcagt tacgatcaca tcgaattgac 540

gcggattgcg tatgagctgc atggcacagt tgtcgacgta catgtggctg aattcgacgt 600

caggatactc cagagctact cgattggcca cctcgcgcca taacctagag ctttctagaa 660

cattggcctt gtccaccgat gtcacttttct ttctccgttt cctcgccgcc tcgcaggcca 720

aacgaactat gcgttcgatc tcatacgtcg agtactccag aacatcgata gccctttctc 780

cgcccagaag cttctcccgc cgcttctccc cgaagtacaa cccgccggtc agttccctca 840

ctaccaagag atctactccc tcgataatat cgggtttcag ggaggaagca tgaaccagtt 900

ccgggaacag gtaagcgggc cgcaggttag cgtaaagccc aagttcctta cgcagagcca 960

acagcgctgc cgcctcgggc ctgagcgcag ccggcaggtt atcccatttg ggaccaccta 1020

tggctcctag aagaacagcg tcgctatctt tgcacagggc cagggtttct tcaggcaaag 1080

gaacccccac ctcgtcgata gccgctcccc cgaccagggc ttcggtaaaa gcgaattcgt 1140

gtttgaacct cttagcaact gctttcaata ctttttgcgc ttcaggtacg atctcggtcc 1200

cgataccatc cccgggtaac acggctatct taaacactga tttagtttcg gtgtctatct 1260

cttaatagcc tcgatttatt ttcggggcta ttaatcaact ctcagaggcg acaagcttct 1320

tcttccctta cgacgttttt attggttgga catggcaagg ttctctcttc tgccgtta 1378

<210> SEQ ID NO 122
<211> LENGTH: 1327
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 122, Example 122: designer Prochlorococcus marinus MIT9313 groE-promoter-controlled 3-Methylbutanal Reductase DNA construct (1327 bp)

<400> SEQUENCE: 122

agaaaatctg gcaccacacc ccctttcaga gcggcgcaac attaccactg catggcgaga 60

tcttctcagg gttcggtgac ccgcacaggt atccactagt cggcacagca tcaacacaca 120

tagggttggc actcaatggc cacgagtgct actcatgatg tcagttttcg tttcaggtgc 180

taacgggttc attgcccaac acattgtcga tctcctgttg aaggaagact ataaggtcat 240

cggttctgcc agaagtcaag aaaaggccga gaatttaacg gaggcctttg gtaacaaccc 300

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aaaattctcc atggaagttg tcccagacat atctaagctg gacgcatttg accatgtttt 360

ccaaaagcac ggcaaggata tcaagatagt tctacatacg gcctctccat tctgctttga 420

tatcactgac agtgaacgcg atttattaat tcctgctgtg aacggtgtta agggaattct 480

ccactcaatt aaaaaatacg ccgctgattc tgtagaacgt gtagttctca cctcttctta 540

tgcagctgtg ttcgatatgg caaaagaaaa cgataagtct ttaacattta acgaagaatc 600

ctggaaccca gctacctggg agagttgcca aagtgaccca gttaacgcct actgtggttc 660

taagaagttt gctgaaaaag cagcttggga atttctagag gagaatagag actctgtaaa 720

attcgaatta actgccgtta acccagttta cgtttttggt ccgcaaatgt ttgacaaaga 780

tgtgaaaaaa cacttgaaca catcttgcga actcgtcaac agcttgatgc atttatcacc 840

agaggacaag ataccggaac tatttggtgg atacattgat gttcgtgatg ttgcaaaggc 900

tcatttagtt gccttccaaa agagggaaac aattggtcaa agactaatcg tatcggaggc 960

cagatttact atgcaggatg ttctcgatat ccttaacgaa gacttccctg ttctaaaagg 1020

caatattcca gtggggaaac caggttctgg tgctacccat aacacccttg gtgctactct 1080

tgataataaa aagagtaaga aattgttagg tttcaagttc aggaacttga aagagaccat 1140

tgacgacact gcctcccaaa ttttaaaatt tgagggcaga atataatgat ttagtttcgg 1200

tgtctatctc ttaatagcct cgatttattt tcggggctat taatcaactc tcagaggcga 1260

caagcttctt cttcccttac gacgttttta ttggttggac atggcaaggt tctctcttct 1320

gccgtta 1327

<210> SEQ ID NO 123
<211> LENGTH: 2004
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 123, Example 123: designer Cyanothece sp. ATCC 51142 nirA-promoter-controlled 2-Isopropylmalate Synthase DNA construct (2004 bp)

<400> SEQUENCE: 123

agaaaatctg gcaccacacc tattaaatct aaaatagctg ttttagctaa aatagtcaat 60

agcaagtctt ataggtaatc aaacgcaact aaaatgcaaa aaatccataa ttaaaatgca 120

aaaaacggat ttttaataca attttgttac attagctaca aaatatctca aatggtagag 180

gttaaatagg tacaactcga ccagatggag ggttttccct gtgatgaact gttccttctt 240

cccttatact ctccttggat agaatgtagt tccttctcat gatggctctg tttaaggcat 300

ctacaaaacc gcttacgctg gcttttatta tgtccgtatc cacgcctcta cctgaggctt 360

ttacattatc cagctctatc acaaggcgcg cctctgcctg cgcatccgtg ttgggggtga 420

gagcttttat agaaaagtca atgagtctgg gctccacctt aagagctttc tgtatggctt 480

ttatcacagc atccacagga ccgtttcccg tagatgtggc agtcctttct tcacctctaa 540

agctcagcac tactgtagcg gtaggaagca ggttgtcccc tgtctgaacc tgatagtgtt 600

ttacctttat aggctcttcc tcctccacct tcataaactc ttcgtatatg agggcttcca 660

aatcctcatc atatacctcc tttttcttat ccgcaagagc cttgaacttt tcaaagatcc 720

tctccaggtc ttcatcgctt agcttaaagc caagttcatt cagtctcctc tttagagcgt 780

gcctccctga gtgtttacca agtattattc tggtggaggg aaaacctaca tcctcggggt 840

-continued

tcattatctc gtaggtgaga gggtgagcca gcacaccgtg ctggtgtatg cccgattcat 900

gagcaaaggc attatccccc actatagcct tgttgggttg aacaaaagag ccggttatcc 960

tgcaaaggag cctgctggtt ttgtatatct ctctggtgtt tatgtccgtg tagagccctc 1020

caaagaagtc tttgcgcact ttgagagcca tcactatctc ctcaagggct gcgtttcctg 1080

ctctttcacc tatgccgttg atggtgcact ctacctgtct tgcaccgtgc tttaccgcca 1140

taagggagtt ggcaacagcc atcccaaggt catcatgaca gtgcacgctt ataatggctc 1200

tgtctatgtt gggcacgttg ttccttatgt cctctatgag ccttgcaaac tcttctggca 1260

ccgcatagcc aacggtgtcg ggaatgttta taacggtagc acctgccttt atggctgttt 1320

ctatcaccct gtagaggaac tctctctggc ttctggtggc atcctcgcag gaaaactcca 1380

catcgtcagt aaaccttctg gcaaactcca cagctttttt agcccctttcc agaacctcct 1440

ctggggacat cctaagcttg tacttcatgt gtatctcgga agtagctatg aaggtgtgta 1500

tcctctttct tctggctggc tttagagcct cccctgctag ctctatgtcc ttttccaatg 1560

ctctggcaag ggagcatatt atcggacctt ctacctgctg tgctatcaga tggacgctct 1620

caaagtctcc cttagatgct gctgcaaagc ctgcctctat aacatccacc cccagcttgg 1680

caagttggtg agccatctga agtttttcat cagcagtcat agaaaaaccc ggcgcttgct 1740

ctccgtctct cagcgtggtg tcaaatatgt aaaccttctc cattaagctg ttttagagaa 1800

atttgttcgg taaatattag cctacctaca gttgttgtgg gtaggctaat attatgaatt 1860

gagtcctact gaaccaatga ttatcgttac gactaaaagt aataaatgtc atcagcagga 1920

taggggttga taggaaaagt tttttaatcg gatggttttc gagttagagg ttagggtttc 1980

tttaggttct ctcttctgcc gtta 2004

<210> SEQ ID NO 124
<211> LENGTH: 2648
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 124, Example 124: designer Cyanothece sp. ATCC 51142 nirA-promoter-controlled Isopropylmalate Isomerase large/small subunits DNA construct (2648 bp)

<400> SEQUENCE: 124

agaaaatctg gcaccacacc tattaaatct aaaatagctg ttttagctaa aatagtcaat 60

agcaagtctt ataggtaatc aaacgcaact aaaatgcaaa aaatccataa ttaaaatgca 120

aaaaacggat ttttaatata attttgttac attagctaca aaatatctca aatggtagag 180

gttaaatagg tacaactcga ccagatggag ggttttccct gtgatggtgc caaagacgat 240

tattgaaaaa atttgggatg aacacgtggt ttaccgtgaa gatgggaaac ccgatttatt 300

atatattgat ttacatctcg ttcatgaagt gacatcgccg caagcttttg aaggattgcg 360

acaaaaagga agaaaagtgc gtcgcccaga tttaacattt gcgacgatgg accataacgt 420

tccaacgatt aatcggtccg ttgttgaaga tgaagtggcg aaaaatcaaa tgacagcatt 480

ggagcggaac tgtcgtgagt tcggtgttcc gcttgccgat ttaaacagtc cagaacaagg 540

gattgttcat gtcatcggtc cagaactcgg gttgacacag cctgggaaaa ccattgtgtg 600

tggagatagc catacgtcta cacatggcgc ttttggggca ttagcgttcg ggatcggaac 660

gagtgaagtc gaacacgtat tagcgacgca aacgttatgg caacatcgtc caaagacgat 720

-continued

gcaagtgaac gttacgggat cgttagcacc gggcgtatca gcaaaagacg ttattttagc 780

gatcattggc aagtttggag ttgattttgg cacaggctac gtgcttgagt ttacaggcga 840

tgttattcgt cgtatgtcaa tggaagagcg gatgacaatt tgcaatatgt cgattgaagc 900

aggggcacga gctgggttaa ttgccccaga tgatgtgacg tttgcatatt taaaagagag 960

aaaatatgca ccgaaaggag aagcgtttga gcaggcagtt gaaaagtgga agcagttatg 1020

cacagatgaa ggagcggtat acgatcgtgt cgttcatatt gatggaagtg aaattgctcc 1080

aacagtgaca tggggcacaa cgccagcaat gagctctccg atcgatggaa ctgttccaga 1140

tccgaacgag tttgcgacag aaacagagag aaaagctgta cagttagcgt tgcaatatat 1200

gggattaaag ccaggaacga aaatgacgga tattgcggtg caacatgtgt ttatcggatc 1260

atgcacaaac tcgcgcataa gcgatttacg ggaagcggcg caaattgtaa aaggaaaaaa 1320

agtcgcaccg ggcgtcagag cgctcgtcgt tccgggctca caacaagtaa aaaagcaggc 1380

agaagaagaa ggaattgctc aaacgtttat tgacgcaggc tttgaatggc gcgattccgg 1440

ctgtagcatg tgtcttggaa tgaatccaga tactgttcca gcaggggaac attgcgcctc 1500

aacgtcaaac cgcaatttcg aagggagaca aggaaaaggg gcgcgcacgc atctcgtgag 1560

tccagcaatg gcagccgcgg ctgcgattta cgggcatttt gtcgatgtgc gtacattgta 1620

taaagaagtg gtaagatagt attaaatcta aaatagctgt tttagctaaa atagtcaata 1680

gcaagtctta taggtaatca aacgcaacta aaatgcaaaa aatccataat taaaatgcaa 1740

aaaacggatt tttaatacaa ttttgttaca ttagctacaa aatatctcaa atggtagagg 1800

ttaaataggt acaactcgac cagatggagg gttttccctg tgatggaacc attcgtcgtt 1860

cataaaggaa aagtggctgg cttagatcga gcaaatatag atacggatca aattattccg 1920

aaacaatttt taaaacgaat tgaacgcacc ggatttggtc aatttctttt ttacgattgg 1980

cgttatttat cggacggaac accaaaccca cattttgagt taaaccgtcc tgaaaacgag 2040

ggcgcgacca ttttagtcgc aaatgaaaat ttcggatgtg gttcatcgcg cgaacacgct 2100

ccttgggcgc ttgcggatta cggatttcgt gccattattg ctccttcatt tgctgatatt 2160

ttttacaaca actgtttgaa aaatagttta cttcctatta aacttccaaa agaagacgtc 2220

gcttatttgt taaaacaagc ggaacgggca gattacgaac taacgatttc gcttgaacaa 2280

caagtcgttt ttgatgatga agggtttaca agctcgttcg acatcgatcc gtatcgaaaa 2340

cagctccttt taaaaggttg ggacgaaatt gatttaacgt tcgtgtatga accatatatt 2400

atcgcctacg aaaaaaaacg ctcttgataa gctgttttag agaaatttgt tcggtaaata 2460

ttagcctacc tacagttgtt gtgggtaggc taatattatg aattgagtcc tactgaacca 2520

atgattatcg ttacgactaa aagtaataaa tgtcatcagc aggatagggg ttgataggaa 2580

aagtttttta atcggatggt tttcgagtta gaggttaggg tttctttagg ttctctcttc 2640

tgccgtta 2648

<210> SEQ ID NO 125
<211> LENGTH: 1530
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 125, Example 125: designer Cyanothece sp. ATCC 51142 nirA-promoter-controlled 3-Isopropylmalate Dehydrogenase DNA construct (1530 bp)

<400> SEQUENCE: 125

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agaaaatctg gcaccacacc tattaaatct aaaatagctg ttttagctaa aatagtcaat 60

agcaagtctt ataggtaatc aaacgcaact aaaatgcaaa aaatccataa ttaaaatgca 120

aaaaacggat ttttaataca attttgttac attagctaca aaatatctca aatggtagag 180

gttaaatagg tacaactcga ccagatggag ggttttccct gtgatggcaa ccacgtatcg 240

cattgctgtt ttggcggggg atggtattgg cccagaaatt acggccgttg cccttgatgt 300

attgcgggcg atcgcccctc gctttgggtt ggactttgac tttgttcccg cccttgtggg 360

gggctgcgcc attgatgctg tgggggaacc cttgccagca gcaacgctag ccacctgtcg 420

tcagagtgat gccgtgctcc tagctgccat tggcggaacg cagtgggata gcctaccccg 480

tcatctgcgc ccggaaaccg gattacttgc cctgcggtct ggtctaggtt tatttgccaa 540

cctacgcccc gccaaaatct ttccccagct tctccatgcc tcctccctca agccggaagt 600

gattgccggt gtggatctca tggtggtgcg cgaactgacg ggtggcattt actttggtca 660

accgcgcggt attttcacca ctgaaacggg tgagcagcgg ggggtgaata cgatggccta 720

taccgccacg gaaattgatc gcattggccg tgttgccttt gaaaccgctc gcaaacggca 780

gggcaaactc tgctccgtgg ataaggccaa tgtccttgaa gtctcccaac tgtggcgcga 840

tcgcctgacc gccctcagtg ctgagtaccc ggatgtggaa ctgacgcacc tttatgtgga 900

caatgcagca atgcaactgg tgcgcgcccc gaaacagttt gacacgattg tgaccagtaa 960

cctctttggt gatatcctct ccgatattgc cgccatgctc accggtagta ttggcatgct 1020

tccctccgcc agcctagggg aatcggggcc agctctgttt gaaccggttc atggctctgc 1080

ccccgacatt gccggccaag acaaggccaa ccccctcgcc atggtgctca gtgcggcaat 1140

gatgctgcgt tatggtctga accaaccagc ggcagcgcaa gcgatcgaag aggccattac 1200

tgccgtttta gatcagggct accgcaccgg cgatttaatg tctgagggct gcacgcttgt 1260

gggctgtcgc gaaatgggca acctcctaat caaggaattg tcccgataat aagctgtttt 1320

agagaaattt gttcggtaaa tattagccta cctacagttg ttgtgggtag gctaatatta 1380

tgaattgagt cctactgaac caatgattat cgttacgact aaaagtaata aatgtcatca 1440

gcaggatagg ggttgatagg aaaagttttt taatcggatg gttttcgagt tagaggttag 1500

ggtttcttta ggttctctct tctgccgtta 1530

<210> SEQ ID NO 126
<211> LENGTH: 2088
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 126, Example 126: designer Cyanothece sp. ATCC 51142 nirA-promoter-controlled 2-Keto Acid Decarboxylase DNA construct (2088 bp)

<400> SEQUENCE: 126

agaaaatctg gcaccacacc tattaaatct aaaatagctg ttttagctaa aatagtcaat 60

agcaagtctt ataggtaatc aaacgcaact aaaatgcaaa aaatccataa ttaaaatgca 120

aaaaacggat ttttaataca attttgttac attagctaca aaatatctca aatggtagag 180

gttaaatagg tacaactcga ccagatggag ggttttccct gtgatgtata cagtaggaga 240

ttacctgtta gaccgattac acgagttggg aattgaagaa atttttggag ttcctggtga 300

ctataactta caatttttag atcaaattat ttcacgcgaa gatatgaaat ggattggaaa 360

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tgctaatgaa ttaaatgctt cttatatggc tgatggttat gctcgtacta aaaaagctgc 420

cgcatttctc accacatttg gagtcggcga attgagtgcg atcaatggac tggcaggaag 480

ttatgccgaa aatttaccag tagtagaaat tgttggttca ccaacttcaa aagtacaaaa 540

tgacggaaaa tttgtccatc atacactagc agatggtgat tttaaacact ttatgaagat 600

gcatgaacct gttacagcag cgcggacttt actgacagca gaaaatgcca catatgaaat 660

tgaccgagta ctttctcaat tactaaaaga aagaaaacca gtctatatta acttaccagt 720

cgatgttgct gcagcaaaag cagagaagcc tgcattatct ttagaaaaag aaagctctac 780

aacaaataca actgaacaag tgattttgag taagattgaa gaaagtttga aaaatgccca 840

aaaaccagta gtgattgcag gacacgaagt aattagtttt ggtttagaaa aaacggtaac 900

tcagtttgtt tcagaaacaa aactaccgat tacgacacta aattttggta aaagtgctgt 960

tgatgaatct ttgccctcat ttttaggaat atataacggg aaactttcag aaatcagtct 1020

taaaaatttt gtggagtccg cagactttat cctaatgctt ggagtgaagc ttacggactc 1080

ctcaacaggt gcattcacac atcatttaga tgaaaataaa atgatttcac taaacataga 1140

tgaaggaata attttcaata aagtggtaga agattttgat tttagagcag tggtttcttc 1200

tttatcagaa ttaaaaggaa tagaatatga aggacaatat attgataagc aatatgaaga 1260

atttattcca tcaagtgctc ccttatcaca agaccgtcta tggcaggcag ttgaaagttt 1320

gactcaaagc aatgaaacaa tcgttgctga acaaggaacc tcatttttg gagcttcaac 1380

aattttctta aaatcaaata gtcgttttat tggacaacct ttatggggtt ctattggata 1440

tacttttcca gcggctttag gaagccaaat tgcggataaa gagagcagac acctttttatt 1500

tattggtgat ggttcacttc aacttaccgt acaagaatta ggactatcaa tcagagaaaa 1560

actcaatcca atttgtttta tcataaataa tgatggttat acagttgaaa gagaaatcca 1620

cggacctact caaagttata acgacattcc aatgtggaat tactcgaaat taccagaaac 1680

atttggagca acagaagatc gtgtagtatc aaaaattgtt agaacagaga atgaatttgt 1740

gtctgtcatg aaagaagccc aagcagatgt caatagaatg tattggatag aactagtttt 1800

ggaaaaagaa gatgcgccaa aattactgaa aaaaatgggt aaattatttg ctgagcaaaa 1860

taaatagtaa gctgttttag agaaatttgt tcggtaaata ttagcctacc tacagttgtt 1920

gtgggtaggc taatattatg aattgagtcc tactgaacca atgattatcg ttacgactaa 1980

aagtaataaa tgtcatcagc aggatagggg ttgataggaa aagtttttta atcggatggt 2040

tttcgagtta gaggttaggg tttctttagg ttctctcttc tgccgtta 2088

<210> SEQ ID NO 127
<211> LENGTH: 1503
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 127, Example 127: designer Cyanothece sp. ATCC 51142 nirA-promoter-controlled Hexanol Dehydronase DNA construct (1503 bp)

<400> SEQUENCE: 127

agaaaatctg gcaccacacc tattaaatct aaaatagctg ttttagctaa aatagtcaat 60

agcaagtctt ataggtaatc aaacgcaact aaaatgcaaa aaatccataa ttaaaatgca 120

aaaaacggat ttttaataca attttgttac attagctaca aaatatctca aatggtagag 180

gttaaatagg tacaactcga ccagatggag ggttttccct gtgatggaac tcgacctcga 240

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cggtcccggg gttggtgaag tgctgatcaa gtacaccgcc gcggggttgt gccattcgga 300

cctgcacttg accgacgggg acctaccgcc gcgctatcca atcgtcgggg ggcacgaggg 360

gtcaggcatc atcgaggacg tcggacctgg ggtcaccaag gtcaaaccag gcgatcacgt 420

tgtttgcagc ttcatcccga actgcggaac ctgtcggtac tgcgccaccg gacgctccaa 480

cctctgcgat atgggcgcca ccatcctcga agggtgcatg cccgacggca gttaccggtt 540

ccacagtaac ggcctggatt tcggtgcgat gtgcatgctc ggcacattct ccgaacgcgc 600

aactatctcc cagcattcgg tggtcaagat cgacgactgg ctgccgctcg agaccgcggt 660

ggtcgtcggc tgcggcgtgc cgactggctg gggcacctcc gtctatgccg gcggggttcg 720

ttgcggtgac accaccgtca tctatggcgt cggcggcctg ggagtcaacg ccgtccaagg 780

cgcggtgagt gcgggcgcga agtacatcgt ggtcgtcgat ccggttgcgt tcaaacgcga 840

caccgcgctc aagttcggcg ccacccacgc gttcgccgac gccgccaccg ccgcggccaa 900

ggtcgacgaa ctgacctggg gacagggtgc cgatcaggcg ctgatcctgg tcggcaccgt 960

cgacgaggac gtggtctcgg cggcgactgc ggtgatcggt aagggaggca ccgtcgtgat 1020

caccggactg gcggacccag caaagctcac ggtgcacgtt tcgggaacgg acctgacgct 1080

taacgagaag acaatcaagg gcacgttgtt cggctcgtcc aatccgcaat acgacatcgt 1140

acggctgctc cgtctctacg acgccggcca gctaaaactc gacgatctga tcaccacccg 1200

atacacgctc gaccaggtca accagggcta ccaggatctg cgagacggca agaacatccg 1260

cggcgtgatc atccacgcct gataagctgt tttagagaaa tttgttcggt aaatattagc 1320

ctacctacag ttgttgtggg taggctaata ttatgaattg agtcctactg aaccaatgat 1380

tatcgttacg actaaaagta ataaatgtca tcagcaggat aggggttgat aggaaaagtt 1440

ttttaatcgg atggttttcg agttagaggt tagggtttct ttaggttctc tcttctgccg 1500

tta 1503

<210> SEQ ID NO 128
<211> LENGTH: 1149
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 128, Example 128: designer Cyanothece sp. ATCC 51142 nirA-promoter-controlled short-chain Alcohol Dehydrogenase DNA construct (1149 bp)

<400> SEQUENCE: 128

agaaaatctg gcaccacacc tattaaatct aaaatagctg ttttagctaa aatagtcaat 60

agcaagtctt ataggtaatc aaacgcaact aaaatgcaaa aaatccataa ttaaaatgca 120

aaaaacggat ttttaataca attttgttac attagctaca aaatatctca aatggtagag 180

gttaaatagg tacaactcga ccagatggag ggttttccct gtgatgaagg ttgccgtaat 240

tactggggca tcccgtggaa tcggggaagc tatagcaaag gcccttgctg aagatggata 300

ttcccttgcc ttaggggcta gaagtgttga taggttagag aagattgcca aggaactcag 360

cgaaaaacat ggggtggagg tattttacga ctacctcgat gtatcaaaac cagaaagcgt 420

tgaagagttt gcaaggaaaa cgctagctca ctttggagat gtggacgttg ttgtggccaa 480

tgcggggctt ggttactttg gtaggcttga agagcttaca gaagagcagt tccacgaaat 540

gattgaagta aacctttttgg gagtttggag aacaataaaa gctttcttaa actccttaaa 600

-continued

gcggactgga ggagtggcta ttgttgttac ttcagatgtt tctgcaaggc tacttccata 660

cggtggaggt tatgtggcaa ctaaatgggc tgcaagagca ttggtaagga ccttccagat 720

tgagaatcca gatgtgaggt tcttcgagct aagacctgga gcagtagata catattttgg 780

agggagcaaa gctgggaagc caaaggagca agggtattta aaacctgagg aagttgctga 840

ggcagtaaaa tacctcctaa gacttccaaa ggatgttagg gttgaggaat taatgttgcg 900

ctcaatttat caaaaacctg agtattgata agctgtttta gagaaatttg ttcggtaaat 960

attagcctac ctacagttgt tgtgggtagg ctaatattat gaattgagtc ctactgaacc 1020

aatgattatc gttacgacta aaagtaataa atgtcatcag caggataggg gttgatagga 1080

aaagtttttt aatcggatgg ttttcgagtt agaggttagg gtttctttag gttctctctt 1140

ctgccgtta 1149

<210> SEQ ID NO 129
<211> LENGTH: 1910
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 129, Example 129: a designer Nial-promoter-controlled chloroplast-targeted Phosphoglycerate Mutase DNA construct (1910 bp)

<400> SEQUENCE: 129

agaaaatctg gcaccacacc atggtagggt gcgagtgacc ccgcgcgact tggaagggtt 60

caaacgaccc cgccgtacga acttttgtcg gggggcgctc ccggatggta gggtgcgagt 120

gaccccgcgc gacttggaag ggttcaaacg accccgccgt acgaactttt gtcgggggggc 180

gctcccggat ggccgccgtc attgccaagt cctccgtctc cgcggccgtg gctcgcccgg 240

cccgctccag cgtgcgcccc atggccgcgc tgaagcccgc cgtcaaggct gcccccgtgg 300

ctgccccggc tcaggccaac cagatgactc gtgtcatcat tgtgcgtcat ggtcaaagta 360

catataatgt tgaacgacgt atccaaggac gtactgatgc gtcaacttta acggataaag 420

gtcggagcga tgctggtaaa gtgggtaaag ccctgagtaa tatagcattt acagcaatat 480

atagcagtcc tctcaaccga gcgaagacga cagcggaaat tattcgcagt gagttggttg 540

aacattcgtc cgtgattcag gtttctgaac atctggttga agtagattta cctttgtggg 600

caggaatgtt atctcttgat gtgaaagaga agtttcctga tgactatagt atttggaaaa 660

aacgtcccca cgaattgcat atgattgtca gtgacgcaca cgggacacga gaacttttcc 720

cagttctggc tttatatgaa caagccaagc agttttggca agaaatgtta tctcgtcatc 780

aaggggaaac tattctcatt gttggacata atggtattaa ccgcgctctg attagtacgg 840

ctttgggtat tcctcccagt gtttatcacg gactacaaca gtctaattgc gcgattagcg 900

ttttaaattt tgcgggtggt ttgggtgata cggttcagct agattcaatg aatcagacgc 960

aacatttgga agatacttta cccactttgc gaccaaatca tcaaggattt agattattat 1020

tagtacgtca tggggaaaca gaatggaatc gtcaaggtaa gtttcaaggc caaattgacg 1080

ttcctctgaa tgataatggc agagcgcaag caggaaaaac tggggagttt ctccaagagg 1140

tggcgcttga ttttgctttt agtagcacta tggcgcgtcc aaaagaaaca gcggaaatta 1200

ttcttcagaa gcatgctgat ataaagttgg aattactaga tggtttacgg gaaatcagtc 1260

acggcagttg ggaaggcaag tttgagtcag aaatagaaca agagtttccc ggagtgttgg 1320

aacgctggcg tactgtacct gctgaagtac aaatgccgca aggggaaaat ttacaacagc 1380

-continued

tatgggaacg tagtgtggct gcttggcagt caatattaca atcggctgag gtaaatcaat 1440

ggcaaattgg gttggtagtg gctcacgatg ctactaataa aactttactc tgcaatatct 1500

tgggtttatc tccagaaaat ttctggaatt tccgtcaagg taatggggca gttagtgtta 1560

ttgactaccc tttaggcgct agtggtttac cagtactgca agcgatgaac attactagtc 1620

atttgagtgg tggtgtatta gataaaacgg cagcaggagc attgtagtaa atggaggcgc 1680

tcgttgatct gagccttgcc ccctgacgaa cggcggtgga tggaagatac tgctctcaag 1740

tgctgaagcg gtagcttagc tccccgtttc gtgctgatca gtctttttca acacgtaaaa 1800

agcggaggag ttttgcaatt ttgttggttg taacgatcct ccgttgattt tggcctcttt 1860

ctccatgggc gggctgggcg tatttgaagc ggttctctct tctgccgtta 1910

<210> SEQ ID NO 130
<211> LENGTH: 1856
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 130, Example 130: designer Nial-promoter-controlled chloroplast-targeted Enolase DNA construct (1856 bp)

<400> SEQUENCE: 130

agaaaatctg gcaccacacc atggtagggt gcgagtgacc ccgcgcgact tggaagggtt 60

caaacgaccc cgccgtacga acttttgtcg gggggcgctc ccggatggta gggtgcgagt 120

gaccccgcgc gacttggaag ggttcaaacg accccgccgt acgaactttt gtcgggggggc 180

gctcccggat ggccgccgtc attgccaagt cctccgtctc cgcggccgtg gctcgcccgg 240

cccgctccag cgtgcgcccc atggccgcgc tgaagcccgc cgtcaaggct gcccccgtgg 300

ctgccccggc tcaggccaac cagatgctta ggtcctaaac caacagtacc agcataaaca 360

gcgcgatcgc ctaattcatc ttcaattctg agtaaacgat tgtattttgc tacccgttca 420

ctacgacaaa gagaaccagt tttaatttga cctgcacgag tggctacagc caaatcagca 480

atagttgtat cctcagtttc accagaacga tggctaatga ctgagcggaa accgttgcga 540

gtagctaaat caatagtttc caaagtttca gtcagtgaac caatttgatt caacttaatc 600

aaaatcgagt tacctgcttt ttgctcaatc ccttttttgta accgagtagc gttagtaaca 660

aataaatcat cacccaccaa ctgtactcgt gaacccaact tctgagtcag taattgccaa 720

ctttcccaat cttcctcatg taaaccatct tcaatggaaa caatcggata ttggtcaacc 780

aactggccta aataatcaat aaactcaact gggctatggg gtttaccatc ataaacatac 840

tgcccatttt tgtaaaactc actcgctgcc acatccaagg ctaaagcaac ttcttcccca 900

ggcttgtaac cagcttgttt aatagcagct agcaataatt ctaaagctac ttggttagag 960

tccaggttag gtgcaaaacc accttcatca ccaacaccag tcagcaaacc cttatcatcc 1020

aaaaccttgc tgagagttgc aaaaacttcc gcaccccaac gcaaagcttc ctggaaggaa 1080

ggcgcactga cgggtacaat cataaactcc tgaaaatcga cattattggc tgcgtgcgct 1140

ccaccattga tcacattcat caaaggtaca ggtagcaaat ttgctaaagg cccacccaca 1200

tagcgataca aaggaattcc caaagactca gcagcagctt tagcagctgc tagtgaaacc 1260

gacaaaattg catttgcgcc caaattagct ttattgggtg aaccatccaa agagatcatg 1320

attttatcta atgattcttg gtctagggca tccaagccta acaattgggg tgctaatacc 1380

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tctttcacat tctgcactgc cttgagtact cctttgccac cataacggct tttatcacca 1440

tctcgcagtt catgagcctc aaaagtacct gtggaagcac cgctaggaac ttgcgctagt 1500

cctactgtac cattagccaa atgtactgca gcctcaacag tcggtcttcc ccgtgaatca 1560

agaatttcgc gggcgataat agcttcaata gcggtatcca gaaattttgt cattaaatgg 1620

aggcgctcgt tgatctgagc cttgcccccc gacgaacggc ggtggatgga agatactgct 1680

ctcaagtgct gaagcggtag cttagctccc cgtttcgtgc tgatcagtct ttttcaacac 1740

gtaaaaagcg gaggagtttt gcaatttttgt tggttgtaac gatcctccgt tgattttggc 1800

ctctttctcc atgggcgggc tgggcgtatt tgaagcggtt ctctcttctg ccgtta 1856

<210> SEQ ID NO 131
<211> LENGTH: 1985
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 131, Example 131: designer Nial-promoter-controlled chloroplast-targeted Pyruvate-Kinase DNA construct (1985 bp)

<400> SEQUENCE: 131

agaaaatctg gcaccacacc atggtagggt gcgagtgacc ccgcgcgact tggaagggtt 60

caaacgaccc cgccgtacga acttttgtcg gggggcgctc ccggatggta gggtgcgagt 120

gaccccgcgc gacttggaag ggttcaaacg accccgccgt acgaactttt gtcgggggggc 180

gctcccggat ggccgccgtc attgccaagt cctccgtctc cgcggccgtg gctcgcccgg 240

cccgctccag cgtgcgcccc atggccgcgc tgaagcccgc cgtcaaggct gcccccgtgg 300

ctgccccggc tcaggccaac cagatgaaac ccttaaattt tcggactaaa attgttgcta 360

ctatcggtcc tgcgagtaat actcccgaag tattacgtca aatgctctta gccggagtca 420

atgttgcgcg gttgaatttt tcccacggta gctacgaaga tcacgctcag atggttaaac 480

tcttacgttc tttgtccgaa gaattagact tacccctgac cattttacaa gaccttcaag 540

gtccaaaaat tcgggtaggc aaattacccc cagacggact taacctcatc gaaggacaat 600

ctctaacctt ggttcccctt gctgcttgga aaaatcaagc caataccgtt ggcattgatt 660

atccctacgt cgctgaagaa gcgcaacccg gtactcaagt gctgcttgat gacggtttat 720

tggagttaac cgttgaacaa gtcaagggaa atgaggtcat ctgtcaagtg gttgaaggag 780

gcattctcaa aagcaataag ggggttaatt tgccaaccct caatctacgc ttgccttcca 840

tgaccgaaaa agataagaaa gatctcgaat ttggactatc ccaaggcgtt gacatcattt 900

ccctaagctt tgtccgcaaa cccgaagata ttcaagaact caaggaattt attgcccaaa 960

gatcggcaaa agttcccgtt ttagcgaaaa ttgaaaagcc ccaagccgtt gacaatattg 1020

aagccattat cgatgaatgc gatgctatta tggttgcgcg gggagactta ggggtagaaa 1080

tgcgccccga aaaggttcca ggtatccaaa aacgcatcat taagctgtgt aaccaaaaag 1140

gcatccccgt tattaccgcc acccagatgc tcgatagcat gattcgtaac ccccgtccca 1200

cccgtgctga agccagtgac gtagccaatg ctatcattga tggaaccgat gcggttatgt 1260

tatcaggaga atcagcgatc ggagattatc ccgtgcaagc ggtgcaaatg ctggctaata 1320

ttgccaaaga tattgaacca ggactgaatt ttgccaatta tcctcctcga cggcagaata 1380

aagcccacgc catagccgaa gctctcaata ccatcgacaa gattcttgat ttacaatgta 1440

ttgtcacctt tacggaaacc gggtattctg ctaaattagc tgctgctgaa cggccacggg 1500

-continued

ttcccatagt ggctttaaca cctgatcacc aagtttatca tcgccttaat ttagtttggg 1560

gagtccgacc cattttattt gactacgatg agtcttccct agacgacttg atggttaaag 1620

tagaagatat gttaaaaacc cgaaactacg cgacatcagg ggataaagtg ttgattatgg 1680

gtggtttacc cctcagaaaa gccagtacca cgagttttct cgatattcat acgattactt 1740

aataaatgga ggcgctcgtt gatctgagcc ttgccccctg acgaacggcg gtggatggaa 1800

gatactgctc tcaagtgctg aagcggtagc ttagctcccc gtttcgtgct gatcagtctt 1860

tttcaacacg taaaaagcgg aggagttttg caattttgtt ggttgtaacg atcctccgtt 1920

gattttggcc tctttctcca tgggcgggct gggcgtattt gaagcggttc tctcttctgc 1980

cgtta 1985

<210> SEQ ID NO 132
<211> LENGTH: 1568
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 132, Example 132: designer Nial-promoter-controlled NADPH-dependent chloroplast-targeted NADPH-dependent Glyceraldehyde-3-phosphate dehydrogenase DNA construct (1568 bp)

<400> SEQUENCE: 132

agaaaatctg gcaccacacc atggtagggt gcgagtgacc ccgcgcgact tggaagggtt 60

caaacgaccc cgccgtacga acttttgtcg gggggcgctc ccggatggta gggtgcgagt 120

gaccccgcgc gacttggaag ggttcaaacg accccgccgt acgaactttt gtcgggggggc 180

gctcccggat ggccgccgtc attgccaagt cctccgtctc cgcggccgtg gctcgcccgg 240

cccgctccag cgtgcgcccc atggccgcgc tgaagcccgc cgtcaaggct gcccccgtgg 300

ctgccccggc tcaggccaac cagatgtcaa cgaatattgc aattaatgga atgggtagaa 360

ttggaagaat ggtgctaaga atagcactaa agaatgaagc attgaatgta gttgccatca 420

atgctagcta tcctcctgaa acaattgcac atttaattaa ttatgacaca acacatggga 480

gatacgataa aagagtagaa cctattgaaa gtggaattcg agtggaaggc catgatatta 540

aattagtgtc tgatagaaac ccagaaaatt taccctggaa agatttagaa atagatatcg 600

tcattgaagc gaccggtaaa tttaaccatg gtgataaagc taaggcacat attcaagcag 660

gagctaaaaa agtgttattg acaggaccat caaaaggcgg aaaagtacag atggtggtta 720

aaggtgttaa cgatcaagac ttagatacag atacatatga catatttagt aatgcgtcgt 780

gtactacgaa ttgtatcgga ccagttgcaa aagttttaaa tgatagtttt ggcattgaaa 840

atggcttaat gacaacggta catgcaatta caaatgatca aaataatata gataatccgc 900

ataaagattt gagaagagcg cgttcttgtg gggaaagtat tataccaaca tcaacaggtg 960

ctgctaaagc attaaaagaa gttatgccag aattgaatgg caaactacat ggcatagcac 1020

ttcgtgtgcc aactcaaaat gtatcattag ttgatttagt cattgattta aaacaaaaag 1080

tgacagtaga tgaagttaat catgcattta gagatgcaaa cttacaagga attattgatg 1140

ttgaagaggc ccctctagtt tctaaggact ataatacaaa tcctcattca gcagttatag 1200

atgctaaaaa tacaatggtc atgggagata ataaggttaa agttatagcc tggtatgata 1260

acgaatgggg atattctaat agagtagttg aggtagcaaa tcaacttgga gaactaatta 1320

aataataaat ggaggcgctc gttgatctga gccttgcccc ctgacgaacg gcggtggatg 1380

-continued

gaagatactg ctctcaagtg ctgaagcggt agcttagctc cccgtttcgt gctgatcagt 1440

ctttttcaac acgtaaaaag cggaggagtt ttgcaatttt gttggttgta acgatcctcc 1500

gttgattttg gcctctttct ccatgggcgg gctgggcgta tttgaagcgg ttctctcttc 1560

tgccgtta 1568

<210> SEQ ID NO 133
<211> LENGTH: 1571
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 133, Example 133: designer Nial-promoter-controlled chloroplast-targeted NAD-dependent Glyceraldehyde-3-Phosphate Dehydrogenase DNA construct (1571 bp)

<400> SEQUENCE: 133

agaaaatctg gcaccacacc atggtagggt gcgagtgacc ccgcgcgact tggaagggtt 60

caaacgaccc cgccgtacga acttttgtcg gggggcgctc ccggatggta gggtgcgagt 120

gaccccgcgc gacttggaag ggttcaaacg accccgccgt acgaactttt gtcgggggggc 180

gctcccggat ggccgccgtc attgccaagt cctccgtctc cgcggccgtg gctcgcccgg 240

cccgctccag cgtgcgcccc atggccgcgc tgaagcccgc cgtcaaggct gcccccgtgg 300

ctgccccggc tcaggccaac cagatgtaaa ctggctgaat gtacaagcat atccgcaagt 360

ttgttggagt aacccatttc gttatcgtac catgaaacta ctttcacgaa atttggagat 420

aacataattc ccgcatcctt gtcgaatacc gaagttctct tctcgcccac gaaatcctga 480

gaaaccacag cgtcttcagt ataccctaaa attcctttaa gttcaccttc cgatgccgct 540

ttcattgctg cacagatttc ttcgtatgaa gtagatttct ctaatctgac cgttaaatcc 600

actacagaaa catctgcagt tgggactctg aatgacatac cggttaattt accgttaagg 660

gcaggaatta cttttcctac tgcttttgca gctccggtag aagatgggat gatgttgttc 720

aatgcagaac gcccgcctct ccagtctttc atagaaggcc cgtcaacagt tttctgggtt 780

gcagtagttg cgtgcacggt cgtcattaaa ccttcgatga ttccgaaatt atcgtgaagt 840

acttttgcta atggagcaag acagttagtc gtacagctcg cgttagaaaa aatagtaacg 900

tcatctgtaa gatccttgtg gttaacaccc attacgaaca tcggcgtatc gtcttttgaa 960

ggagcagaaa ggattgcttt ttttgcaccc gcgttgatat gtgcctgtgc cgcctccttg 1020

gtaaggaata aaccggttga ttccacgatg tattctgcgc ctacttcgtt ccatttcagg 1080

ttgttaggat ctttttcggc ggttacacga atctttttgc cattcacgat aaggtcgttt 1140

ccttctacag aaacttcgcc cgcaaatgtg ccgtgtaccg agtcatactt aagcatgtac 1200

gccatatatt tggcatcgat aagatcgtta attcccacca cttcgatgtt ttctctctcg 1260

gccatcgctc tgaaaaccaa gcgtccaatc ctaccgaatc cgttgattcc tactttaatt 1320

gttgacatta aatggaggcg ctcgttgatc tgagccttgc cccctgacga acggcggtgg 1380

atggaagata ctgctctcaa gtgctgaagc ggtagcttag ctccccgttt cgtgctgatc 1440

agtctttttc aacacgtaaa aagcggagga gttttgcaat tttgttggtt gtaacgatcc 1500

tccgttgatt ttggcctctt tctccatggg cgggctgggc gtatttgaag cggttctctc 1560

ttctgccgtt a 1571

-continued

<210> SEQ ID NO 134
<211> LENGTH: 2150
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 134, Example 134: designer Nial-promoter-controlled chloroplast-targeted Citramalate Synthase DNA construct (2150 bp)

<400> SEQUENCE: 134

agaaaatctg gcaccacacc atggtagggt gcgagtgacc ccgcgcgact tggaagggtt 60

caaacgaccc cgccgtacga acttttgtcg gggggcgctc ccggatggta gggtgcgagt 120

gaccccgcgc gacttggaag ggttcaaacg accccgccgt acgaactttt gtcgggggggc 180

gctcccggat ggccgccgtc attgccaagt cctccgtctc cgcggccgtg gctcgcccgg 240

cccgctccag cgtgcgcccc atggccgcgc tgaagcccgc cgtcaaggct gcccccgtgg 300

ctgccccggc tcaggccaac cagatggagc aggtttttat ctacgacacc accttgaggg 360

atggctcgca ggcagaaggt ataaactttt ccgtagagga taagatgcgc atacttcaaa 420

aactggacga atttggagtg cattacatag agtgcggatg gcccggtgcg aacccaaaag 480

acactattct ctttgaaagg ctgagaaaga taaaaactca aaatgccaaa atagtagcct 540

ttggtgcaac aagaaaagct ggaaagaagg cgcacgaaga taagcaggtg gaaaaccttt 600

tgaaatcggg tgccaaggtg ataaccgtat ttggcaagag ctgggacttt catgtaacgc 660

atgccatagg gaccacctta gaggaaaacc tggacatggt ttacgagacg gtaagctatc 720

ttaaaaagca tgtggaggag gttatctttg acgcagagca cttctttgac ggatacaggc 780

acaacgaaag ctatgctttt aaggtattgg aggcagcttt tcaggcaggt gcggactgga 840

tagtcctctg cgataccaac ggtggcaccc ttcccaatga ggtttatgag ataaccaaaa 900

aggttgtaca aaagtttcca caggcacgcg taggcataca cgctcacaac gattcagata 960

ctgctgtggc taactctctt atggcggtgc ttgcaggtgc aaggcaggtt cacggcacta 1020

taaacggctt gggggaaaga acgggcaatg ctaatctgtg ttccataata cctaaccttc 1080

agctcaagct gggctttagt gtagtgcctt cccaaaacct caaaaagctc accgagcttg 1140

ctcactttgt ctccgaaatc tccaacacgc cactgcccaa aaacatgcct tatgtagggg 1200

agagtgcttt tacccacaaa gcaggcgtac acgcctctgc agttatgaaa aggtcagaaa 1260

catacgaaca catagaccct tctttggtag gaaacagaag gaaggtgaca gtgtctgacc 1320

tttctggaag gagtaatata ctttacaagc tcagggaaat ggggcttgag gtggatgata 1380

agtcccctga gcttatcaaa ctccttgaaa agataaagga acttgagaag gaaggctacc 1440

actttgaagc agctgaagct tcttttgagc ttctttgcaa gaggcatttt gggcttgtta 1500

aaaactattt tgaccttgat gcttacaggg tgctaatagc cagaaggagt acagacctat 1560

ctcctgtttc ggaagccacc gtaagactct atgtggaaga cataaaggag catacagcag 1620

ctcttggtaa cggaccagtg agcgcccttg acagagccct cagaaaagcc ttggaagagt 1680

tttatccaag ccttaaagat gttcagctca tagactacaa ggtgagaata gttaacgaat 1740

cggagggtac atctgccaaa gtgagggtgc ttatagaatc taccgatggt agaagaaagt 1800

ggggaacggt gggagtttcg gaaaacataa tagaagcctc ttggatagcc ttaactgata 1860

gcctcgtata taaactctta aaagacgaag aagagggtat aatgtgataa atggaggcgc 1920

tcgttgatct gagccttgcc ccctgacgaa cggcggtgga tggaagatac tgctctcaag 1980

-continued

tgctgaagcg gtagcttagc tccccgtttc gtgctgatca gtctttttca acacgtaaaa 2040

agcggaggag ttttgcaatt ttgttggttg taacgatcct ccgttgattt tggcctcttt 2100

ctccatgggc gggctgggcg tatttgaagc ggttctctct tctgccgtta 2150

<210> SEQ ID NO 135
<211> LENGTH: 3125
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 135, Example 135: designer Nial-promoter-controlled chloroplast-targeted 3-Isopropylmalate/(R)-2-Methylmalate Dehydratase large/small subunits DNA construct (3125 bp)

<400> SEQUENCE: 135

agaaaatctg gcaccacacc atggtagggt gcgagtgacc ccgcgcgact tggaagggtt 60

caaacgaccc cgccgtacga acttttgtcg gggggcgctc ccggatggta gggtgcgagt 120

gaccccgcgc gacttggaag ggttcaaacg accccgccgt acgaactttt gtcgggggggc 180

gctcccggat ggccgccgtc attgccaagt cctccgtctc cgcggccgtg gctcgcccgg 240

cccgctccag cgtgcgcccc atggccgcgc tgaagcccgc cgtcaaggct gcccccgtgg 300

ctgccccggc tcaggccaac cagatgtacc atgtctgctg ttgctatctc gcccttgatt 360

gctgatgctg taacagtagc cgctgaagca agatatacaa aagaatcttt atgtcctgca 420

cgtcccttga agtttcgtgt acctgtactg ataagagtct caccctcacc gataacaccc 480

tgacagcttc cccagcatac agagcagtta ggattcataa caattgcacc tgcgtccatg 540

aatatatcaa ggagtccctc tttcatagcc tgaagatata ccgaacggct tgcaggaact 600

acaaggaatc ttaccttagg agcaaccttt ttccctttga tgatcgctgc gccaactctt 660

aaatcctcga ttcgtccatt gttacatgaa ccaagaaatg cttcatcaat ctttacacca 720

agtgattcct tagccggaac tacattgtca acaaaatgtg gctttgcaac aattggctgt 780

attgttgaaa ggtcaatatc ataaacctgc tcaaatactg catcatcatc tgatgtaaag 840

catgcctttg gctctctgcc atgctcctta agataatcca ttgcaacatc atcaacttcc 900

atgagtgcag tcttagcacc tgcctctaca caaaggttac agattgatat tctgtctgcc 960

attgaaaggc tgtgtaagcc ttctcctgca aattccattg ctttatagtt agcaccgtta 1020

gcgccaatct ttccaataat agagagtatt aaatctcttg catatactcc atcgttaagc 1080

tttcccttaa ggttgaatct taatgttccc ggaaccatta cccatgatgt tcctgtaacc 1140

attgcataca aataatctgt acaaccaaca cctgtaccaa atgcacctaa cgcaccatat 1200

gcacaagtat ggctgtctgc tccaaatata agctcacccg gcactacatg attttccatc 1260

ataacctgat gacacacacc ctcgccctcg tagaacttaa tatcattagc cttagcaaag 1320

tctctcatct tcttctgtga ggctgctgtc ttaggactgt ctgatggaat attgtggtct 1380

acaatccata caagcttatc cttgtcagca atatgaggat tctttaactt ctcatacata 1440

ccaatagtaa gatgtgttgt tccatcatta ctcataagtc tgtcaagagt aacagttgca 1500

atatcaccag ccttaacctg tgaaagacct gctgcccttg cgataatctt ctctgcaata 1560

gtcatgccat gctttgcctc atctgcaggt acggctgtac tctcagactc ttctttctca 1620

ccatcaagtg atgcaataag accaccctga ttaagaatag cctgcatctt ggctggaagc 1680

ttagtacatg tataagtctt tccattaaca gttataattc catcttctaa tgaaagctca 1740

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cattcatccc ccgcattaac ttcgtcatgg agttctttac atacaataac aggaagtcct 1800

atattaatag cattacgata gaatattctt gcaaatgatt tggcaatcac tgccttgaca 1860

cctaatgcct taagtacgct tggtgcctgc tctcttgatg aaccacatcc aaagttgtca 1920

tctgcaacaa cgaaatctcc cggctttacg gcagaagcaa aatcagagtc taatgattca 1980

aatgtatgac tcttcatctc atcaattgtc ggaaacaaaa gatactgcga tgcaataatc 2040

tgatctgtat caacatcttt atcaaactta aatatcctac ccatatggta gggtgcgagt 2100

gaccccgcgc gacttggaag ggttcaaacg accccgccgt acgaactttt gtcgggggggc 2160

gctcccggat ggtagggtgc gagtgacccc gcgcgacttg gaagggttca aacgaccccg 2220

ccgtacgaac ttttgtcggg gggcgctccc ggatggccgc cgtcattgcc aagtcctccg 2280

tctccgcggc cgtggctcgc ccggcccgct ccagcgtgcg ccccatggcc gcgctgaagc 2340

ccgccgtcaa ggctgccccc gtggctgccc cggctcaggc caaccagatg gtcaagaccg 2400

ttaagctttc tcattgcctt aacaagtccg cctgcattaa gtatatccac aagattatca 2460

ggaagtgaag caataggata tgcttttcca ttgtgtgtaa tctttgcatt tacttcaaca 2520

tcaatagtat cgccttccgt aacttcgtcg tgaaggtctg cattctctat aaggagaagt 2580

ccgttattaa tagaatttct gaagaatatt cttgcatatg atttggcaat aacacattta 2640

atacctaatg ccttaataac ctcaggtgcc tgctctcttg atgaaccaca accaaagttc 2700

tttcctgcaa caatgatgtc gcctggctta atctgacctg caagttctgg tcttaatggc 2760

gaaaatgcat atggtttcat atcttctact gtctttaatg caaggtactc tgtagggata 2820

atgatatctg tatcaatgtc atcaccaagt acccatactt taccgctaaa tttctcgttc 2880

attaaatgga ggcgctcgtt gatctgagcc ttgccccctg acgaacggcg gtggatggaa 2940

gatactgctc tcaagtgctg aagcggtagc ttagctcccc gtttcgtgct gatcagtctt 3000

tttcaacacg taaaaagcgg aggagttttg caattttgtt ggttgtaacg atcctccgtt 3060

gattttggcc tctttctcca tgggcgggct gggcgtattt gaagcggttc tctcttctgc 3120

cgtta 3125

<210> SEQ ID NO 136
<211> LENGTH: 2879
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 136, Example 136: designer Nial-promoter-controlled chloroplast-targeted 3-Isopropylmalate Dehydratase large/small subunits DNA construct (2879 bp)

<400> SEQUENCE: 136

agaaaatctg gcaccacacc atggtagggt gcgagtgacc ccgcgcgact tggaagggtt 60

caaacgaccc cgccgtacga acttttgtcg gggggcgctc ccggatggta gggtgcgagt 120

gaccccgcgc gacttggaag ggttcaaacg accccgccgt acgaactttt gtcgggggggc 180

gctcccggat ggccgccgtc attgccaagt cctccgtctc cgcggccgtg gctcgcccgg 240

cccgctccag cgtgcgcccc atggccgcgc tgaagcccgc cgtcaaggct gcccccgtgg 300

ctgccccggc tcaggccaac cagatgaatg aactgcctta catcagaaac ttttccatta 360

accgccgccg ccactaccat cgctggactc atcaataaag tgcgaccggt tgatgacccc 420

tgacggcctt taaaattacg gttagaagaa gaagcactaa tttgatcgcc aactaactta 480

-continued

tcagggttca tggctaaaca catggaacag ccggcttctc gccattcaaa cccggcttgg 540

gtaaaaattt tatcgagtcc ttcggcttct gcttgttgtt taacccttc cgatccggga 600

acgacaaatg ctttaacccc tgatgctacc tgtcttcctt gggcaaattt agccgcttct 660

cgtagatcgc tgatgcgtcc attggtacaa ctaccaataa aacagacatc gacaggagtc 720

cccataatag gcgatccggg tttgagttgc atatattcat aagcttcttg agcaataaag 780

cgatcgcctt ctggtaaact ttcaggagta ggaaccactt cagtcacgcc tattccttga 840

ccgggggtaa taccccaagt aacagtcggt tcgatctcac cggcatcaaa caccacgaca 900

tcatcatatt gggcattcgc atcactgcgg atactcttcc accattcgac ggccttatcc 960

cagtcttggc ctttgggaga aaagtctctg cctttgaggt attcaaaagt cacctcatca 1020

gggttaatat agccgcatct agcgccgcct tcgatggcca tattacaaac ggtcattcgt 1080

tcttccatcg acatggcctc aaaggtagtg ccggcatatt cataagcgta acctacgccg 1140

ccttttaccc ctaatttgcg gatgatgtgc aggacgacat ctttggcata gactccgggg 1200

ggtaaggttc cgttaacttc aattttacgg actttgagtt tagagagggc tagggtttgg 1260

gtagcgagga catctcgcac ttgggaggtt cctatgccaa aagcgatggc cccaaaagcg 1320

ccatgagtgg aggtatgaga gtcaccgcaa gcaatggtca ttccgggttg agttagtcct 1380

tgttcggggg cgatcacatg aacaataccc tgatttcctg agccgatatt ataaaaaggg 1440

atattattat ctttagcatt agtttcaata gcccgcatca tttcttcagc gaggtcgtct 1500

acaaagggac ggtgttggtt ctcggtgggt acaatatgat ccactgtggc gacggtgcga 1560

tcggggaata ataccttcag ttttctgtcc cgtagcatag caaaagcttg tggactggta 1620

acttcatgaa tgaggtgaag tcctataaat agttgggttt gtcccgatgg taagatgcgg 1680

acggtatgta agtcccaaac tttgtcaaac agtgttcctg tactcatatg gtagggtgcg 1740

agtgaccccg cgcgacttgg aagggttcaa acgaccccgc cgtacgaact tttgtcgggg 1800

ggcgctcccg gatggtaggg tgcgagtgac cccgcgcgac ttggaagggt tcaaacgacc 1860

ccgccgtacg aacttttgtc ggggggcgct cccggatggc cgccgtcatt gccaagtcct 1920

ccgtctccgc ggccgtggct cgcccggccc gctccagcgt gcgccccatg gccgcgctga 1980

agcccgccgt caaggctgcc cccgtggctg ccccggctca ggccaaccag ttatacctct 2040

acggcatttt tccaatttaa ataaggtaat tttttagcag tttcttgaat ttcagaaagg 2100

ttttgaatga gttgtccgca gctatcccaa gagccttcaa ttaacatttg tctagaccct 2160

tctcccatgc taacatcagc aacaaattcg ccacattgca ctttcatagc ggctaaatct 2220

aaactgaggg acaaggcagg attttcttgc aggagagatt gtatttttc tacggtttca 2280

ggagaagctg tcacacaggg aaccccgtta gcaatacaat tgccaaagaa aatttcagca 2340

aaactttcac cgataattgc tttaattccc caacgaataa tggcttgtgg ggcgtgttct 2400

cttgaagatc cacagccaaa attagcgtta actaccaaga gattagctcc ctgatattgc 2460

ggcagatcaa agggatgttt tccttgcatc tgttggcgat catcaataaa aacttgttct 2520

cctaagcctt caaaggtgac gcaacgtaga aaccgcgcag gaataatacg atcagtatcg 2580

atatcatcgc ccactaaagg gatacctcgt cctgaaattt gggtgacttg actcattaaa 2640

tggaggcgct cgttgatctg agccttgccc cctgacgaac ggcggtggat ggaagatact 2700

gctctcaagt gctgaagcgg tagcttagct ccccgtttcg tgctgatcag tctttttcaa 2760

cacgtaaaaa gcggaggagt tttgcaattt tgttggttgt aacgatcctc cgttgatttt 2820

-continued

ggcctctttc tccatgggcg ggctgggcgt atttgaagcg gttctctctt ctgccgtta 2879

<210> SEQ ID NO 137
<211> LENGTH: 1661
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 137, Example 137: designer Nial-promoter-controlled chloroplast-targeted 3-Isopropylmalate Dehydrogenase DNA construct (1661 bp)

<400> SEQUENCE: 137

agaaaatctg gcaccacacc atggtagggt gcgagtgacc ccgcgcgact tggaagggtt 60

caaacgaccc cgccgtacga acttttgtcg gggggcgctc ccggatggta gggtgcgagt 120

gaccccgcgc gacttggaag ggttcaaacg accccgccgt acgaactttt gtcgggggggc 180

gctcccggat ggccgccgtc attgccaagt cctccgtctc cgcggccgtg gctcgcccgg 240

cccgctccag cgtgcgcccc atggccgcgc tgaagcccgc cgtcaaggct gcccccgtgg 300

ctgccccggc tcaggccaac cagatgactc ggcaacaccg cataacccta cttcctggcg 360

atggtatcgg acctgaaatt ttagccgtaa ccgtagatgt cctaaaggtg ataggcaaac 420

aattcgacct aaattttgag tttacagaag ccctcatcgg cggtgctgcc attgatgcaa 480

ccggaaaccc cttacccgaa gaaaccttaa agatttgtcg caacagtgat gcagtgcttt 540

tagccgccat cgggggttat aagtgggata atttgccccg tcatcaacgc ccagaaacgg 600

gattattagg catcagagcc ggcttaggat tatttgctaa cttacgtccg gccaccattt 660

taccgcagtt aatcgacgct tccaccctca aacgagaagt cgtcgaaggc gtggacatta 720

tggtggtgcg agaactcacc ggcggcattt attttggtca accgaaggga atttttgaga 780

cagaaagcgg cgaaaaacgg ggcgtgaata ccatggccta tacagaatca gaaatagacc 840

gcattgctca aatcggcttt gaaacagccc aaaaacgtcg aggaaagctc tgttctgtgg 900

ataaagccaa tgtcttagat gtctcccaat tatggcgcga tcgcgtaact ttaatggccg 960

aaaaataccc agatgtagaa ctgtctcatc tctatgttga caatgcggct atgcagctag 1020

tgcgtaaccc aaaacaattt gataccatcg tcaccggcaa tttatttggc gatatcctct 1080

cggatgcagc cgctatgtta accggtagta ttgggatgtt accctctgct agtttaggtt 1140

cagatggacc cggactattt gaaccggtac atggttcagc ccccgatatt gcaggacttg 1200

ataaagctaa cccgcttgct caggtactca gtgccgccat gatgttgaaa tatggcttaa 1260

atgagccaga agccgccgat caaatcgaac aagcggtttt agccgtatta gaaaaaggct 1320

atcgtacagg agacatcatg tcagaaggaa tgacgttagt gggatgtaag ggcatgggag 1380

aagttttgat taatgtctta gaatctttac aagggtgata aatggaggcg ctcgttgatc 1440

tgagccttgc cccctgacga acggcggtgg atggaagata ctgctctcaa gtgctgaagc 1500

ggtagcttag ctccccgttt cgtgctgatc agtctttttc aacacgtaaa aagcggagga 1560

gttttgcaat tttgttggtt gtaacgatcc tccgttgatt ttggcctctt tctccatggg 1620

cgggctgggc gtatttgaag cggttctctc ttctgccgtt a 1661

<210> SEQ ID NO 138
<211> LENGTH: 2174
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

-continued

<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 138, Example 138: designer Nial-promoter-controlled chloroplast-targeted 2-Isopropylmalate Synthase DNA construct (2174 bp)

<400> SEQUENCE: 138

agaaaatctg gcaccacacc atggtagggt gcgagtgacc ccgcgcgact tggaagggtt 60

caaacgaccc cgccgtacga acttttgtcg gggggcgctc ccggatggta gggtgcgagt 120

gaccccgcgc gacttggaag ggttcaaacg accccgccgt acgaactttt gtcgggggggc 180

gctcccggat ggccgccgtc attgccaagt cctccgtctc cgcggccgtg gctcgcccgg 240

cccgctccag cgtgcgcccc atggccgcgc tgaagcccgc cgtcaaggct gcccccgtgg 300

ctgccccggc tcaggccaac cagatgtgat gctgtaacag ccgcttgttc tttttgggtt 360

ttttcttgtt ctagggcaac ataaagacgg ttaagagcgc taatataagc ccgtgccgaa 420

gcaacgataa tatcagtatt agcggcatga cccgagaaag ttcggttttc gtatttcaga 480

cgaatggtga cttctcccat tgcatcaatg ccttctgtga ctgacttaac cgaaaattca 540

atcaactggt taggaacatt aaccactcgg ttaatcgctt tataaaccgc atctacgggt 600

ccggttccaa tagccgcatc cattaattct tcgccgttgg gacctttttaa gatcacggtt 660

gctgttggac gggcctgatc gccacatgac acttgtacta attcgagacg gaagatttct 720

ggggcaacat gaatttcatc attgacgatg gcttctaagt cccagtcagt aatttctttg 780

cgcttgtctg ccacttcttt aaagcgtaca aaggctttat ttagctcagt ttccgtcaat 840

tcaaagccta attcttttag acgagtgccg aaagcattac gccctgagag tttcccgagg 900

acaatttgat tattggttaa cccgatagac tcagcgtcca taatttcgta ggttaattta 960

ttttttagca cgccatcctg atgaataccg gattcatgag cgaaagcatt agcgccgaca 1020

attgccttat tcggttgtac cgccatcccg gtgagactgg aaactaaacg ggatgttttg 1080

tagatttctt tggtattgat attggttagg ggttcagtgg agtctgctgg tcgtcctaag 1140

aaaggattgt aataggagcg gcgtacatga agcgccatca ctaattcttc taaggcggcg 1200

ttgccggctc gttctcctat gccgttaata gtacattcta actgtctggc tccatttttа 1260

acggcttcaa ggaagttagc caccgctaac cctaaatcat tatgtccatg aaccgagata 1320

atagcattgt ctatgttagg aacattttct ttgatgccgc gaatcaattg accaaattca 1380

gagggagtta aatagcctac ggtatcggga atattaacgg tagttgctcc ggctgctatg 1440

gctctttcta atacttgata caaaaattct gggtcactac ggcctgcatc ttctggggaa 1500

aattctacat catctacaaa agacttcgca taagccacca tttctgggac gatttctagg 1560

acttcttgac gagtcttttt gagtttatag gccaagtgaa tatcggaggt agccaaaaag 1620

gtatgaatgc ggggtttagc ggcgggtttg agggcttctg cggctttagt gatatcttgt 1680

cgagtggctc ttgccaagcc gcaaattgtg gggcctcctt ggactcctac tactttagcg 1740

atttttgta cagcttcaaa atctccggga cttgcgtaag gaaaacccgc ttctatgaca 1800

tctactccca gtcgtgccag tgcgcgagca acggttagct tctcatcaac attcagggtt 1860

gctcccgggg actgttcccc atctcggaga gtggtatcga agatgataac gcgatcgggt 1920

tgtttactca ttaaatggag gcgctcgttg atctgagcct tgccccctga cgaacggcgg 1980

tggatggaag atactgctct caagtgctga agcggtagct tagctccccg tttcgtgctg 2040

atcagtcttt ttcaacacgt aaaaagcgga ggagttttgc aattttgttg gttgtaacga 2100

tcctccgttg attttggcct ctttctccat gggcgggctg ggcgtatttg aagcggttct 2160

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ctcttctgcc gtta 2174

<210> SEQ ID NO 139
<211> LENGTH: 2882
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 139, Example 139: designer Nial-promoter-controlled chloroplast-targeted Isopropylmalate Isomerase large/small subunits DNA construct (2882 bp)

<400> SEQUENCE: 139

agaaaatctg gcaccacacc atggtagggt gcgagtgacc ccgcgcgact tggaagggtt 60

caaacgaccc cgccgtacga acttttgtcg gggggcgctc ccggatggta gggtgcgagt 120

gaccccgcgc gacttggaag ggttcaaacg accccgccgt acgaactttt gtcgggggggc 180

gctcccggat ggccgccgtc attgccaagt cctccgtctc cgcggccgtg gctcgcccgg 240

cccgctccag cgtgcgcccc atggccgcgc tgaagcccgc cgtcaaggct gcccccgtgg 300

ctgccccggc tcaggccaac cagatgcaac aactcccgca catccgcaac ttcaccctga 360

atcgccgcag tagcgaccat cgccggactc attaacaaag tgcgaccgga agctgatcct 420

tgtcgtcctt taaagttgcg gttggaggag gaagcactaa tttgtctacc ttccagcttg 480

tcggggttca tggctagaca catagaacat ccaggttcgc gccattcaaa gcctgctgct 540

tcaaagattt tatctaaacc ttcagcttcg gcagcttttt tcactcgttc ggaaccggga 600

accacaaaag ccttgactcc ttccgctacg tggcgacctt tggcaatttt cgcggcttct 660

tgcaggtcac taagtctacc gttagtgcag ctaccgataa agcaaacgtc aattttcgtt 720

cccttaatcg gttgaccagg atataaatcc atgtaacggt aagcttcttc agctacaaag 780

cggtcttctt ctaggagttc ttctggctgg ggaatcaact gattcacacc aataccttga 840

ccgggggtaa ttccccaggt aacagtgggg ggaatatccg cagcgttgaa tactattaca 900

tcatcgtatt cagcatcagc atcactcttg attgattccc accaagccac ggctttttcc 960

caatcagcgc cttgggggggc aaagtctcta ccttggagat aatcataggt aacttgatca 1020

ggattgacat aaccgcatct agcgccaccc tcaatggcca tgttgcagac agtcatccgt 1080

tcttccatat tcatttgctc aaaagtcgta cccgcgtatt cgtaggcgta acctacacca 1140

cctttcactc ccagggtacg gatgatatgc aggatgacat ctttggcata aaccccaggg 1200

ttgagtgtgc cgttaacttc aattttacgg actttgagtt tggataggga taaggtttgg 1260

gaggcgagaa cgtcccgcac ttggctagta ccaataccaa aagcgatcgc cccaaacgcc 1320

ccatgacttg aagtgtggct atcaccacag gcgatcgtca ttcccggctg tgtcagtccc 1380

agttctggcg caatcacatg aactatacct tgattgccgg aaccaatgtt ataaaaagta 1440

atgttatttt cttgacaatt ctgctctagg gcttggatca tttcctcagc caagcgatcg 1500

acaaaaggac gcgcctgatt ctctgtaggc acgatgtgat ccacagtagc cacagtccgc 1560

tcaggaaata gtacctttaa acctcgttcc cgtaacatag caaaggcttg tggactagta 1620

acttcatgga ctaggtgcag gccaataaat agctgtgtta gccctgaagg aagtgtacca 1680

acagtgtgta agtcccaaac tttatcaaac agggtgcctt tgctcatatg gtagggtgcg 1740

agtgaccccg cgcgacttgg aagggttcaa acgaccccgc cgtacgaact tttgtcgggg 1800

ggcgctcccg gatggtaggg tgcgagtgac cccgcgcgac ttggaagggt tcaaacgacc 1860

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ccgccgtacg aacttttgtc ggggggcgct cccggatggc cgccgtcatt gccaagtcct 1920

ccgtctccgc ggccgtggct cgcccggccc gctccagcgt gcgccccatg gccgcgctga 1980

agcccgccgt caaggctgcc cccgtggctg ccccggctca ggccaaccag atgaccagca 2040

gccagtttac cccaactcac ataaggtaac ttagcagatg ttacccgcac ttgctcggtg 2100

ttcgctacca actgaccgca agcatcccaa gccccagtaa taaaggtgct tctggttcct 2160

tcaccaatgg agattggcgc ggtgaaatca ccaacttgta cttgcagagt ttctaagttg 2220

atgctgacat tagcttgagg attagcggct actaactctt gcaattgttt aacgatcgcc 2280

tcatcagcag tgacacaagg tacaccgatg gctacgcaat taccgaagaa aatttctgca 2340

aaactttcac caatcacgga ttgaatcccc catttagaaa gggcttgggg tgcgtgttcc 2400

cgtgaagaac cacagccaaa gttgcggtta actatgagga tatttgcgcc ttgatactgc 2460

ggttggtcaa aaggatgctc ccctttttagg gctgtgcggt catcaataaa cgcgccttca 2520

cgtaacccat caaaggtaat ggctttgaga taacgagcag gaataatgcg atcggtatca 2580

atatcattac ccactaaggg tatgccacgc cctgtaactt ctttaacttc actgaccatt 2640

aaatggaggc gctcgttgat ctgagccttg ccccctgacg aacggcggtg gatggaagat 2700

actgctctca agtgctgaag cggtagctta gctccccgtt tcgtgctgat cagtcttttt 2760

caacacgtaa aaagcggagg agttttgcaa ttttgttggt tgtaacgatc ctccgttgat 2820

tttggcctct ttctccatgg gcgggctggg cgtatttgaa gcggttctct cttctgccgt 2880

ta 2882

<210> SEQ ID NO 140
<211> LENGTH: 2210
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 140, Example 140: designer Nial-promoter-controlled chloroplast-targeted 2-Keto Acid Decarboxylase DNA construct (2210 bp)

<400> SEQUENCE: 140

agaaaatctg gcaccacacc atggtagggt gcgagtgacc ccgcgcgact tggaagggtt 60

caaacgaccc cgccgtacga acttttgtcg gggggcgctc ccggatggta gggtgcgagt 120

gaccccgcgc gacttggaag ggttcaaacg accccgccgt acgaactttt gtcgggggggc 180

gctcccggat ggccgccgtc attgccaagt cctccgtctc cgcggccgtg gctcgcccgg 240

cccgctccag cgtgcgcccc atggccgcgc tgaagcccgc cgtcaaggct gcccccgtgg 300

ctgccccggc tcaggccaac cagatgtata cagtaggaga ttacctgtta gaccgattac 360

acgagttggg aattgaagaa atttttggag ttcctggtga ctataactta caatttttag 420

atcaaattat ttcacgcgaa gatatgaaat ggattggaaa tgctaatgaa ttaaatgctt 480

cttatatggc tgatggttat gctcgtacta aaaaagctgc cgcatttctc accacatttg 540

gagtcggcga attgagtgcg atcaatggac tggcaggaag ttatgccgaa aatttaccag 600

tagtagaaat tgttggttca ccaacttcaa aagtacaaaa tgacggaaaa tttgtccatc 660

atacactagc agatggtgat tttaaacact ttatgaagat gcatgaacct gttacagcag 720

cgcggacttt actgacagca gaaaatgcca catatgaaat tgaccgagta ctttctcaat 780

tactaaaaga aagaaaacca gtctatatta acttaccagt cgatgttgct gcagcaaaag 840

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cagagaagcc tgcattatct ttagaaaaag aaagctctac aacaaataca actgaacaag 900

tgattttgag taagattgaa gaaagtttga aaaatgccca aaaaccagta gtgattgcag 960

gacacgaagt aattagtttt ggtttagaaa aaacggtaac tcagtttgtt tcagaaacaa 1020

aactaccgat tacgacacta aattttggta aaagtgctgt tgatgaatct ttgccctcat 1080

ttttaggaat atataacggg aaactttcag aaatcagtct taaaaatttt gtggagtccg 1140

cagactttat cctaatgctt ggagtgaagc ttacggactc ctcaacaggt gcattcacac 1200

atcatttaga tgaaaataaa atgatttcac taaacataga tgaaggaata attttcaata 1260

aagtggtaga agattttgat tttagagcag tggtttcttc tttatcagaa ttaaaaggaa 1320

tagaatatga aggacaatat attgataagc aatatgaaga atttattcca tcaagtgctc 1380

ccttatcaca agaccgtcta tggcaggcag ttgaaagttt gactcaaagc aatgaaacaa 1440

tcgttgctga acaaggaacc tcatttttttg gagcttcaac aattttctta aaatcaaata 1500

gtcgttttat tggacaacct ttatggggtt ctattggata tacttttcca gcggctttag 1560

gaagccaaat tgcggataaa gagagcagac acctttttatt tattggtgat ggttcacttc 1620

aacttaccgt acaagaatta ggactatcaa tcagagaaaa actcaatcca atttgtttta 1680

tcataaataa tgatggttat acagttgaaa gagaaatcca cggacctact caaagttata 1740

acgacattcc aatgtggaat tactcgaaat taccagaaac atttggagca acagaagatc 1800

gtgtagtatc aaaaattgtt agaacagaga atgaatttgt gtctgtcatg aaagaagccc 1860

aagcagatgt caatagaatg tattggatag aactagtttt ggaaaaagaa gatgcgccaa 1920

aattactgaa aaaaatgggt aaattatttg ctgagcaaaa taaatagtaa atggaggcgc 1980

tcgttgatct gagccttgcc ccctgacgaa cggcggtgga tggaagatac tgctctcaag 2040

tgctgaagcg gtagcttagc tccccgtttc gtgctgatca gtctttttca acacgtaaaa 2100

agcggaggag ttttgcaatt ttgttggttg taacgatcct ccgttgattt tggcctcttt 2160

ctccatgggc gggctgggcg tatttgaagc ggttctctct tctgccgtta 2210

<210> SEQ ID NO 141
<211> LENGTH: 1724
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 141, Example 141: designer Nial-promoter-controlled chloroplast-targeted NADH-dependent Alcohol Dehydrogenase DNA construct (1724 bp)

<400> SEQUENCE: 141

agaaaatctg gcaccacacc atggtagggt gcgagtgacc ccgcgcgact tggaagggtt 60

caaacgaccc cgccgtacga acttttgtcg gggggcgctc ccggatggta gggtgcgagt 120

gaccccgcgc gacttggaag ggttcaaacg accccgccgt acgaactttt gtcgggggggc 180

gctcccggat ggccgccgtc attgccaagt cctccgtctc cgcggccgtg gctcgcccgg 240

cccgctccag cgtgcgcccc atggccgcgc tgaagcccgc cgtcaaggct gcccccgtgg 300

ctgccccggc tcaggccaac cagatgggcg gcggcttcga gtatctgacg gctgacgtca 360

agggtaatat cgccgttttc acccagatgg gtcatgccgt ggtcctccaa ctgctgcacc 420

aggtcggtaa tgccttgcgc accgatgtca taggcggaca ggcgggtcgg cacaccaagg 480

ttttcaaaga attcctccgt cttgcggata accgcattga tccgctcatc ttccgttcca 540

tcggtcaggt tccatacccg tactgcatac tgaagcagtt tggcacgctt ttcctcgcga 600

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cgcaccttca gcagggcagg aaataccatg gccagcgtcc gggcgtggtc aatgtggtat 660

tttgccgtga tttcgtggcc gatcatatgc gtgctccagt catgtggcac ccctgcgccg 720

atcaggccat taagcgccaa tgtcgccacc cacatgaggt tggagcgcag gtcataatca 780

tcgggtgccg ccatgatacg tggcccgatt tccacaaggc tggagagcag cccttcggaa 840

aagcgatcct gcgccattcc gtccacagga taggtcatgt actgttccat cacatggacg 900

aaggagtcca caacaccgtt gataacctgc ttcatcggca ggctcatggt gcgtgtcggg 960

tcaagcacgg aaaagcgtgg atagaccagg ggattggaaa acaggagctt atccccagtg 1020

gactgccgtg aaatcacgct catgcagttc atttcagacc ccgtggcagg cagggtgacc 1080

accgtgccca gtggcagggc cttggtcgcg gctgtgcctt tgctggtcag gatgtcccat 1140

gcctcacctt catatgggac agcggcagcg acgaacttgg tcccatccat gacagagccc 1200

ccacccacgg caagcaggaa gtcgagccct tcttcacgca ccatggttac ggccttcatc 1260

agggtttcat aggtgggatt ggcctcgatg ccaccgaatt cccgaaaggt ccggctaccg 1320

agggcggcgc gtacctcggc aagcgtcccg ctgcgctcgg cgcttgaacc gccatacagg 1380

acgaggacac gggcctgggg tgacaactga tcatctagac ggccaatcat gcctttgccg 1440

aacaggacac gtgttgggtt atagaattcg aaattctgca ttaaatggag gcgctcgttg 1500

atctgagcct tgcccccctga cgaacggcgg tggatggaag atactgctct caagtgctga 1560

agcggtagct tagctccccg tttcgtgctg atcagtcttt ttcaacacgt aaaaagcgga 1620

ggagttttgc aattttgttg gttgtaacga tcctccgttg attttggcct ctttctccat 1680

gggcgggctg ggcgtatttg aagcggttct ctcttctgcc gtta 1724

<210> SEQ ID NO 142
<211> LENGTH: 1676
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 142, Example 142: designer Nial-promoter-controlled chloroplast-targeted NADPH-dependent Alcohol Dehydrogenase DNA construct (1676 bp)

<400> SEQUENCE: 142

agaaaatctg gcaccacacc atggtagggt gcgagtgacc ccgcgcgact tggaagggtt 60

caaacgaccc cgccgtacga acttttgtcg gggggcgctc ccggatggta gggtgcgagt 120

gaccccgcgc gacttggaag ggttcaaacg accccgccgt acgaactttt gtcgggggggc 180

gctcccggat ggccgccgtc attgccaagt cctccgtctc cgcggccgtg gctcgcccgg 240

cccgctccag cgtgcgcccc atggccgcgc tgaagcccgc cgtcaaggct gcccccgtgg 300

ctgccccggc tcaggccaac cagatgccta tacacttttt caaataattt ctttaaatct 360

tttaaattta cttctctgac atttccacta gtacaaatat cttcaagagc agatttagac 420

ataatattta tttcattaaa atatttttct tcatctattg ctaaatcttt tacacaacta 480

ggaagtccta agtttttatt taaaacttcc actgccacag ctaaactttc tgctccttct 540

tctgtattat ttgcaggaaa acctaaatct tttgaaattt cataatatct ttgagcagta 600

gttttatttt ctgaattgaa tctaattatg tagggtaata tagttccatt tatttttcca 660

tgagctatat gaaactttcc accaatagcg tgggctatac tatgatttat tcctaaacca 720

gatttttcaa aagcaaaacc tgctatacaa gatgcctttg ccatttcaat cctagcttcc 780

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tcatctttta tatctctata cattctcaaa agatttttaa aaataagtct tatagctgaa 840

agagcatata tttgagtata aaaatttgct tctttgcaag tgtatgactc aatagcatga 900

gttagagcat ctatacctga atcagctaca actgattttg gtagtgtttt tgtaagttca 960

ggatctagta ttgcatattc aggtatcatc tcattatctt ttaatggaat ttttacatta 1020

ttctttttat ctgtaagaac tgcataggaa cttacttctg aacctgttcc acttgtagtt 1080

ggtaaggcta ttaaagggat agataatcca gatttttta caaaatattt aattgactta 1140

gcagtatcaa gagaagaacc tcctcctatt gctaccatca catctggaag aaaatcaata 1200

accttatcta aggctttact aactatttca aatgctggat caacttcaac ttcattaaaa 1260

atcctataat ctatattttt ttgcttaaat atattttcaa attttttagt cattcctatt 1320

tttgacataa ctgaatcagt tactataaag gctttttag ctttaatttt attaataact 1380

tcatcaaatt tgtctcctac ataaacattt gtatttactt caaaaatttt cattaaatgg 1440

aggcgctcgt tgatctgagc cttgcccct gacgaacggc ggtggatgga agatactgct 1500

ctcaagtgct gaagcggtag cttagctccc cgtttcgtgc tgatcagtct ttttcaacac 1560

gtaaaaagcg gaggagtttt gcaattttgt tggttgtaac gatcctccgt tgattttggc 1620

ctctttctcc atgggcgggc tgggcgtatt tgaagcggtt ctctcttctg ccgtta 1676

<210> SEQ ID NO 143
<211> LENGTH: 3629
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Coonstruct- Sequence No. 143, Example 143: designer Nial-promoter-controlled chloroplast-targeted Phosphoenolpyruvate Carboxylase DNA construct (3629 bp)

<400> SEQUENCE: 143

agaaaatctg gcaccacacc atggtagggt gcgagtgacc ccgcgcgact tggaagggtt 60

caaacgaccc cgccgtacga acttttgtcg gggggcgctc ccggatggta gggtgcgagt 120

gaccccgcgc gacttggaag ggttcaaacg accccgccgt acgaactttt gtcgggggggc 180

gctcccggat ggccgccgtc attgccaagt cctccgtctc cgcggccgtg gctcgcccgg 240

cccgctccag cgtgcgcccc atggccgcgc tgaagcccgc cgtcaaggct gcccccgtgg 300

ctgccccggc tcaggccaac cagatgaccg gtatttctca ttcctgccgc aattccatta 360

atggttaata gcgctcctct gagcaactct tccttagaat aacggaaatt aatgactcca 420

gactcagctt gtgcgttgta ctgacgtagg cgtttgatga gagatacttg caaaaatcct 480

agaggaacaa ttgttccatt gcgtaactga acagaacgct gtaaggtggg atcgccatct 540

aggagccgtt tattctcggt aatttctaag actaagcggc aagtgcgatg atattcttgg 600

gctatttgct caaacagccg ctcaaagcgt tctctatctt ccggttgaga caattccttt 660

acataatgat aggcaatttg caaatctacc ttagataagg tcatttccac ttttgagatg 720

accattttaa agaagggcca tttgagataa aaatagcgca acagtttcaa atgttcttca 780

ggttcggtgc taataaactg ttctaaagcg gttcctaccc cataccaagc gggtaacaga 840

aaacgggttt gagtccaact aaagacccaa ggaattgcgc gtagggtact gaggtctttt 900

ttcccacttt tacgtctagc cgggcgagaa ctaatttgga gttgactaat ttcttgaatg 960

ggggtgacag acatgaagaa atccacaaaa tccggttctt cataaatcaa ggcacgatag 1020

gctttacgag aacaactggc gagttcttcc atgatctcat tccaaacctg aatatcatca 1080

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aagccgcagc ctaacaaact cgattgaata acggcagtaa caatggtttc taggttataa 1140

agggctaatt cagggagaga atatttagaa gcgaggactt ctccctgttc agtaatttta 1200

attctgccat taaccgtcgc tgtcggttga gcgagaatag cggcataagc gggtccaccg 1260

cctcgtccta ctgaaccccc gcgtccgtga aacaggcgta aatctaagcc atatctttta 1320

gcgacttttt gtaaagcttt ttgggcttta tgaatctccc aattactgct taaaaaccca 1380

gaatctttgt tactgtcgga ataaccgacc ataatttctt gtaggttagt gggttctaag 1440

agggggggtt taagttcgcc cacattttcc ccctgtaaag aggctaaatg atcatatcct 1500

cctgccaaag tggcgcggta aagagtcaat tcaaatagcg cccgcatgat ttcgggtgcc 1560

cgtttaaggt cttctacggt ttcaaatagg ggtacaatgc ggatcgtgct ggaacaagtg 1620

gccgggtcat agagtccggc ttcttgtgcc aagagaagaa cctctaagac atcgctgacc 1680

tcattagtca tactgataat gtaggtatga cagatctcta aaccaaattc ttgttgtagc 1740

tgccgcaaca tcctcaaggt ttctatcact tcgcaggttt tctcagaaaa cggcatttcc 1800

tggggaatga gaggacgacg agtttttaat tcttcgatta accaggcggt tctttcggct 1860

tcagtcagtt ggttgtaggg tttaggcaga atttgtaaat attctgctat ttcgttgatc 1920

gcatctgagt ggttactcga ctcttggcgg aaatctagtt gcgtgaggtt aaacccataa 1980

acttctacct gacaaattaa gctatctaat tcttgacaac ttaagccagt gctttctagg 2040

ttacgccgca ttaatttgag ttcttctata aactcttctt tattttggta attgttggcg 2100

ttggttgtct tgaacactaa aaggcgttct tctgggttag ctaggcggct attgcggtcg 2160

cgggtatttt ccaggcgttt tttaatataa gctaacttaa gacgataggg ttcttgacgg 2220

taacgaatgg ctaactgatt ataaacttgt gggatttgta cgcggtcttt ttctagggag 2280

tctaacaaat ccggcaggac gttacaccaa tggagggaag gactaaggat attcgataac 2340

tcatctaccc tttcgatata tttttcgata acgacattgc gttgataaca ggccgtggcc 2400

caagtcactt ctggtgtaac aaaggggttc ccatctcgat cgcctcccac ccaagagcca 2460

aaataacaga aattattctt cggtgggcgt agtctgggga aggcactttt tagagttcgt 2520

ttgagacgaa gggctaattg aggaattgcc tcaaagagga cttcattaaa atagtgtagg 2580

gagtagtcca cttcatctaa cacggtgggt ttaaactggt gtaactcatc ggtacgccac 2640

cagaggcgaa tttcttcttt aagctgttct ttagcttctt ctgcttccca ggagttggtt 2700

agccccattc ctctaaaggt ttcttctgcc tggtctaact tttgtaaaat atgagcgata 2760

cgccgttgtt tgcgtcgaat ggtgtggcga acaatttcgg tgggatgggc tgtaaaaacc 2820

aggcgcacat ctagttgttc gagtaggcgt tgaatttgtt gaggtggaac atttaattgt 2880

tttaaatagg gaaatagcca gtgaaaagtt cctatttttt gatcattttg tttttcatcg 2940

ttcaaacttc tttctaacca atttgctcca aatgccgagg agaatatact ggtttgctcg 3000

ccgttaatgc catttttggc actggactct ccttcattgt aggtggcccg tcgtgagagt 3060

tgttggtctc gttgttcgta gtgttgttca acaatattaa tgagttggaa atagagagca 3120

aaagcgcgag acgttcttac tgcttcattg aggtcgagtt tttcaatcaa ttgggtaatg 3180

gagtcttcta acgctttttg ggcttgtcct tgttcagaac aaattgcacg cagttttatg 3240

agcagatcca ccaaatcttg cccgcattct gcctttagca cggcttccca taaatcttcg 3300

actaatttta gtctagcttg taaaaataag tctgatgtgg agaagaattg taatggggtt 3360

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gtggggactt gaactagcga actcattaaa tggaggcgct cgttgatctg agccttgccc 3420

cctgacgaac ggcggtggat ggaagatact gctctcaagt gctgaagcgg tagcttagct 3480

ccccgtttcg tgctgatcag tctttttcaa cacgtaaaaa gcggaggagt tttgcaattt 3540

tgttggttgt aacgatcctc cgttgatttt ggcctctttc tccatgggcg ggctgggcgt 3600

atttgaagcg gttctctctt ctgccgtta 3629

<210> SEQ ID NO 144
<211> LENGTH: 1745
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 144, Example 144: designer Nial-promoter-controlled chloroplast-targeted Aspartate Aminotransferase DNA construct (1745 bp)

<400> SEQUENCE: 144

agaaaatctg gcaccacacc atggtagggt gcgagtgacc ccgcgcgact tggaagggtt 60

caaacgaccc cgccgtacga acttttgtcg gggggcgctc ccggatggta gggtgcgagt 120

gaccccgcgc gacttggaag ggttcaaacg accccgccgt acgaactttt gtcgggggcc 180

gctcccggat ggccgccgtc attgccaagt cctccgtctc cgcggccgtg gctcgcccgg 240

cccgctccag cgtgcgcccc atggccgcgc tgaagcccgc cgtcaaggct gcccccgtgg 300

ctgccccggc tcaggccaac cagatgaacc gagacaccaa gcaggctgtt ttggaagagc 360

tgtaaccgtt ccagaccctt ttcaatcgtt tggcagtcag tggcgtagga gagccggatg 420

ctgcgatcgt cgccaaaggc aatgccggga atggctgcaa cttgatgttg atccaacagt 480

tgacggcaat aggtcatcga gtcgagacct gttttgctga tgtccacgaa gacgtagaac 540

gccccttccg gtattggaca ggagagcccc gcgatttgat tcagtccgtt caagatcaac 600

tgacgccgct ccgtaaaggc agccagcatt tctgccacac aatcctgtgg accttgcaga 660

gctgcgatcg cgccgtactg ggcaaaggtg cagacgtttg aggtgctgtg gctttgcagc 720

gatgcagcag cagcaattag ctcgctcgga cccgcgaggt agccaacccg ccatcctgtc 780

atcgagtagg ctttggcgaa gccgttgctg atcagcgttc gttcaaaaca ggcggggctc 840

aagctgccaa tgctgtggtg atcggctccg tcgtaaagga tcttttcgta aatttcatca 900

gaaacgaccc aaaagtcatg ggcttcaatg atcggcgcga tcgcttccag ttcttgccgg 960

ctatagacca tccccgtggg attggagggg gaattcagca ctagcagccg tgtccgaggc 1020

gtaatcgccc ctgccaattg ctgcggctgg agtttaaagc cgtcgctggc gaaagtttca 1080

acgatgacgg gcacaccgcc cgccaacttg accatttcgg gatagctcaa ccagtaaggt 1140

gcggggataa tcacctcatc gcccggatcg agcagcacct gcatcaggtt gtagagtgac 1200

tgcttaccgc cattggtgac gagaatgttg gcggcttggt aatcgagtcc gttgtcggcg 1260

cgcaattttt gggcgatcgc ttcgcgcaga tcaggttcac cggctgcagg accgtagcga 1320

gttttgccct ctgctagcgc ttgagctgct gcattgcgaa tgtgcaaagg tgtttcaaag 1380

tcgggctccc cggcgctgaa gctgcagaca tccaagccct cagctttcat cgctttggct 1440

tgggcagcga tcgcgagagt caacgatggt gacactcgcc ccacacgctc ggatagtttc 1500

attaaatgga ggcgctcgtt gatctgagcc ttgccccctg acgaacggcg gtggatggaa 1560

gatactgctc tcaagtgctg aagcggtagc ttagctcccc gtttcgtgct gatcagtctt 1620

tttcaacacg taaaaagcgg aggagttttg caattttgtt ggttgtaacg atcctccgtt 1680

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gattttggcc tctttctcca tgggcgggct gggcgtattt gaagcggttc tctcttctgc 1740

cgtta 1745

<210> SEQ ID NO 145
<211> LENGTH: 2366
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 145, Example 145: designer Nial-promoter-controlled chloroplast-targeted Aspartokinase DNA construct (2366 bp)

<400> SEQUENCE: 145

agaaaatctg gcaccacacc atggtagggt gcgagtgacc ccgcgcgact tggaagggtt 60

caaacgaccc cgccgtacga acttttgtcg gggggcgctc ccggatggta gggtgcgagt 120

gaccccgcgc gacttggaag ggttcaaacg accccgccgt acgaactttt gtcggggggc 180

gctcccggat ggccgccgtc attgccaagt cctccgtctc cgcggccgtg gctcgcccgg 240

cccgctccag cgtgcgcccc atggccgcgc tgaagcccgc cgtcaaggct gcccccgtgg 300

ctgccccggc tcaggccaac cagatggcgt taattgtcca aaaatacggt ggaacctctg 360

tcggttcagt agaacgcatt caaacagttg cccaacggat tcaaaaaaca gcccaaaatg 420

gcaatcaagt cgtggttgtt gtttcggcca tgggaaaaac caccgatact ttagtcaatt 480

tagccaaaga gattacccca aatccctgtc gtcgggaaat ggatatgtta ttgtccacgg 540

gagaacaagt atcgatcgcc ttgatgagta tggccttaca gaaattagga caagcggcca 600

tctccttaac tggggcacaa gtggggatcg tcaccgaagc agaacacagt cgagcccgca 660

tcctttccat taaaccccat cgcattcaac gccatctcga tcgcggtgaa gttgtcgtgg 720

tcgccgggtt tcaaggcatt actaacgcag atgacttaga aattaccacc ctagggcgag 780

ggggctcaga tacctccgcc gtcgccattg cggcagcctt aaaagccagt tgctgcgaaa 840

tctatacaga tgtccccggc attctcacca ccgatccccg catcgtcccc gatgcccaat 900

taatgggggа aattacctgc gatgagatgc tagagttggc cagtttaggg gctaaggttc 960

ttcatccgag ggcggtggaa attgcgcgta attatggcat tcctttagtg gtgcgatcga 1020

gttggagtga tgcccccgga acccgcgtga cttctcccat tcctaaaccg cgatcgctag 1080

aaggcttaga actgacaaaa gccgttgatg gggtgcaatt tgaccccgat caagccaaaa 1140

tcgccttgtt acgagtcccc gatcgccccg gagtcgctgc ccgcctattt ggggaaattg 1200

cccaccagca ggtggatgta gacttaatta ttcaatcgat ccacgaaggg aatagtaacg 1260

atatcgcctt tacggtggtt aaaaatgtac tcactaaggc cgaagccgtc gctgaagcga 1320

tcgccccggc tttacggagt cattcagcga atagcgatga agcagaggta ttagtcgaga 1380

cgggagtggc gaaaattgcc atttcagggg caggaatgat cggacggcca ggtattgccg 1440

cgaaaatgtt caaaattctc gcccaagagg ggattaatat cgaaatgatc tccacctcgg 1500

aagtgaaggt cagttgtgtg attcgtcaag aagagggcga tcgcgccatt aaagccctat 1560

gccaagggtt tgaggtggaa ttgtccccga cggggattcc tgagtcagta gtagcggtgt 1620

tacctccagt tcgaggagtc gctttagatg aaaaacaagc acaaatcgcc ctaattcatg 1680

ttcaagatcg gccggggatg gctgctagta tctttggagt cttagcggat cataacatca 1740

gtattgatac gattattcaa tcccaacgct gtcgaattgt tgagggaata cccacccgtg 1800

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atatcgcctt taccgttgcc caaattgatg tagaagctgc tcaaaatgcg ttaaaaaccc 1860

tagccagtgc gtttagtgaa atgatcgtcg atagcgatgt tgctaaagtc agtattgtag 1920

gggcgggaat ggcgggacaa cccggggtag cggccaagtt ttttgatgct ttagctagac 1980

atcaaattaa tattaaaatg attgcaactt cagaaataaa aattagttgt gttgttagca 2040

aagatcaagg aattaaagct ttaaaagcag ttcatgaagc ctttcaatta gccggagaag 2100

aacgggtaga agttccagct taataaatgg aggcgctcgt tgatctgagc cttgcccct 2160

gacgaacggc ggtggatgga agatactgct ctcaagtgct gaagcggtag cttagctccc 2220

cgtttcgtgc tgatcagtct ttttcaacac gtaaaaagcg gaggagtttt gcaattttgt 2280

tggttgtaac gatcctccgt tgattttggc ctctttctcc atgggcgggc tgggcgtatt 2340

tgaagcggtt ctctcttctg ccgtta 2366

<210> SEQ ID NO 146
<211> LENGTH: 1604
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 146, Example 146: designer Nial-promoter-controlled chloroplast-targeted Aspartate-Semialdehyde Dehydrogenase DNA construct (1604 bp)

<400> SEQUENCE: 146

agaaaatctg gcaccacacc atggtagggt gcgagtgacc ccgcgcgact tggaagggtt 60

caaacgaccc cgccgtacga acttttgtcg gggggcgctc ccggatggta gggtgcgagt 120

gaccccgcgc gacttggaag ggttcaaacg accccgccgt acgaactttt gtcgggggggc 180

gctcccggat ggccgccgtc attgccaagt cctccgtctc cgcggccgtg gctcgcccgg 240

cccgctccag cgtgcgcccc atggccgcgc tgaagcccgc cgtcaaggct gcccccgtgg 300

ctgccccggc tcaggccaac cagatgtcag attcatacag agtagcaata ttaggagcaa 360

ctggtgcagt aggtacggaa ttactagaat tactggaaac tcggaacttt ccagtaggag 420

aattaaaact cttagcttca gaattttcag cgggtaagac cttaaaattt aaggaacaaa 480

gtttacaagt agaagctgta acaaatgatt catttaataa agtagattta gtgctagcat 540

cagcaggtgc atctgtatca aaagtatggg caaagaaagc agtagaggct ggagctgtag 600

ttattgacaa ttctagtgct tttcgtatgg actcccaagt acctcttgta gtcccagaag 660

ttaacccaga agcagcggct ttacataaag gtatagttgc taaccctaac tgcacaacaa 720

tattaatgag tgtagcagtg tggccattgc acaaaatcca gccagtccaa aggttagtag 780

tggccactta tcaatcagca agtggggccg ggtcaagggc tatggcagaa atgaaaattc 840

aggcccaaga aatcttagat ggaaaaactc caacaacaga tatttttccc tacccattag 900

catttaattt gttccctcat aattctcaac tcaatgagca gggatattgt caagaagaaa 960

tgaaaatgct tgatgaaacc agaaaaatat ttggctctaa ggaactgaga attacagcaa 1020

cttgtattcg agtaccagta ttaagagctc attcagaagc aattaatttg gaatttgctg 1080

aaccatttag tgtagttaaa gcacgggaag tattaagtca agcaccagga gtgacactgg 1140

tagaaaattg gcaagaaaat tattttccta tgcctatggt tgcaagtggt aaagatgatg 1200

tattggtggg gagaattcgt caggatattt ctcaagctga ggggttagaa ttatggttaa 1260

gtggagacca ggtaagaaaa ggagctgcct tgaatgcagt acaaatagct gaattattgg 1320

tggcaaaaaa ttggctgaga ataccagtag gaacatttta ataaatggag gcgctcgttg 1380

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atctgagcct tgccccctga cgaacggcgg tggatggaag atactgctct caagtgctga 1440

agcggtagct tagctccccg tttcgtgctg atcagtcttt ttcaacacgt aaaaagcgga 1500

ggagttttgc aattttgttg gttgtaacga tcctccgttg attttggcct ctttctccat 1560

gggcgggctg ggcgtatttg aagcggttct ctcttctgcc gtta 1604

<210> SEQ ID NO 147
<211> LENGTH: 1868
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 147, Example 147: designer Nial-promoter-controlled chloroplast-targeted Homoserine Dehydrogenase DNA construct (1868 bp)

<400> SEQUENCE: 147

agaaaatctg gcaccacacc atggtagggt gcgagtgacc ccgcgcgact tggaagggtt 60

caaacgaccc cgccgtacga acttttgtcg gggggcgctc ccggatggta gggtgcgagt 120

gaccccgcgc gacttggaag ggttcaaacg accccgccgt acgaactttt gtcgggggggc 180

gctcccggat ggccgccgtc attgccaagt cctccgtctc cgcggccgtg gctcgcccgg 240

cccgctccag cgtgcgcccc atggccgcgc tgaagcccgc cgtcaaggct gcccccgtgg 300

ctgccccggc tcaggccaac cagatgaagc actcgcagga cgctaggaat gctattaatc 360

gcttgagatt gctcaatttc agctaaggct tgccgaaaat tgccttctcg tacatcatga 420

gtgaccacga cgatttctgc taactgtccc tgaaatccaa tttgaacgac ggattctaga 480

ctaacatggt gctgaccaaa acaagttcct aaatgcccaa tcaccccagg gacatcttca 540

cagagaaagc gggcataaaa gcgagttttt aaatcttcaa ttggggtcag actacaataa 600

tgttgatggg tgacgttcaa taaaggatct aaagattgtg cttgtcctcc actgctttgc 660

agaatgccga cgatattcat aatatctgaa acgactgcac tggcggttgg acctgccccc 720

gcaccgggtc caaaaaacat cacttgtcct aacggttctc ccttgaccaa aatggcgtta 780

taaaccccat taatactggc tagtggatga tctttggcta ttaaagtggg atgtactcgc 840

acttgtaagg tttctgaatc atctccttta gaaccttggg caatggctaa taatttaatc 900

acaaatccga gtttatcagc ataagtaata tcggcggcac tgacttgacg aatgccctca 960

caataaatct cttcgcgttt tacccgtccg gcaaaaccga tggaggccaa aatagcaatt 1020

ttatcggctg catctaatcc gtctacatct gccgtcggat cggcttcagc atagcctaat 1080

ttttgggctt ctgctaatac ctcgccaaaa tcggctccct cagaggtcat ttggctgagg 1140

atataattgg tcgttccgtt aataatgcca ataatattac taatccgatt ggcccctaat 1200

gattgtttga ggggtttaat cactggaatt ccccccccca cagccgcttc taataacaca 1260

taaacgccgg ctgcattggc cgcttcataa atttcatccc cataacgagc gatcactgcc 1320

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cgcactcctg cccgtttaat ctcgatatct tttaagatag gattacgtcc ccagggatcg 1560

agtagaattt gtgctgtccc cgttcccaca gttcccaagc ctaataaacc tattttaaat 1620

gccactaaat ggaggcgctc gttgatctga gccttgcccc ctgacgaacg gcggtggatg 1680

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gaagatactg ctctcaagtg ctgaagcggt agcttagctc cccgtttcgt gctgatcagt 1740

ctttttcaac acgtaaaaag cggaggagtt ttgcaatttt gttggttgta acgatcctcc 1800

gttgattttg gcctctttct ccatgggcgg gctgggcgta tttgaagcgg ttctctcttc 1860

tgccgtta 1868

<210> SEQ ID NO 148
<211> LENGTH: 1472
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 148, Example 148: designer Nial-promoter-controlled chloroplast-targeted Homoserine Kinase DNA construct (1472 bp)

<400> SEQUENCE: 148

agaaaatctg gcaccacacc atggtagggt gcgagtgacc ccgcgcgact tggaagggtt 60

caaacgaccc cgccgtacga acttttgtcg gggggcgctc ccggatggta gggtgcgagt 120

gaccccgcgc gacttggaag ggttcaaacg accccgccgt acgaactttt gtcgggggggc 180

gctcccggat ggccgccgtc attgccaagt cctccgtctc cgcggccgtg gctcgcccgg 240

cccgctccag cgtgcgcccc atggccgcgc tgaagcccgc cgtcaaggct gcccccgtgg 300

ctgccccggc tcaggccaac cagatgatta acaattttgg ccccttccat atctaaagag 360

agtgcttgca cttgcgccgc tacccccttca ttttcccacg ccaccctcat cgcttcagtc 420

accctatccg cttcaccctg agaacttaaa gcgagtaaag tgggacctgc cccactgatt 480

accataccat aagccccggc tgcgatagcc gctcgtttca ccgcttcgta acctttaatt 540

aaaccttgac gatagggttg atgcagctta tcctccatcg ccatagctaa ccagtctcct 600

cgcccctgtt cgagtccttg taacaataac cctaaacgtg caatattaaa aatagcatca 660

gcgcggctat actgagtggg taaaacgcct ctcgcttctt gagtagataa ttcaaaatcc 720

ggaatagcca caatgggaat cagtttgtca taccagggaa tctcgcaaat ttgccaattc 780

cccatttccc ccacacataa gcgactgctt cccaataaag cgggaaccac attatcggga 840

tgtccttcta aagatatggc taattccatc acttcagatt gagttaaagg gttaccggct 900

agataatttg cccccactaa acccccctaca atggctgtgg ctgaacttcc taaccctctg 960

gctaaaggaa cccctaattt gatctcaatt tctacagcag gaaccggttg attgagatgt 1020

tgatagaaaa gcgcaaaaga ttgataaagt aaattagttt tatctcgact aacccgttct 1080

gcttctgcgc cgcttacgag aattttctct tcggtttctg aagtgagagt aaacttaaat 1140

tgattataaa gggttaaagc ggctcctaga caatcaaagc ctggaccaag attagcggta 1200

gtagcaggaa cggttagggt aacggtcatt aaatggaggc gctcgttgat ctgagccttg 1260

ccccctgacg aacggcggtg gatggaagat actgctctca agtgctgaag cggtagctta 1320

gctccccgtt tcgtgctgat cagtcttttt caacacgtaa aaagcggagg agttttgcaa 1380

ttttgttggt tgtaacgatc ctccgttgat tttggcctct ttctccatgg gcgggctggg 1440

cgtatttgaa gcggttctct cttctgccgt ta 1472

<210> SEQ ID NO 149
<211> LENGTH: 1655
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 149, Example

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149: designer Nial-promoter-controlled chloroplast-targeted Threonine Synthase DNA construct (1655 bp)

<400> SEQUENCE: 149

agaaaatctg gcaccacacc atggtagggt gcgagtgacc ccgcgcgact tggaagggtt 60

caaacgaccc cgccgtacga acttttgtcg gggggcgctc ccggatggta gggtgcgagt 120

gaccccgcgc gacttggaag ggttcaaacg accccgccgt acgaactttt gtcggggggc 180

gctcccggat ggccgccgtc attgccaagt cctccgtctc cgcggccgtg gctcgcccgg 240

cccgctccag cgtgcgcccc atggccgcgc tgaagcccgc cgtcaaggct gcccccgtgg 300

ctgccccggc tcaggccaac caggtgaccc taacttggcc tatttctaaa tctgcgtcct 360

ggtcaggtct gatcaacgcc taccgttcct atttacctgt cacggaagcc actccgattg 420

tcaccctgca tgaagggaac acgcccctga ttccggtgcc cagcattgcc gctgaaattg 480

gccggcaagt tcaggtctat gtcaagtacg acggtttgaa ccccacgggc agctttaaag 540

atcggggtat gaccatggcg atctccaagg ctaaggaagc cggagccaag gcggtgatct 600

gtgccagtac cggcaatacc tctgcggcgg cagcggccta tggacggcgg ggcggcatgc 660

gggtctttgt cctcatcccc gatggttatg tcgctctggg aaaattagcc caagccctgg 720

tctatggcgc agaggtgctg gccattcagg gcaactttga tcaggcattg accctggtgc 780

agcaattagc cgaaacccag cccgtcaccc tggtgaattc cgtcaacccc taccggctgg 840

aaggtcagaa aactgctgcc tttgaagtgg tggatgccct gggtaatgcc cccgactggc 900

tctgtattcc cgtgggcaat ggcggcaata tcaccgctta ctggatggga ttctgtcagt 960

atcgggaaca ggatcgttgc gatcgtctac cccggatgat gggttttcaa gcagccggct 1020

ctgctccccct tgtccatggc caggtggtga cccatcctga aactgtagcg accgccattc 1080

ggattggtaa cccggccaac tggcagcggg cgatggccgt gcgggatgcc agccagggag 1140

aattcaatgc tgtcagcgat gccgaaattc tcgctgccta ccgtctgctg gccagtcagg 1200

aagggatctt ttgtgaaccc gccagtgccg cgtccgtcgc cggtctatta aaggtgaaag 1260

atcaggttcc gacgggggca acggtggtct gtgtcctgac ggggaatgga ttgaaagatc 1320

ctgatagcgc aattaagcag caaagtaacc agttccatca gggcatccca gctcagctcg 1380

aagccgtggc agccgtgatg ggcttccgtt agtaaatgga ggcgctcgtt gatctgagcc 1440

ttgccccctg acgaacggcg gtggatggaa gatactgctc tcaagtgctg aagcggtagc 1500

ttagctcccc gtttcgtgct gatcagtctt tttcaacacg taaaaagcgg aggagttttg 1560

caattttgtt ggttgtaacg atcctccgtt gattttggcc tctttctcca tgggcgggct 1620

gggcgtattt gaagcggttc tctcttctgc cgtta 1655

<210> SEQ ID NO 150
<211> LENGTH: 2078
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 150, Example 150: designer Nial-promoter-controlled chloroplast-targeted Threonine Ammonia-Lyase DNA construct (2078 bp)

<400> SEQUENCE: 150

agaaaatctg gcaccacacc atggtagggt gcgagtgacc ccgcgcgact tggaagggtt 60

caaacgaccc cgccgtacga acttttgtcg gggggcgctc ccggatggta gggtgcgagt 120

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gaccccgcgc gacttggaag ggttcaaacg accccgccgt acgaactttt gtcgggggc    180

gctcccggat ggccgccgtc attgccaagt cctccgtctc cgcggccgtg gctcgcccgg    240

cccgctccag cgtgcgcccc atggccgcgc tgaagcccgc cgtcaaggct gcccccgtgg    300

ctgccccggc tcaggccaac cagatgtaag aagagtcgat aggctggatt gtcactttcg    360

ttccagtacc gatagcccag ggttttgaga aatgattccc actgagccat ctcttgtgga    420

gggacttgca tcccgacgac gattctgccg tagtctgcgc cgtgattgcg gtagtggaat    480

aggctgatgt tccaatctgg gctcattttc gtgacaaagt tagctaatgc gcccggtcgc    540

tcaggaaatt caaaccgata gagcagttcg ttttgagcta gcggtgactt gccgcctacc    600

atgtgccgca aatgcatctt ggctagctca tcatcagtta gatctagcgt cttaaatcca    660

ttgtctctaa acttgtgggc gatcgcctgc gcatcggctc tattttctat ctgaatgccc    720

acaaaaatat gagcttgatc ggcatctgca atccgatagt tgaattcgct aaggctgtgg    780

ctaccgagga tatcgcaaaa tttgctgaga ctgcctgccc gctctggaat cgtaacggca    840

aagacggctt ctcttccttc tcctagctcg gctcgctcgg ctacaaagcg cagacgatca    900

aagttcatat tggccccaca agcgatcgcc accaacgttt ctccctgaat ttcttctcgc    960

tctacatagg ctttgatacc tgcgatcgcg agcgccccag cgggttccaa aattgagcga   1020

gtatcttcaa atacgtcctt gatcgcggcg caggtatcat ctgtagttac cagcaacaca   1080

tcatcgacat actgttggca cagacgaaac gtttcctccc cgacctggcg caccgctacg   1140

ccatctgcaa acaggcctac ttgatccaac ttgacacgat tccctttttgc taatgattga   1200

cgcatggcat cagcatccac cggctccaca ccaatgatct taacttcagg acgtaagcgt   1260

ttgatataag cggcaatgcc cgaaattaaa ccacccccccc caatcgcaac aaaaatggca   1320

tgaatcggct tctgatgctg tcgcaagatc tccatgccga tcgttccctg cccggcaatg   1380

acgtctggat cgtcaaacgg atgcacaaag gtaagtcctt tttccacttc tagctggcgt   1440

gcgtgtgcat aggcatcgtc gtaggtgtca ccgtgtaaga caacgagtcc gcctctggcc   1500

ttcaccgcat caatcttgac ttgcggcgtc gtgatcggca taacaattac cgctgacgta   1560

cccaattctc tagcgcctag cgccaccccc tgtgcgtggt tgcccgcaga agctgcaatc   1620

accccacgct gcaacagttc tgaaggtagc tgcgccattt tgttataggc accgcgtagt   1680

ttgaaggaga aaacagactg tacatcttcc cgttttagca gcacctgatt acctagccgc   1740

tccgatagcc tcggcgcgat atctaaaggc gtttcttgcg ccacgtcata aacgcgggcc   1800

ttcaaaatgc gttctaaata gtcagaataa accactaaat ggaggcgctc gttgatctga   1860

gccttgcccc ctgacgaacg gcggtggatg gaagatactg ctctcaagtg ctgaagcggt   1920

agcttagctc cccgtttcgt gctgatcagt ctttttcaac acgtaaaaag cggaggagtt   1980

ttgcaatttt gttggttgta acgatcctcc gttgattttg gcctctttct ccatgggcgg   2040

gctgggcgta tttgaagcgg ttctctcttc tgccgtta                           2078
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<210> SEQ ID NO 151
<211> LENGTH: 2282
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 151, Example 151: designer Nial-promoter-controlled chloroplast-targeted Acetolactate Synthase DNA construct (2282 bp)

<400> SEQUENCE: 151

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agaaaatctg gcaccacacc atggtagggt gcgagtgacc ccgcgcgact tggaagggtt 60

caaacgaccc cgccgtacga acttttgtcg gggggcgctc ccggatggta gggtgcgagt 120

gaccccgcgc gacttggaag ggttcaaacg accccgccgt acgaactttt gtcggggggc 180

gctcccggat ggccgccgtc attgccaagt cctccgtctc cgcggccgtg gctcgcccgg 240

cccgctccag cgtgcgcccc atggccgcgc tgaagcccgc cgtcaaggct gcccccgtgg 300

ctgccccggc tcaggccaac cagatgttga caaaagcaac aaaagaacaa aaatcccttg 360

tgaaaaacag aggggcggag cttgttgttg attgcttagt ggagcaaggt gtcacacatg 420

tatttggcat tccaggtgca aaaattgatg cggtatttga cgctttacaa gataaaggac 480

ctgaaattat cgttgcccgg cacgaacaaa acgcagcatt catggcccaa gcagtcggcc 540

gtttaactgg aaaaccggga gtcgtgttag tcacatcagg accgggtgcc tctaacttgg 600

caacaggcct gctgacagcg aacactgaag gagaccctgt cgttgcgctt gctggaaacg 660

tgatccgtgc agatcgttta aaacggacac atcaatcttt ggataatgcg gcgctattcc 720

agccgattac aaaatacagt gtagaagttc aagatgtaaa aaatataccg gaagctgtta 780

caaatgcatt taggatagcg tcagcagggc aggctggggc cgcttttgtg agctttccgc 840

aagatgttgt gaatgaagtc acaaatacga aaaacgtgcg tgctgttgca gcgccaaaac 900

tcggtcctgc agcagatgat gcaatcagtg cggccatagc aaaaatccaa acagcaaaac 960

ttcctgtcgt tttggtcggc atgaaaggcg gaagaccgga agcaattaaa gcggttcgca 1020

agcttttgaa aaaggttcag cttccatttg ttgaaacata tcaagctgcc ggtacccttt 1080

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atttactgct agagcaggca gatgttgttc tgacgatcgg ctatgacccg attgaatatg 1200

atccgaaatt ctggaatatc aatggagacc ggacaattat ccatttagac gagattatcg 1260

ctgacattga tcatgcttac cagcctgatc ttgaattgat cggtgacatt ccgtccacga 1320

tcaatcatat cgaacacgat gctgtgaaag tggaatttgc agagcgtgag cagaaaatcc 1380

tttctgattt aaaacaatat atgcatgaag gtgagcaggt gcctgcagat tggaaatcag 1440

acagagcgca ccctcttgaa atcgttaaag agttgcgtaa tgcagtcgat gatcatgtta 1500

cagtaacttg cgatatcggt tcgcacgcca tttggatgtc acgttatttc cgcagctacg 1560

agccgttaac attaatgatc agtaacggta tgcaaacact cggcgttgcg cttccttggg 1620

caatcggcgc ttcattggtg aaaccgggag aaaaagtggt ttctgtctct ggtgacggcg 1680

gtttcttatt ctcagcaatg gaattagaga cagcagttcg actaaaagca ccaattgtac 1740

acattgtatg gaacgacagc acatatgaca tggttgcatt ccagcaattg aaaaaatata 1800

accgtacatc tgcggtcgat ttcggaaata tcgatatcgt gaaatatgcg gaaagcttcg 1860

gagcaactgg cttgcgcgta gaatcaccag accagctggc agatgttctg cgtcaaggca 1920

tgaacgctga aggtcctgtc atcatcgatg tcccggttga ctacagtgat aacattaatt 1980

tagcaagtga caagcttccg aaagaattcg gggaactcat gaaaacgaaa gctctctagt 2040

aaatggaggc gctcgttgat ctgagccttg ccccctgacg aacggcggtg gatggaagat 2100

actgctctca agtgctgaag cggtagctta gctccccgtt tcgtgctgat cagtcttttt 2160

caacacgtaa aaagcggagg agttttgcaa ttttgttggt tgtaacgatc ctccgttgat 2220

tttggcctct ttctccatgg gcgggctggg cgtatttgaa gcggttctct cttctgccgt 2280

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ta 2282

<210> SEQ ID NO 152
<211> LENGTH: 1562
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 152, Example 152: designer Nial-promoter-controlled chloroplast-targeted Ketol-Acid Reductoisomerase DNA construct (1562 bp)

<400> SEQUENCE: 152

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caaacgaccc cgccgtacga acttttgtcg gggggcgctc ccggatggta gggtgcgagt 120

gaccccgcgc gacttggaag ggttcaaacg accccgccgt acgaactttt gtcgggggggc 180

gctcccggat ggccgccgtc attgccaagt cctccgtctc cgcggccgtg gctcgcccgg 240

cccgctccag cgtgcgcccc atggccgcgc tgaagcccgc cgtcaaggct gcccccgtgg 300

ctgccccggc tcaggccaac cagatgagcc ttttttagcc aactaaacat agctcgtaaa 360

tctttaccga cttcttcaat aggatgttca gcttcttgac gacgcatggc gataaatccg 420

ggttttcctg actggttttc taagacaaat tcccgagcaa attgaccgga ttgaatttct 480

ttaaggattt tccgcatttc ttgccgggtt tgatccgtaa caatacgagg acctctagta 540

tagtctccat attctgccgt attggaaatg ctatcgcgca tcttagctaa tccgccttct 600

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cagaggacta cttgttcacc aaataaatca gtttctgttt cttctcggaa agtcgtttct 780

aaaacaccgg cacgagttcc tccaatccct ttagcataag ccatagcgcg atcgcgggct 840

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gtacgtctga cgagatgtcc tggacctttt ggtgccacca taaccacatc taccgtagaa 960

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tcttttaaat ggggttcaat ttcattttta tagacgcttt tttgtacctc atctggcagc 1080

aaaatcataa tccagtcggc ggcggcggcg gcatcggcta cacttttaac cgttaagccg 1140

gcttcagtgg ctttttgggc tgacttactc ccaggataca gccccacaat aacattaact 1200

ccgctatctt taagattaag ggcatgggca tggccttgag aaccatagcc gataatggca 1260

accgttttat tagcaagtaa gtctaaattg gcatcttcat cgtaatacat tcgagccatt 1320

aaatggaggc gctcgttgat ctgagccttg ccccctgacg aacggcggtg gatggaagat 1380

actgctctca agtgctgaag cggtagctta gctccccgtt tcgtgctgat cagtcttttt 1440

caacacgtaa aaagcggagg agttttgcaa ttttgttggt tgtaacgatc ctccgttgat 1500

tttggcctct ttctccatgg gcgggctggg cgtatttgaa gcggttctct cttctgccgt 1560

ta 1562

<210> SEQ ID NO 153
<211> LENGTH: 2252
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 153, Example 153: designer Nial-promoter-controlled chloroplast-targeted Dihydroxy-Acid Dehydratase DNA construct (2252 bp)

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<400> SEQUENCE: 153

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cccgctccag cgtgcgcccc atggccgcgc tgaagcccgc cgtcaaggct gcccccgtgg 300

ctgccccggc tcaggccaac cagatgtcag ataattacag aagtcgcatc attacacaag 360

gcagtcaacg tacaccaaac cgggccatgc ttcgggcggt aggttttgga gataatgact 420

ttactaagcc cattgtggga gtggctaacg gatacagcac cattacccct tgtaatatgg 480

gcatcaatga tctcgcgctg cgggccgaag ccggactcaa gcaagcggga gccatgccgc 540

aaattttcgg caccattacc gtgagtgacg gaatttctat gggaacagaa ggaatgaaat 600

actccctcgt ctcgcgcgat gtgatcgctg actctatcga aaccgcttgt aacggtcaaa 660

gtatggatgg tgtgcttgcc attggcggct gtgataaaaa tatgcccggg gccatgatcg 720

ccatcgctcg tatgaatatc cctgctatct tcgtctatgg cggtaccatt aaacccggaa 780

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aaaaatccgc ttttgtgctg gtagatgcca tcagaaagca aattttgccc agtcagattt 1080

taacccgtaa agcctttgag aatgcgattt ccgtgattat ggccgttggg ggatcgacca 1140

acgcggtttt acatttatta gcgatcgctc ataccatagg ggtagaactg agcatcgatg 1200

actttgaagc cattagagct agagttcccg tactttgtga cctcaaaccg agtggacgct 1260

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cagtgtataa agaaggacac ctagcgatct taaaaggaaa tttagccacc gagggagcag 1500

tcgctaaaat tagcggggtc aaaaatccta aaattaccgg tccggcgcga gtatttgaat 1560

ccgaggaaag ctgtctagag gcgattcttg caggtaaaat tcaagctggc gatgtgatta 1620

ttgttcgtta tgaagggccc aaaggtggcc ccggtatgag agaaatgtta gccccgactt 1680

cagccattat tggggcagga ttgggagatt ccgtaggatt aattactgat gggcgttttt 1740

ctgggggaac ttacgggcta gtcgtcggtc atgttgcccc agaagcagca gtaggcggaa 1800

atattgccct cgtacaagag ggagatagca ttaccattga tgcgaaagag cgattattac 1860

agcttaatgt agctgaagat gaattaatcc gtcgtcgcgc taactggcaa ccgcccatcc 1920

ctcgttatac caaaggtgta ttagcgaaat atgccaaatt agtctcttct agtagtatag 1980

gagcggttac cgacaaagat ttattctaat aaatggaggc gctcgttgat ctgagccttg 2040

ccccctgacg aacggcggtg gatggaagat actgctctca agtgctgaag cggtagctta 2100

gctccccgtt tcgtgctgat cagtcttttt caacacgtaa aaagcggagg agttttgcaa 2160

ttttgttggt tgtaacgatc ctccgttgat tttggcctct ttctccatgg gcgggctggg 2220

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cgtatttgaa gcggttctct cttctgccgt ta 2252

<210> SEQ ID NO 154
<211> LENGTH: 1496
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 154, Example 154: designer Nial-promoter-controlled chloroplast-targeted 2-Methylbutyraldehyde Reductase DNA construct (1496 bp)

<400> SEQUENCE: 154

agaaaatctg gcaccacacc atggtagggt gcgagtgacc ccgcgcgact tggaagggtt 60

caaacgaccc cgccgtacga acttttgtcg gggggcgctc ccggatggta gggtgcgagt 120

gaccccgcgc gacttggaag ggttcaaacg accccgccgt acgaactttt gtcgggggggc 180

gctcccggat ggccgccgtc attgccaagt cctccgtctc cgcggccgtg gctcgcccgg 240

cccgctccag cgtgcgcccc atggccgcgc tgaagcccgc cgtcaaggct gcccccgtgg 300

ctgccccggc tcaggccaac cagatggcag ttccatccaa ttctactaaa actttcaagc 360

tgaacaacgg cctgtccatt ccagcagtcg gtctcggaac atggcaatcc accgatgaag 420

aggcttacaa tgccgttatt gctgcattga aagctggata cagacacatc gacacagctt 480

actgttacgg aaatgaagag ccaattggca aagctattaa ggactctgga gttgcaagaa 540

aggacatttt tattactacc aaactttggg gaactgacca caccagaact gaggaaggtt 600

tggataggtc tctgaaattg ttgggtttgg actatgttga tctgttcttg atgcattggc 660

cagttccaat gaaccctaat ggaaaccacg acaaatttcc tacattacca gacggtaaac 720

gtgacattct gtttgactgg aacttcgttg atacatacag agagatgcaa aaattagttg 780

cctctggaaa gaccaaggca atcggtgtgt ccaatttttc tatcactaac ttgaagaaat 840

tgcttgcaga cccagaaatc accatcaagc cagttgtcaa ccaagttgaa attcacgggt 900

atctgccgca gcagagactt ttggagtatg cgaaggaaaa tgatattgtt ttggaggcat 960

attcaccgtt gggatccact ggtgccccat tgctgaaaga tgagctggtg caggacctag 1020

ccaagaagaa tggtatttct gaatctactc tcttaatttc ctgggcagtg tggagaggta 1080

tcgtcgtttt accaaaatct gtaacgcctt ccagaattgc tgataatctt aagatcattg 1140

agttgtgtga ggaggatgga aaaaaactta atgaattggc ctcgattaga ggagaaaaac 1200

gattagttag ccctccttgg gatcctattg tcgtcttcaa cgatgaagac taataaatgg 1260

aggcgctcgt tgatctgagc cttgcccccc gacgaacggc ggtggatgga agatactgct 1320

ctcaagtgct gaagcggtag cttagctccc cgtttcgtgc tgatcagtct ttttcaacac 1380

gtaaaaagcg gaggagtttt gcaattttgt tggttgtaac gatcctccgt tgattttggc 1440

ctctttctcc atgggcgggc tgggcgtatt tgaagcggtt ctctcttctg ccgtta 1496

<210> SEQ ID NO 155
<211> LENGTH: 1595
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 155, Example 155: designer Nial-promoter-controlled chloroplast-targeted 3-Methylbutanal Reductase DNA construct (1595 bp)

<400> SEQUENCE: 155

agaaaatctg gcaccacacc atggtagggt gcgagtgacc ccgcgcgact tggaagggtt 60

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caaacgaccc cgccgtacga acttttgtcg gggggcgctc ccggatggta gggtgcgagt 120

gaccccgcgc gacttggaag ggttcaaacg accccgccgt acgaactttt gtcgggggggc 180

gctcccggat ggccgccgtc attgccaagt cctccgtctc cgcggccgtg gctcgcccgg 240

cccgctccag cgtgcgcccc atggccgcgc tgaagcccgc cgtcaaggct gcccccgtgg 300

ctgccccggc tcaggccaac cagatgtcag ttttcgtttc aggtgctaac gggttcattg 360

cccaacacat tgtcgatctc ctgttgaagg aagactataa ggtcatcggt tctgccagaa 420

gtcaagaaaa ggccgagaat ttaacggagg cctttggtaa caacccaaaa ttctccatgg 480

aagttgtccc agacatatct aagctggacg catttgacca tgttttccaa aagcacggca 540

aggatatcaa gatagttcta catacggcct ctccattctg ctttgatatc actgacagtg 600

aacgcgattt attaattcct gctgtgaacg gtgttaaggg aattctccac tcaattaaaa 660

aatacgccgc tgattctgta gaacgtgtag ttctcacctc ttcttatgca gctgtgttcg 720

atatggcaaa agaaaacgat aagtctttaa catttaacga agaatcctgg aacccagcta 780

cctgggagag ttgccaaagt gacccagtta acgcctactg tggttctaag aagtttgctg 840

aaaaagcagc ttgggaattt ctagaggaga atagagactc tgtaaaattc gaattaactg 900

ccgttaaccc agtttacgtt tttggtccgc aaatgtttga caaagatgtg aaaaaacact 960

tgaacacatc ttgcgaactc gtcaacagct tgatgcattt atcaccagag gacaagatac 1020

cggaactatt tggtggatac attgatgttc gtgatgttgc aaaggctcat ttagttgcct 1080

tccaaaagag ggaaacaatt ggtcaaagac taatcgtatc ggaggccaga tttactatgc 1140

aggatgttct cgatatcctt aacgaagact tccctgttct aaaaggcaat attccagtgg 1200

ggaaaccagg ttctggtgct acccataaca cccttggtgc tactcttgat aataaaaaga 1260

gtaagaaatt gttaggtttc aagttcagga acttgaaaga gaccattgac gacactgcct 1320

cccaaatttt aaaatttgag ggcagaatat aataaatgga ggcgctcgtt gatctgagcc 1380

ttgccccctg acgaacggcg gtggatggaa gatactgctc tcaagtgctg aagcggtagc 1440

ttagctcccc gtttcgtgct gatcagtctt tttcaacacg taaaaagcgg aggagttttg 1500

caattttgtt ggttgtaacg atcctccgtt gattttggcc tctttctcca tgggcgggct 1560

gggcgtattt gaagcggttc tctcttctgc cgtta 1595

<210> SEQ ID NO 156
<211> LENGTH: 1739
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 156, Example 156: designer Nial-promoter-controlled chloroplast-targeted NADH-dependent Butanol Dehydrogenase DNA construct (1739 bp)

<400> SEQUENCE: 156

agaaaatctg gcaccacacc atggtagggt gcgagtgacc ccgcgcgact tggaagggtt 60

caaacgaccc cgccgtacga acttttgtcg gggggcgctc ccggatggta gggtgcgagt 120

gaccccgcgc gacttggaag ggttcaaacg accccgccgt acgaactttt gtcgggggggc 180

gctcccggat ggccgccgtc attgccaagt cctccgtctc cgcggccgtg gctcgcccgg 240

cccgctccag cgtgcgcccc atggccgcgc tgaagcccgc cgtcaaggct gcccccgtgg 300

ctgccccggc tcaggccaac cagatgaata attttacttt ttataatcct actaaaatta 360

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actttggtag aggagttgaa tcctctgttg gagaagagat taaaagctta ggagctagta    420

aagtgctttt tcattatggt ggaggaagta ttagaaaaaa tgggttatat gatagaattt    480

tagattcttt aaataaagca ggattacatg taatagaact tggaggagtt aagcctaatc    540

ctagattaag cttagttaaa aagggaatag aactttgtaa aaatagtaaa gttgatttta    600

tacttgcagt tggaggagga agtgttattg actcagctaa agccatagct cttggtgttc    660

cttatgatgg agatgtatgg gatttcttta ctaaaaatat taaaatagaa aaagctttac    720

cattaggtac agtattaaca ataccagcgg caggaagtga atcaagctca ggaactgtta    780

taactaatga agatggatgg tataagagat caacaggatc accacttcta tatcctaaat    840

tttcaatgtt aaatccagaa ctatgcttta ctttaccaga atatcaaata gcatcaggaa    900

gtgcagatat tttagcacat ttaatggaaa gatatttcac aaacacaaag aatgttgaac    960

ttatagatag attaattgag ggaacaatga aaacagtaat aaataatgtt cctaaggtat   1020

taaaaaataa ggaagactat gatagctttg cagaggttat gtgggctgga acaatagcac   1080

ataataatct tttaagcaca ggaagagaaa cagattgggc atcacataat atagaacatg   1140

aattaagtgg aatatatgat gttactcatg gtgcaggatt agctgttata ttcccagctt   1200

ggatgaagtt tgtttataag catgatttag atagattcaa ccaatttgct actagagtat   1260

ttgatgttca agttgaagat aaaactaagg aagaggttgc cttagaagga attaagaaac   1320

ttgaagaatt cttcaaatca ataaatcttc cagtaacttt aaaagagtta gaaataggtg   1380

aagatagatt agaagaaatg gctaaaaaat gcacagataa tgatgagcat acagtaggtc   1440

attttgtaga attaaacaca gaggacatcc ttgaaatata caaattagct ttatagtaaa   1500

tggaggcgct cgttgatctg agccttgccc cctgacgaac ggcggtggat ggaagatact   1560

gctctcaagt gctgaagcgg tagcttagct ccccgtttcg tgctgatcag tctttttcaa   1620

cacgtaaaaa gcggaggagt tttgcaattt tgttggttgt aacgatcctc cgttgatttt   1680

ggcctctttc tccatgggcg ggctgggcgt atttgaagcg gttctctctt ctgccgtta    1739
```

<210> SEQ ID NO 157
<211> LENGTH: 1733
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 157, Example 157: designer Nial-promoter-controlled NADPH-dependent chloroplast-targeted NADPH-dependent Butanol Dehydrogenase DNA construct (1733 bp)

<400> SEQUENCE: 157

```
agaaaatctg gcaccacacc atggtagggt gcgagtgacc ccgcgcgact tggaagggtt     60

caaacgaccc cgccgtacga acttttgtcg gggggcgctc ccggatggta gggtgcgagt    120

gaccccgcgc gacttggaag ggttcaaacg accccgccgt acgaactttt gtcgggggggc   180

gctcccggat ggccgccgtc attgccaagt cctccgtctc cgcggccgtg gctcgcccgg    240

cccgctccag cgtgcgcccc atggccgcgc tgaagcccgc cgtcaaggct gcccccgtgg    300

ctgccccggc tcaggccaac cagatgatga gatttacatt accaagagat atttattatg    360

gaaaaggatc actagaacaa ctaaaaaatc ttaaaggtaa aaaggcaatg ctagtacttg    420

gtggcggttc gatgaaaaga tttggatttg tcgataaggt gttaggatac ttaaaggaag    480

ctggaataga agtaaaatta atagaaggag ttgaaccaga cccatcagtt gaaacagtgt    540
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tcaagggcgc tgagttaatg agacaatttg aaccagattg gattatagct atgggtggtg 600

gatcaccaat tgatgctgca aaagcaatgt ggatttttta tgaacaccca gaaaaaactt 660

ttgatgacat taaagatccg tttacagtac cagaattaag aaataaggct aagttcctag 720

cgattccatc aacaagtggt acagcaacag aagtaacagc attttctgta attacagatt 780

ataagactga aataaaatat cctttagctg attttaatat aactccagat gtagctgtag 840

tagattcaga attagctgaa acaatgccac ctaagttaac tgcccataca ggaatggatg 900

cattaactca tgcaattgaa gcttatgtag caacattaca ttcaccattt actgatccac 960

tagctatgca agcgattgaa atgattaatg aacatttatt taaatcatat gaaggcgata 1020

aagaagctag agaacaaatg cattatgctc aatgtttagc tggaatggct ttctctaatg 1080

cactattagg aatatgtcat agtatggcgc ataaaacagg ggctgtattc catatccctc 1140

atggatgtgc gaatgcaatc tatttaccat atgtaattaa gtttaattca aaaacttcat 1200

tagaaagata tgctaaaata gcaaaacaaa tttcattagc aggaaataca aatgaggaat 1260

tagttgattc attaataaac ttagttaaag aattaaataa gaagatgcaa ataccaacaa 1320

cattaaaaga atatggtatt catgaacaag aatttaagaa taaggttgat ttgatttcag 1380

aaagagctat tggagatgct tgtactggat caaatccaag acaattaaat aaagatgaaa 1440

tgaaaaagat ttttgaatgc gtatattatg gtacagaagt tgatttttaa taaatggagg 1500

cgctcgttga tctgagcctt gccccctgac gaacggcggt ggatggaaga tactgctctc 1560

aagtgctgaa gcggtagctt agctccccgt ttcgtgctga tcagtctttt tcaacacgta 1620

aaaagcggag gagttttgca attttgttgg ttgtaacgat cctccgttga ttttggcctc 1680

tttctccatg ggcgggctgg gcgtatttga agcggttctc tcttctgccg tta 1733

<210> SEQ ID NO 158
<211> LENGTH: 1745
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 158, Example 158: designer Nial-promoter-controlled chloroplast-targeted 3-Ketothiolase DNA construct (1745 bp)

<400> SEQUENCE: 158

agaaaatctg gcaccacacc atggtagggt gcgagtgacc ccgcgcgact tggaagggtt 60

caaacgaccc cgccgtacga acttttgtcg gggggcgctc ccggatggta gggtgcgagt 120

gaccccgcgc gacttggaag ggttcaaacg accccgccgt acgaactttt gtcgggggggc 180

gctcccggat ggccgccgtc attgccaagt cctccgtctc cgcggccgtg gctcgcccgg 240

cccgctccag cgtgcgcccc atggccgcgc tgaagcccgc cgtcaaggct gcccccgtgg 300

ctgccccggc tcaggccaac cagatgaccg acatcgtcat cgtcgccgca gcccgcaccg 360

ccgtgggcaa gttcggcggc tcgctggcca agatcccggc gcctgagctg ggcgctgccg 420

tgatcaaggc cctgctggaa aaaaccggcg tgggcgccga ccagatcggt gaagtcatca 480

tgggccaggt gctggccgcc ggcgcgggcc agaacccggc tcgccaggcc atgatgaagg 540

cgggcatcgc caaggaaacg ccggcgctga ccatcaacgc cgtgtgcggc tccggcctga 600

aggccgtgat gctggcggcc caagccatcg cctggggcga cagcgagatc gtcatcgccg 660

gcggccagga aaacatgtcc gccagcccgc acgtgctgca aggcagccgc gacggccagc 720

gcatgggcga ctggaagatg gtcgacacca tgatcaacga cggcctgtgg gacgtgtaca 780

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acaagtacca catgggcatc acggccgaga acgtcgccaa ggcgcacgac atcacccgtg 840

agcagcagga cgccctggcc ctggccagcc agcaaaaggc caccgccgcc caggaagccg 900

gcaagttcaa ggacgagatc gttcccgtcg ccattccgca gcgcaagggc gatccggtga 960

tgttcgacac cgacgagttc atcaacaaga agaccaacgc cgaagcgctg gccggcctgc 1020

gtccggcctt cgacaaggcc ggctcggtga ccgcgggcaa cgcctccggc atcaacgacg 1080

gcgccgccgc cgtgatggtc atgtcggccg ccaaggccga gcaactgggc ctgaagccgc 1140

tggcgcgcat cgccagcttc ggcaccagcg gcctggaccc cgccaccatg ggcatgggcc 1200

cggtgccggc cacgcgcaag gcgctggagc gcgccggctg gcaagtcggc gacgtggacc 1260

tgttcgagct gaacgaagcc ttcgccgccc aagcctgcgc ggtgaacaag gagctgggcg 1320

tggacccggc caaggtcaac gtcaacggtg gcgccatcgc catcggccac cccatcggcg 1380

cctccggctg ccgcgtgctg gtgacgctgc tgcacgaaat gcagcgccgc gacgccaaga 1440

agggcgtggc cgcgctgtgc atcggtggcg gcatgggcgt gtcgctggcc gtcgagcgct 1500

gataaatgga ggcgctcgtt gatctgagcc ttgccccctg acgaacggcg gtggatggaa 1560

gatactgctc tcaagtgctg aagcggtagc ttagctcccc gtttcgtgct gatcagtctt 1620

tttcaacacg taaaaagcgg aggagttttg caattttgtt ggttgtaacg atcctccgtt 1680

gattttggcc tctttctcca tgggcgggct gggcgtattt gaagcggttc tctcttctgc 1740

cgtta 1745

<210> SEQ ID NO 159
<211> LENGTH: 1439
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 159, Example 159: designer Nial-promoter-controlled chloroplast-targeted 3-Hydroxyacyl-CoA dehydrogenase DNA construct (1439 bp)

<400> SEQUENCE: 159

agaaaatctg gcaccacacc atggtagggt gcgagtgacc ccgcgcgact tggaagggtt 60

caaacgaccc cgccgtacga acttttgtcg gggggcgctc ccggatggta gggtgcgagt 120

gaccccgcgc gacttggaag ggttcaaacg accccgccgt acgaactttt gtcgggggggc 180

gctcccggat ggccgccgtc attgccaagt cctccgtctc cgcggccgtg gctcgcccgg 240

cccgctccag cgtgcgcccc atggccgcgc tgaagcccgc cgtcaaggct gcccccgtgg 300

ctgccccggc tcaggccaac cagatggaga ttcggaagat cggcgtgatc ggcgcagggc 360

agatggggtc gggcatcgcc caggtggcgg cccagtcggg ttacgaggtc gtgctaatgg 420

acgtcgagga gctgagcctc aagaaggggc tcgaggccat ccgaaggtcg ctcgaccgct 480

tcctgcgcaa ggagaagatc acccaggagg aggccgaaaa ggccctggcc cgcatcaaga 540

cgacgctcaa ccccgccgac ttcgcggact gcgacctggt cgtcgaggcc atcgtggaga 600

acgagtcggt caagggtaag ctcttccaga cgctcgacaa ggtggtgaag cctgaggccg 660

tcttcgcttc caacacctcc tcgattccca tcaccaagct ggccagctac acctcccgcc 720

ccgagcgttt catcggcatg cacttcatga acccggtgcc gctgatgaag ctcgtcgagg 780

tcatccgcgg ctacaagacc tcggacgagg tcacccgggt ggtcatggcg acggccgaga 840

agatgggcaa ggtgccggtc gaggtcaacg actaccccgg cttcgtctcc aaccgcgtgc 900

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tcatccccat gctcaacgag gccatccaag cggtcatgga gggcgtggcc acccccgagg 960

ccatcgacac cgtgatgaag ctgggcatga accaccccat gggcccgctg acgctcgccg 1020

acttcatcgg cctcgacacc gtgctggcca tcatggaggt gctgcacgag ggctttggcg 1080

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gcaagagcgg gcaggggttc tacaagtacg acgagaaggg gaacaagatc ggctagtaaa 1200

tggaggcgct cgttgatctg agccttgccc cctgacgaac ggcggtggat ggaagatact 1260

gctctcaagt gctgaagcgg tagcttagct ccccgtttcg tgctgatcag tctttttcaa 1320

cacgtaaaaa gcggaggagt tttgcaattt tgttggttgt aacgatcctc cgttgatttt 1380

ggcctctttc tccatgggcg ggctgggcgt atttgaagcg gttctctctt ctgccgtta 1439

<210> SEQ ID NO 160
<211> LENGTH: 1337
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 160, Example 160: designer Nial-promoter-controlled chloroplast-targeted Enoyl-CoA Dehydratase DNA construct (1337 bp)

<400> SEQUENCE: 160

agaaaatctg gcaccacacc atggtagggt gcgagtgacc ccgcgcgact tggaagggtt 60

caaacgaccc cgccgtacga acttttgtcg gggggcgctc ccggatggta gggtgcgagt 120

gaccccgcgc gacttggaag ggttcaaacg accccgccgt acgaactttt gtcgggggggc 180

gctcccggat ggccgccgtc attgccaagt cctccgtctc cgcggccgtg gctcgcccgg 240

cccgctccag cgtgcgcccc atggccgcgc tgaagcccgc cgtcaaggct gcccccgtgg 300

ctgccccggc tcaggccaac cagatgacgg ttcgactgga atacgatggc gggttcgcgc 360

acctgacgct cagccgcccg caggtcctga atgcgctcag tttcgagctg ctcgccgagt 420

tgagccgggc gcttgccggc gtcgccgaat ccgatgcgcg cgccctgatc gtcacgggcg 480

agggcgacaa ggcgttctgc gccggcgcgg acattcccga gctgatgaat cggccgctca 540

tgcaagagct cgaaggggcc gcgaaaggcc aggcggtgtt cagccggatc gccgagctga 600

agattccgtc tgtcgccgtc atccagggtt atgccttcgg cggcgggctg gagcttgccc 660

tggcatgcac attccgcgtt gccactgatc gcgcccgcat ggggctgccc gaggtcaagc 720

tcggcctgat cccgggttat ggcggaacgc agcgtctgcc gaggctgatc ggcgaggggc 780

gcgcactcga cctgatcatg tccggccgca cgatagacgg cggggaagcc gagcgaatcg 840

gcctggtcaa tcgcatagac aacgagggga cgcccctgga gatcggcaag cggtttctgg 900

agccttatct caagcacagt ctctgcgcct tgtattttgc ccgcgaggcc gtgcagaggg 960

gaggcggtgt cgccattgcg gatggcctgc gcatcgagcg ggatctttcc acgctggctt 1020

accggagcca ggatgcggcc gaggggctgc gcgcttttgt ggaaaaacgg cccgcgtctt 1080

tcaaggactg ctgataaatg gaggcgctcg ttgatctgag ccttgccccc tgacgaacgg 1140

cggtggatgg aagatactgc tctcaagtgc tgaagcggta gcttagctcc ccgtttcgtg 1200

ctgatcagtc tttttcaaca cgtaaaaagc ggaggagttt tgcaattttg ttggttgtaa 1260

cgatcctccg ttgattttgg cctctttctc catgggcggg ctgggcgtat ttgaagcggt 1320

tctctcttct gccgtta 1337

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<210> SEQ ID NO 161
<211> LENGTH: 1736
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 161, Example 161: designer Nial-promoter-controlled chloroplast-targeted 2-Enoyl-CoA Reductase DNA construct (1736 bp)

<400> SEQUENCE: 161

agaaaatctg gcaccacacc atggtagggt gcgagtgacc ccgcgcgact tggaagggtt 60

caaacgaccc cgccgtacga acttttgtcg gggggcgctc ccggatggta gggtgcgagt 120

gaccccgcgc gacttggaag ggttcaaacg accccgccgt acgaactttt gtcgggggggc 180

gctcccggat ggccgccgtc attgccaagt cctccgtctc cgcggccgtg gctcgcccgg 240

cccgctccag cgtgcgcccc atggccgcgc tgaagcccgc cgtcaaggct gcccccgtgg 300

ctgccccggc tcaggccaac cagatggccg gcgcgcagca ggatcttgcc gctgcgtccg 360

ggcttgtcgc tggccgcggc ggccttggcg gcatcgtgca ggtcgaacac cgcttccacc 420

ggcagcgcca ggctgccatc gagcgcggcg gtgagcagtt cgccgatcat gcggcgcttg 480

tcctcggcct tggtggcctg catcaccttg ctgccccaga agccacgcac ggtggcctgc 540

ttgaagatca catcgccgct ggatatctgc agcggctcgc cggtcatcga gccaaaggaa 600

atcagctcgc cgccttcggc cagcaaggcc atcagctcac ccgctgcatt gccggccacc 660

gaatcgatgg cgcgcacgat gggcgcatcg ccggccagcg cgcgcacctt gtcctgccag 720

cctgcttgcg cagtggagat tgcgttgccg atgcccagcg ctttcagctc gtccacgccg 780

gcgtcgcggc gcaccaggtt gatcacgttg atgccgcgtg cggcggcgag catcgccacc 840

gtcttgccga ccgcaccgtt ggcggtgttc tgcacgatcc agtcgccctg tttcacctgc 900

aggaattcga tcagcatcag cgcgctcagc ggcatggcga tcaactggca accacgctcg 960

tcgtccaggc catccggcaa cggcaccacg ccggaggcgt cggcaaggaa gtactcggcc 1020

caggcctcat gcacaccggc ggcgaccacg cgctggccaa cctgcaagcc ctcgacaccc 1080

tcacccagcg catcgatgac acccgccgct tcgctgccgc cgatggctgg cagttccggc 1140

ttgtagccgt aattgccgcg cacggtccac aggtcatggt tatggatcgg cgcgcgccgc 1200

atcgcaacgc gcacctggcc cttgcctggc tgcggcgtgg ggcgctcgcc cagttcgagc 1260

accttggccg gatcgccgaa ttgggtatgg atggctgcgc gcatggaggt ctcctgccgg 1320

gcacgctctt gctgcgacgc gcccgatcgt tgtgaaaggt ggcgcgatgc tatcggcagg 1380

gctgcaagga agggatgaag cgaacggaac tgctgtgtga agttgttggc gtgcgcgcgt 1440

agtgacgatg ctctgctgca gcgccggagg actgcgtgca ggccgaccct cattaaatgg 1500

aggcgctcgt tgatctgagc cttgcccccc gacgaacggc ggtggatgga agatactgct 1560

ctcaagtgct gaagcggtag cttagctccc cgtttcgtgc tgatcagtct ttttcaacac 1620

gtaaaaagcg gaggagtttt gcaatttttgt tggttgtaac gatcctccgt tgattttggc 1680

ctctttctcc atgggcgggc tgggcgtatt tgaagcggtt ctctcttctg ccgtta 1736

<210> SEQ ID NO 162
<211> LENGTH: 2036
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 162, Example 162: designer Nial-promoter-controlled chloroplast-targeted Acyl-

-continued

CoA Reductase DNA construct (2036 bp)

<400> SEQUENCE: 162

agaaaatctg gcaccacacc atggtagggt gcgagtgacc ccgcgcgact tggaagggtt 60

caaacgaccc cgccgtacga acttttgtcg gggggcgctc ccggatggta gggtgcgagt 120

gaccccgcgc gacttggaag ggttcaaacg accccgccgt acgaactttt gtcgggggggc 180

gctcccggat ggccgccgtc attgccaagt cctccgtctc cgcggccgtg gctcgcccgg 240

cccgctccag cgtgcgcccc atggccgcgc tgaagcccgc cgtcaaggct gcccccgtgg 300

ctgccccggc tcaggccaac cagatggatg acgataatgt tgtaaaaccc atttactatg 360

gtaaaataga ggttcaaaat aatggcacgg gagtatggga gcctaccgtt gagtggttga 420

atgagttttt aaaccggagt atggaactat cacagagtct tttacaacta ggctttagta 480

gaagggttag agtgttgagc gagatgggga agatttggag ggagaagctt tcgttagtcg 540

aggagaaact agctcctaat atttctaaga atacaggcta cagcgtggag aatgtgaaaa 600

tggacttaag actggttgaa gaagtgttta atgagaccaa tattgttgag ctcttcgata 660

aaggcttaat cgggggatgg cgtagtcttg acaagcccgt tgaaatcatt gatggggagt 720

tcgtgtggaa tagaccgcta ggcgtatccc ttataatatc ctccggaaac accgtcatac 780

cagctattct cccagcagtg gtttctttag catcggggaa cgtaactata ctaaggccgt 840

ctttcagcaa ctaccaagca gtagtcgaaa ttttaaaaac acttttcgat ctagcagaca 900

gctccgtaga aggtgctaga gaaatggctt cggctcttct ggtcgcatac tttaaacatg 960

agagcaaggt atttgaacac ctattagcat cagcacctct cggcatcgtc aattactggg 1020

gcggggagcc aggtagaagc gtgatcgcta gtagggtttt gaagaatccg tttcatccta 1080

agttaatcgt caatggacct ctaacggggt tagcgataat agatgaagag tcagcgtcgg 1140

aaaaagtagc ctacggatta gcgagggatg tggtactgta tgatcaacag ttatgtagct 1200

ctcccactta cgccatattc ataggttcga aagatagcgc gttgaagttt gcacagagac 1260

taggggaagc cctgaataat gtggggagaa ggttcccccg tgatttgaag gaaggagaac 1320

tgtacaattt aatactgctt aggaaaaacc ttgagatcca aggtgtgaga gttttctact 1380

cggaaaaccc cggaaatgct tggacgattg cggtgaaaac actagagtca gtcactaatt 1440

ttgcatatag tttaaaatat ccacatacaa tccctaggag acggttcatt gaaataatag 1500

tgttgaaaga cgccaaagaa ctcaaggaga cgatcttaca cctaattgaa gacttgagga 1560

gaaacggggt tgataagttc cagacagcat cgataaaggt ttctgaaaga aaccttaacc 1620

acttattgaa ggttctctat attcttggga tttacagggt tgtcccaata ggggaatcct 1680

tttttagaac gccgttagaa ccgtacgatg gtgaattctt acctaaatac ttcacttaca 1740

cgatgtatct tagatttatc gagaagtcgg atgcgctaaa acaccctgaa tgataaatgg 1800

aggcgctcgt tgatctgagc cttgcccccc gacgaacggc ggtggatgga agatactgct 1860

ctcaagtgct gaagcggtag cttagctccc cgtttcgtgc tgatcagtct ttttcaacac 1920

gtaaaaagcg gaggagtttt gcaattttgt tggttgtaac gatcctccgt tgattttggc 1980

ctctttctcc atgggcgggc tgggcgtatt tgaagcggtt ctctcttctg ccgtta 2036

<210> SEQ ID NO 163
<211> LENGTH: 1625
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 163, Example 163: designer Nial-promoter-controlled chloroplast-targeted Hexanol Dehydronase DNA construct (1625 bp)

<400> SEQUENCE: 163

agaaaatctg gcaccacacc atggtagggt gcgagtgacc ccgcgcgact tggaagggtt 60

caaacgaccc cgccgtacga acttttgtcg gggggcgctc ccggatggta gggtgcgagt 120

gaccccgcgc gacttggaag ggttcaaacg accccgccgt acgaactttt gtcgggggggc 180

gctcccggat ggccgccgtc attgccaagt cctccgtctc cgcggccgtg gctcgcccgg 240

cccgctccag cgtgcgcccc atggccgcgc tgaagcccgc cgtcaaggct gcccccgtgg 300

ctgccccggc tcaggccaac cagatggaac tcgacctcga cggtcccggg gttggtgaag 360

tgctgatcaa gtacaccgcc gcggggttgt gccattcgga cctgcacttg accgacgggg 420

acctaccgcc gcgctatcca atcgtcgggg ggcacgaggg gtcaggcatc atcgaggacg 480

tcggacctgg ggtcaccaag gtcaaaccag gcgatcacgt tgtttgcagc ttcatcccga 540

actgcggaac ctgtcggtac tgcgccaccg gacgctccaa cctctgcgat atgggcgcca 600

ccatcctcga agggtgcatg cccgacggca gttaccggtt ccacagtaac ggcctggatt 660

tcggtgcgat gtgcatgctc ggcacattct ccgaacgcgc aactatctcc cagcattcgg 720

tggtcaagat cgacgactgg ctgccgctcg agaccgcggt ggtcgtcggc tgcggcgtgc 780

cgactggctg gggcacctcc gtctatgccg gcggggttcg ttgcggtgac accaccgtca 840

tctatggcgt cggcggcctg ggagtcaacg ccgtccaagg cgcggtgagt gcgggcgcga 900

agtacatcgt ggtcgtcgat ccggttgcgt tcaaacgcga caccgcgctc aagttcggcg 960

ccacccacgc gttcgccgac gccgccaccg ccgcggccaa ggtcgacgaa ctgacctggg 1020

gacagggtgc cgatcaggcg ctgatcctgg tcggcaccgt cgacgaggac gtggtctcgg 1080

cggcgactgc ggtgatcggt aagggaggca ccgtcgtgat caccggactg gcggacccag 1140

caaagctcac ggtgcacgtt tcgggaacgg acctgacgct taacgagaag acaatcaagg 1200

gcacgttgtt cggctcgtcc aatccgcaat acgacatcgt acggctgctc cgtctctacg 1260

acgccggcca gctaaaactc gacgatctga tcaccacccg atacacgctc gaccaggtca 1320

accagggcta ccaggatctg cgagacggca agaacatccg cggcgtgatc atccacgcct 1380

gataaatgga ggcgctcgtt gatctgagcc ttgccccctg acgaacggcg gtggatggaa 1440

gatactgctc tcaagtgctg aagcggtagc ttagctcccc gtttcgtgct gatcagtctt 1500

tttcaacacg taaaaagcgg aggagttttg caatttttgtt ggttgtaacg atcctccgtt 1560

gattttggcc tctttctcca tgggcgggct gggcgtattt gaagcggttc tctcttctgc 1620

cgtta 1625

<210> SEQ ID NO 164
<211> LENGTH: 1249
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 164, Example 164: designer Nial-promoter-controlled chloroplast-targeted Octanol Dehydrogenase DNA construct (1249 bp)

<400> SEQUENCE: 164

agaaaatctg gcaccacacc atggtagggt gcgagtgacc ccgcgcgact tggaagggtt 60

-continued

caaacgaccc cgccgtacga acttttgtcg gggggcgctc ccggatggta gggtgcgagt 120

gaccccgcgc gacttggaag ggttcaaacg accccgccgt acgaactttt gtcgggggggc 180

gctcccggat ggccgccgtc attgccaagt cctccgtctc cgcggccgtg gctcgcccgg 240

cccgctccag cgtgcgcccc atggccgcgc tgaagcccgc cgtcaaggct gcccccgtgg 300

ctgccccggc tcaggccaac cagatgttgg gaggccaaga agccgctggt gattgaggac 360

attgaggtgg cgccacctca ggcttggcag gttcgcatca agattacagc cactggcgtt 420

tgccacacgg attctttttc gttgagcggc tctgatcctg agggtctctt tcccgtggtc 480

cttggccatg agggcgccgg catcgtggag agcgttggcg agggcgtaac caactttaag 540

gccggcgatc atgtcattgc cctctacata ccccagtgca atgagtgcaa attctgcaag 600

agcggcaaga caaatctctg ccagaagatt cgcctcaccc agggcgctgg tgtcatgccc 660

aatggatcct cccgcttgtc gtgcaagggt cagcagctgt tccatttcat gggcacctca 720

actttcgccg agtacgcggt ggtggccgac atatcggtga ccaaaatcaa cgagtcggct 780

ccattggaga aggtgtgcct tctgggctgt ggcatttcca cgggctatgg tgccgccttg 840

aacaccttta ggtggaacct ggcagcactt gcgccgtctg gggtctgggt gctgttggac 900

tggcagtggg tctgggctgc aagaaggctg gcgccgccaa ggtctacggc atcgacatca 960

atccctccaa attcgagctg gccaggaagt tcggcttcac cgactttaaa tggaggcgct 1020

cgttgatctg agccttgccc cctgacgaac ggcggtggat ggaagatact gctctcaagt 1080

gctgaagcgg tagcttagct ccccgtttcg tgctgatcag tctttttcaa cacgtaaaaa 1140

gcggaggagt tttgcaattt tgttggttgt aacgatcctc cgttgatttt ggcctctttc 1200

tccatgggcg ggctgggcgt atttgaagcg gttctctctt ctgccgtta 1249

<210> SEQ ID NO 165
<211> LENGTH: 1769
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- Sequence No. 165, Example 165: designer Nial-promoter-controlled chloroplast-targeted Short Chain Alcohol Dehydrogenase DNA construct (1769 bp)

<400> SEQUENCE: 165

agaaaatctg gcaccacacc atggtagggt gcgagtgacc ccgcgcgact tggaagggtt 60

caaacgaccc cgccgtacga acttttgtcg gggggcgctc ccggatggta gggtgcgagt 120

gaccccgcgc gacttggaag ggttcaaacg accccgccgt acgaactttt gtcgggggggc 180

gctcccggat ggccgccgtc attgccaagt cctccgtctc cgcggccgtg gctcgcccgg 240

cccgctccag cgtgcgcccc atggccgcgc tgaagcccgc cgtcaaggct gcccccgtgg 300

ctgccccggc tcaggccaac cagatgatca tcaaaccgcg cgtgcgtggc ttcatctgcg 360

tgaccactca tccggtcggc tgcgaggcca acgtcaagga acagatcgac tacgtgactt 420

cgcacggccc gatcgccaac ggcccgaaga aggtgctcgt gatcggcgcg tcgaccggct 480

acggcctcgc ggcccggatc tcggccgcct tcggctcggg cgcggacacg cttggcgtgt 540

tcttcgagcg cgccggcagc gacaccaagc cgggcaccgc cggctggtac aacagcgccg 600

cgttcgagaa attcgccgcc gaaaaggggc tctatgcgcg cagcatcaac ggcgacgcgt 660

tctccgacaa ggtcaagcag atcacgatcg acacgatcaa gcaggacctc ggcaaggtcg 720

atctggtcgt ctacagcctg gccgcgccgc gccgcacgca tccgaagacg ggcgagacga 780

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tcagctcgac gctgaagccg gtcggcaagt cggtgacgtt ccgcggcctc gacaccgaca 840

aggaaacgat ccgcgaggtg acgctcgagc cggcgacgca ggaagagatc gacggcaccg 900

tcgccgtgat gggcggcgag gactggcaga tgtggatcga cgcgctcgcc gacgccggcg 960

tgctggccga cggcgcgaag accaccgcgt tcacgtatct cggcgagcag atcacgcacg 1020

acatctactg gaacggctcg atcggtgagg cgaagaagga tctcgacaag aaggtcgtgt 1080

cgatccgcga gaagctcgcc gtgcatggcg gcgacgcgcg cgtgtcggtg ctgaaggccg 1140

tcgtcacgca ggcgagctcg gcgatcccga tgatgccgct gtacctgtcg ctgctgttca 1200

aggtgatgaa ggaaaagggc acgcacgaag gctgcatcga gcaggtgtac gggctgctga 1260

aggacagcat gtacggcgcg acgccgcaca tcgacgaaga aggccggctg cgcgcggact 1320

acaaggaact cgatccgcag gtgcaggcgc aggtcgtcgc gatgtgggac aaggtcacga 1380

acgacaacct gtacgagatg accgacttcg ccggttacaa gaccgagttc ctgcgtctgt 1440

tcggcttcga gatcgccggc gtcgactacg acgcggacgt gaacccggac gtgaagatcc 1500

ccggcatcat cgacacgacg gcctgataaa tggaggcgct cgttgatctg agccttgccc 1560

cctgacgaac ggcggtggat ggaagatact gctctcaagt gctgaagcgg tagcttagct 1620

ccccgtttcg tgctgatcag tctttttcaa cacgtaaaaa gcggaggagt tttgcaattt 1680

tgttggttgt aacgatcctc cgttgatttt ggcctctttc tccatgggcg ggctgggcgt 1740

atttgaagcg gttctctctt ctgccgtta 1769

<210> SEQ ID NO 166
<211> LENGTH: 6110
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- SEQ ID NO: 166, example 166: a designer hox-promoter-controlled Formylmethanofuran dehydrogenase (Fmd) DNA construct (6110 bp)

<400> SEQUENCE: 166

agaaaatctg gcaccacacc gcagaaatat aggggctagg agttgagggt actctggttc 60

gtcaagcatt tgggatgatt tcccctcaca agttcctcaa attattctcc tataaacaat 120

agatataagg tcaaaacttg agttatgagt gctgagtaaa aaattactct ccacgcctca 180

gaggtagata tgatgagcgt ctataaaaat gtgacatgtc ccgtctgcgg agggtcttgt 240

gatgacatag aggttctcta tgatgggaaa acaataaaaa caaggaatgc ttgcaggatg 300

gggaatgcaa agtttcagga gatggtcagc tcccacagaa tacttagacc ccagattaaa 360

actgaaagtg gtttcagatc cgcagaatgg gatgaagccc ttgacgctgc agcagagata 420

cttacagagt caaaaagacc aaccctattc atgggtagtg agatgtcaac tgaagccatg 480

gctgcaggtc ttgaacttgg tgagtatcta aatgccatgg tggattcaaa tgcaaccata 540

tgtcatggcc ccacattaat gggaatccag gaagctggac agagcgctgc tacggcaggt 600

gagataaaga atagagctga cgtcatcatt tattggggta caaatgttat ggactccatg 660

cctcgccaca tgtcacgtta cagcatattc atgcgcggat ttttcagaga acgtggtaaa 720

aaagatagaa ctgtcatctc cgtggatccc cgtgaaacag caacaactaa agcctccgat 780

atccatctgc agctgaaacc aaactcagat tatgaacttt tttcagcact gcttacagtt 840

ataaggggca atgaaccgca caggagtatt gagagtataa cagggatatc agttgaaacc 900

-continued

ataaaggaag tcgcagacat aatgctgaat gcgcagtttg gagccatcta tggaggtctt 960

ggacttgcat catcagaagg taagcataga aacgttgaga tggttctcaa actggtagct 1020

gcacttaatg aacacaccaa atttacaata ggagccataa gaggtcattg taatgttgca 1080

ggatttaatc aggtggcttc atgggagtat ggtttcccct ttggtgttga ttttacaagg 1140

ggttatccac gctacaaccc cggagaaaca actatagtcg atcttctcca gagaaaagaa 1200

tccgatgcgg tcctcgttat atgttcagat cttggagctc acctccccaa agaatgcgtt 1260

gagtatatga aagagattcc tgtaatatgc atagatattg ccccatgtcc aacaacactt 1320

gtatctgatg ttgtgatccc tggagttatt gatgctatgg agtccagcgg caccttctac 1380

cgctttgaca atgttcccat ccaccataag gcattcacaa catcaccatt ccctgaaaca 1440

gagagcaacg aacatactct tagacagatc cttgagaggg ttaaatcaat taaaggcgaa 1500

taaatgggat ttgtgttggt accaaaatca gatttccaga tacctctgga agcagatacc 1560

ataagacccg atctgtttga agggctggat cttgatgaaa ttcgttccct tcaagtatac 1620

gaagggaaca tcaaaagacc cctaggcgaa ttttttgaga tagcagagac atcccatgaa 1680

gatcagttaa tacggatcga tggggatgtc agcagggtga agtatatcgg ttcagggatg 1740

aaatccggaa aaatcatcat aaacggcgat gtcggactcc agcttggctg tgaaatgaaa 1800

ggcggtgaaa tagaggtaaa tggaaatgtt tcttcatgga tcggcatgga aatgcatggt 1860

ggcaccataa aaattaatgg aaacgcgggg gattatgttg gctgcgcata taggggagag 1920

tggcgtggca tgaaaggagg taaaatcatt atacagggta atgcagggaa caatattggg 1980

ggtggtatga tggccggaga aatttatata ggtggagatg caggtaattt ctgcggcatc 2040

cgaatgaatg ggggtgaaat aacagtacgc ggggatgctg gaagggcccc cggagcagag 2100

atggtatcag gtatcatcaa aattcatgga cggatctcct ctctcctccc gggattcaag 2160

gagatctcaa cattcaaaga agatggatcc cttatgatcc tattcaaagg agatctatcc 2220

gaaaaaaatc cggagggtaa tctatacatc aattataata agaaccttca cattctagag 2280

aatgagaccg atgaagggag agtcatcaca aaaaagggaa ttaaagtaat ctacaacagt 2340

ggaagtacga tccgtgaagg gcagataata aagggaggca ataaactcac agatgattat 2400

atagatgaat gtgcacgctg ctgtattagt cctgaagact ataagctcct aggtgaaccc 2460

gaaaatgttg tcgtatcatc acatggaaat gaagttgttc tgagagctgt tgaggaccct 2520

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gcttcacaag gtgaaaggat cctgagtgcc gaggaacttg tagaggaata cggggtggga 2700

aaatgagtgg ggcaggtcag agaatacctt gatttaataa aaaatttcag tgggttcgca 2760

agcccgggca gtgtcatagg agctcatatg ttactaatag ccaggaaggt ccttgatttt 2820

gaagtcgatg aagaaattta tgttacatgt gaaacgacaa actgtttacc cgacgcattc 2880

caggccatat gcaaatcaac aataggaaat gggagactga atatcctgga cactggaaaa 2940

atggctgtca tcatcaacag aaagggtatg cctggagaaa cagtccaggc tcttagaata 3000

atactggatc ctgaaaagac cgtcaattac ccgatcatac atgaatggta catgaacacc 3060

cgcaaggtat ccgcagaaga agtgaatcca gaactcataa gagccggtga aaatctatat 3120

tcctggtatt ttgttgatgt gatcgttcca gaaaaagaaa agaagataat tgaaatctgt 3180

aatctttgca acgaaccttt cataaaaaga aatgagctgg atctctgtcc agcttgtctg 3240

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aaaagataaa tggaatatat tttaaaaaat ggtattgtat ttgatccagc aaataatatt 3300

gatggagaaa aaaaggacat actaataaaa gatggataca tagttagtga agtatcaaag 3360

gatgcaaaga ttatagatgt tacaaataaa ttagtaatgc ctggaggagt agatttacac 3420

tcacacatag caggaccaaa actatcagtg ggaagattat atcgtccaga agatacaaga 3480

cgtggaataa aacctgcacc atgtggtgct attgagggat ttgaagcagg attttccata 3540

ccaacatgtc caacaactgg gtacaggtat actcgtatgg gatatacaac agtaacagaa 3600

gcagcagtac caccttaga ggcaaaacat gcacatgaag aaataaacag tattccaaac 3660

cttgatatac caacattaac actctttggt aataactggt tcatgcttaa atatgttaag 3720

gaaaataact tagaaaaact agctttattc atatcaaaat ggttgaaact agcaaagggt 3780

tatggaatta aaatagtaaa tccatgtgga agtgaagcat ggggttgggg aaaaaatgta 3840

gatggacttg atgatccaga accacactgg ggtgtaacag gacgtcaagt aatacaggct 3900

ctaactaaag taaatgaaaa attaggttta ccccattctg tgcatgttca tacaaatgac 3960

cttggacatc ctggaaacta tgaaacaaca cttgaaacat ttgattgtgt aaaggatatt 4020

aagaaaaata agaatgtaac aagagatcaa gtgttacatg caacacacgt acagttccat 4080

gcatataagg gaacatcatg gagggatgtt acatcaggtg caccagaatt gattgattat 4140

ataaataagt caaaacatat gacttgtgat attggacaga taaccttcga tgaaacaaca 4200

acaatgactg cagatgcacc aatggagtat gatttataca gactaacagg acttaaatgg 4260

gcaaataagg atatagaggt tgaaacttca tctggactta ttccatcaat atattctaaa 4320

cgagcaccag taagtgtact tcaatgggct attgggcttg aattcttcct tggaataaaa 4380

gatccatgga aattggcatt aacaactgat tcaccaaatg gtggtccatt tatcagatat 4440

ccacgtgtaa tttcatggat aatgagtaat gaaaaactaa atgatatgct tgataatcaa 4500

gtacatagtt gggcaacaag aagaacatca cttggaagtt atgataggga atattcctgg 4560

aatgaaatag caacaattac aagggcaagt ccagcaaaaa tacttggatt aacagataga 4620

ggacatcttg gtgtaggtgc aaaggctgat gtttcagtat atgatataga tgtctatgac 4680

tttgatacaa cacttcttaa aaattcacaa acacttgaaa acaagttatt aaacagttta 4740

tacactataa aagatggtat gatcatggtt gatcatggaa aaattgttaa attagtagat 4800

agtaaacata tatggactaa tgtttgtggc ttagaaaaag aagaggctaa tcttgtagat 4860

gaaataacac cagaatttaa taagtattat actataaaat atgaaaatta tggtgttcca 4920

gatcattata taaaacctga tacttgtgta gatatagaat atgaggatta gatggatgaa 4980

atggatatta tcataaatac aggtacgagt attatccaag cattttatga aaagaaaggt 5040

tctacattaa aggatgaata cagacaatct acagctgtag cttttatgga tccaagggat 5100

atgaaaaaat tatctctaaa accacgtgat aaaataaatg taacatctaa atggggaagt 5160

gtaacaatat atgcagataa atcccatgat gcaccacatg aaggtatgat attcatacca 5220

aggggaccat gggccaatat agtaataagt ccagaaacat attgctgtaa tattccaaca 5280

tataagggag taaaagcagt aattaaaaaa acagacgatg aagtattact cgtagcaaat 5340

ctaatgcata aaacatacaa taaatataaa tataacacaa aaactcttgg acaaaagcca 5400

gtatataaaa aaatagggga gtaaatgtta tgtgttaatc aagatcattg tttagggtgt 5460

ggagcatgtg ttatagtatg tcctgttaat caagaaatct atccagaggt tattggaggt 5520

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aatgggccag atacaacaga tgtggtaatg ttagttgaaa atggagtaat aaaactattc 5580

catccagaaa aatgtgtaac atgtatgaaa tgtaatgata catgtccaac aaaggcaata 5640

tatcataagg gagactaatg aagtaagtag gaagcaggga gcaggggaaa gaaaattgac 5700

aactgtacaa gattaatcgc gtctctgagc aatgaccaaa tacatctacc tccacggttt 5760

tcttccagcc ccctatctgc gaaagcacaa gatattagca agcgtttcgc ccaaattcac 5820

atacagctaa caatccctga tctcaatgct ggtgaatttt ctcagttaac aatcacgcgc 5880

caaattcaac aagttgccgc aattttccct gataattctg aaccaataac gctgataggt 5940

tctagtttag gcggtttaac tgctgcttat ctaggacagc gatatttaca agtacaacgc 6000

ttagttttat tagcgccagt ttggtttttt atcccattgg ttgcccaaaa tgggtgaaga 6060

agctgtcaca agttggcaac aaacgatata ggttctctct tctgccgtta 6110

<210> SEQ ID NO 167
<211> LENGTH: 1538
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- SEQ ID NO: 167, example 167: a designer hox-promoter-controlled Formyl transferase DNA construct (1538 bp)

<400> SEQUENCE: 167

agaaaatctg gcaccacacc gcagaaatat aggggctagg agttgagggt actctggttc 60

gtcaagcatt tgggatgatt tcccctcaca agttcctcaa attattctcc tataaacaat 120

agatataagg tcaaaacttg agttatgagt gctgagtaaa aaattactct ccacgcctca 180

gaggtagata tgttagaaga ggtcatggag tttgatctgg tatgctccaa ggttgccgcc 240

gtagttccct gcacttatct taattatgcc tggaacggta catgcggcct ttataccttc 300

cttcattgcc tcccttacaa cctcttcgtt gacaccgtct ataactatct catatacccc 360

gttgacgttt tcaggtatct cgctgccctc aacctcatcc ttgagtgtca cgcacatctt 420

ctcattggtt gaggcgttga ggaacttgta cttgtttgat ccaacctttg aacctgaagc 480

caccacacca ccggggaatg gtgttaccgt gccttcaact gcggctattg catccactgc 540

agcctgggcc gcaaggaggg ctgatgcctg actgtcaccc atgatgaaga agtttccgcc 600

tgcaaccccg tcctttattc caaattcgct ttcaatgagg aagtcgcctg acattatcgg 660

gattgagtgg attttccttc catcaatttc aagttccttc tcgtagccat ccccgaagaa 720

cttgagtttg aatcccacat tgagcttctc gtcctcgtca tcgagagcat cgaatactgc 780

ggttgttggt gctgtaagta tacccatccc tatcctttca aggagttcat ggtccaggtt 840

cttctttgat gggttgcaga tcattattat gtatccgggc cttccatcgg gtgtctcctc 900

tggtggaacg tagcagtcta tacctgcctc tgcagggcac cctataacag atgtaccgta 960

acctgttgcc tcggttgcag ctatctttgc aagttttttg gttgctgcag ttacaaggac 1020

ccttgaaacc ttgataccga aggcctccgc aaatgtatcc tctatttcaa caccatttat 1080

ctccattgaa gtaagtagga agcagggagc aggggaaaga aaattgacaa ctgtacaaga 1140

ttaatcgcgt ctctgagcaa tgaccaaata catctacctc cacggttttc ttccagcccc 1200

ctatctgcga aagcacaaga tattagcaag cgtttcgccc aaattcacat acagctaaca 1260

atccctgatc tcaatgctgg tgaattttct cagttaacaa tcacgcgcca aattcaacaa 1320

gttgccgcaa ttttccctga taattctgaa ccaataacgc tgataggttc tagtttaggc 1380

-continued

ggtttaactg ctgcttatct aggacagcga tatttacaag tacaacgctt agttttatta 1440

gcgccagttt ggtttttat cccattggtt gcccaaaatg ggtgaagaag ctgtcacaag 1500

ttggcaacaa acgatatagg ttctctcttc tgccgtta 1538

<210> SEQ ID NO 168
<211> LENGTH: 1631
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- SEQ ID NO: 168, example 168: a designer hox-promoter-controlled 5,10-Methenyl-tetrahydromethanopterin (H4 methanopterin) cyclohydrolase DNA construct (1631 bp)

<400> SEQUENCE: 168

agaaaatctg gcaccacacc gcagaaatat aggggctagg agttgagggt actctggttc 60

gtcaagcatt tgggatgatt tcccctcaca agttcctcaa attattctcc tataaacaat 120

agatataagg tcaaaacttg agttatgagt gctgagtaaa aaattactct ccacgcctca 180

gaggtagata tgatgagtga aagtatgaac atagcagcaa agaaaattgc tgataaaatg 240

gttcaagatg cagaaaaatt aaaagtaatt ccatcaacat tatccaatgg aacatctatt 300

atagattgtg gtgttaatgc taagggaagt attaaaggtg gggaattatt tacaaaagta 360

tgtcttggtg gaatttgtga tgttggaatt tcaatacctg gtgacttaag tgatataatg 420

gctatgcctg ctgttaaggt taaaactgat tttccagcat taaccactct tggttctcag 480

aaagcaggat ggaaaataga tgttaatgga tattatgcta taggttctgg acctgctcag 540

acacataaat ttaaagataa taacatttat aaaataacta actatattga agattcagat 600

attgcagtta ttactcttga agcagataaa ttacctgatg aagatattgc taattatatt 660

gcagatgagt gtggtgtaaa accagaaaat ttaaccatac ttgttgcacc tacatcttct 720

cttgttggat ctattcaaat atctggtaga gctcttgaaa ctggaatata caaaatgtat 780

gaaataatga acttcgatgt tactaaaatt acatatgctg caggtattac ccctattaca 840

ccagttgatc ctgatagtct taaagctatg ggtaaaacta atgatgctat catgtttggt 900

ggaagagcat attattatat tgaacctgat gaaggtgaag atttagaaga attagctgct 960

aatttaccat catctgcttc tgataattat ggtcaaagct ttattgaatt atttaaagaa 1020

gcaaatcagg atttctataa aatgcctaag gatatttttg caccagcaca agttattgtt 1080

aatgatatga taactggtca aatgttccac acaggattta tagatcttaa acgtctaaaa 1140

aaatcttttg aagttaaaga aataatttat gaaaaataat gaagtaagta ggaagcaggg 1200

agcaggggaa agaaaattga caactgtaca agattaatcg cgtctctgag caatgaccaa 1260

atacatctac ctccacggtt ttcttccagc cccctatctg cgaaagcaca agatattagc 1320

aagcgtttcg cccaaattca catacagcta acaatccctg atctcaatgc tggtgaattt 1380

tctcagttaa caatcacgcg ccaaattcaa caagttgccg caattttccc tgataattct 1440

gaaccaataa cgctgatagg ttctagttta ggcggtttaa ctgctgctta tctaggacag 1500

cgatatttac aagtacaacg cttagtttta ttagcgccag tttggttttt tatcccattg 1560

gttgcccaaa atgggtgaag aagctgtcac aagttggcaa caaacgatat aggttctctc 1620

ttctgccgtt a 1631

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<210> SEQ ID NO 169
<211> LENGTH: 1475
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- SEQ ID NO: 169, example 169, a designer hox-promoter-controlled 5,10-Methylene-H4-methanopterin dehydrogenase DNA construct (1475 bp)

<400> SEQUENCE: 169

agaaaatctg gcaccacacc gcagaaatat aggggctagg agttgagggt actctggttc 60

gtcaagcatt tgggatgatt tcccctcaca agttcctcaa attattctcc tataaacaat 120

agatataagg tcaaaacttg agttatgagt gctgagtaaa aaattactct ccacgcctca 180

gaggtagata tgatggttgt aaaaattggt ataataaaat gtggtaacat cgggacctca 240

cctgtgctgg acctgttact tgatgagagg gcagacaggc caaacataga tgtctgtgtc 300

gtgggttcag gtgcaaaaat gaaccccgat gaaatcgaaa gggcagtacc aaccatgctt 360

gaaatggaga gggactttgt tatattcata agcccaaacc ccggtgcacc tggccctgca 420

aaggcaaggg agctcctttc agcggctgat gttccagcca tgatcatagg tgacgcacca 480

ggcctcaggg tcaaggatga aatcgaggag cagggacttg gatacataat agtaaaggcc 540

gacccgatga taggggcaag aagggagttc ctggacccaa cagagatggc atccttcaac 600

tccgacgtta taaaggtcct tgcattcaca ggcgcataca gggttgtgca gaacacaatc 660

gatgcaatga ttgcagatgt tgaagccgga aaggcacctg aacttcctca ggtggtaata 720

gacacagata aggcggttga ggcagcaggc tacaccaacc catatgcaaa ggccaaggcc 780

atggctgcat atgagatagc aaccaaggtg gctgacatag acgtcagggg ctgcttcatg 840

gtacaggacc ctgaccagta cataccaatc gttgcctcag cacacgaaat gctatctgca 900

gctgccaaac ttgcaattga agcaagggaa atcgaaaagg ccaacgacac cgtgctgaga 960

acaccacacg gtaaggaagg caaaacactt agcaagaagg atcttctggc caagccagaa 1020

tagtgaagta agtaggaagc agggagcagg ggaaagaaaa ttgacaactg tacaagatta 1080

atcgcgtctc tgagcaatga ccaaatacat ctacctccac ggttttcttc cagcccccta 1140

tctgcgaaag cacaagatat tagcaagcgt ttcgcccaaa ttcacataca gctaacaatc 1200

cctgatctca atgctggtga attttctcag ttaacaatca cgcgccaaat tcaacaagtt 1260

gccgcaattt tccctgataa ttctgaacca ataacgctga taggttctag tttaggcggt 1320

ttaactgctg cttatctagg acagcgatat ttacaagtac aacgcttagt tttattagcg 1380

ccagtttggt tttttatccc attggttgcc caaaatgggt gaagaagctg tcacaagttg 1440

gcaacaaacg atataggttc tctcttctgc cgtta 1475

<210> SEQ ID NO 170
<211> LENGTH: 2594
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- SEQ ID NO: 170, example 170: a designer hox-promoter-controlled methylenetetrahydrofolate reductase and/or methylene-H4-methanopterin reductase DNA construct (2594 bp)

<400> SEQUENCE: 170

agaaaatctg gcaccacacc gcagaaatat aggggctagg agttgagggt actctggttc 60

gtcaagcatt tgggatgatt tcccctcaca agttcctcaa attattctcc tataaacaat 120

-continued

agatataagg tcaaaacttg agttatgagt gctgagtaaa aaattactct ccacgcctca 180

gaggtagata tgctactcta ccttgggacg gggatacagg ccggcttcct tgacgatggt 240

ggggatgata tcttcccaca tgacggccat gatatggacg ccggctacac cctcgatgga 300

ctgcaggtgt ttaatctgtt ccacacagat ggccacccct tcggccttgg ggtcggaggc 360

tttttccatg cggttgacga tttcgtcggg gacaatcatc ccggccaccg attgttgcat 420

atatttggcg gcccgggcgg atttcagggg catgacgccg gcaataattt tggctctttt 480

atgcaggccg cgctcccgga ccagggccat aaagcgttca aaacgctcca tatcaaaaat 540

gcactgggtt tgaataaagt cggcgccggc attgatcttc ttctccaggc gcatgacccg 600

gaactcaaag gggtcggcaa aggggttggc ggcggcgccg atgaagaagc ggggttcctg 660

gcccttaatc tcttcaccgc aggcgaattt tttctcatcc cggaggtcct tcacgatccg 720

gatcagctgg agggaatcca cgtcatggac gtttttcgcc gtcggatggt taccaaaaga 780

ttgatggtcg ccggacaggc agaggacgtt ccgcatcccc aggctgtagg cacccaggag 840

atcactctgg agggcgatac ggttgcggtc ccgaaccgtc atctggataa tgggttcgcc 900

cccggcctgg aggacgtgga ccccagcggc gatactcgac aggcggacga tggccgtctg 960

gttgtccgtc aggttcatgg catcaacgta gtccttgagg agagcggcgt gcttcttgat 1020

ctctgtagga tcggcgtgct tcggcggtcc aatctcaccg ctgaccagaa attgcccctg 1080

ggagaggatt ttcgccatct tgctttcaac catatgacca ttaaaaaagt tgcaatcttg 1140

ggagcaggat gttacagaac acatgctgca acaggaatca ccaactttgc aagagcatgc 1200

gaagttgcgg aaaaagttgg caaaccggag atagcgatga cgcactccac aattgccatg 1260

gctgcagagt tgaaatacct ggctggaata gacgatatcg tcatctcgga tccgtcattt 1320

gccggtgaat tcactgttgt gaaggacttc gattacaatg aagtcatcaa agcccacaaa 1380

gacaatcccg aaacgattat gccgaagatc agggagaagg ttaacgaact cgccaagaca 1440

gttccaaaac ccccgaaggg cgccatacac tttgttcatc ccgaagacct aggcctgaag 1500

gtaacgactg acgacaggga agcagtacgt gatgcagacc tgataatcac ctggctgcca 1560

aaaggcgaca tgcagaaagg cattatagaa aaattcgcag gagatatcaa agagggagca 1620

ataatcaccc acgcctgtac gattccgaca acccttttct ataagatatt cgaggaactc 1680

ggtatcgcag ataaggtgga agttacatcc tatcaccccg gctcagttcc tgagaacaag 1740

ggccaggtct acatcgcgga aggatatgcc tcagaagaag ctatcaatac aatatacgaa 1800

cttggaaaga aagcccgcgg acatgccttc aaacttcctg cagaacttat cgggccggta 1860

tgcgacatgt gtgcagcact taccgctata acctacgccg gactgcttgt ataccgtgat 1920

gccgttatga atattctcgg tgcacctgcc ggattcagcc agatgatggc gacggaatca 1980

ctggaacaga tcaccgccta tatgaagaag gtaggcataa agaaccttga agagaacctt 2040

gacccgggtg tattccttgg aactgcagac tcaatgaact tcggacctat cgccgagatc 2100

cttcccacag ttcttaaatc acttgagaaa agggcaaaat aatgaagtaa gtaggaagca 2160

gggagcaggg gaaagaaaat tgacaactgt acaagattaa tcgcgtctct gagcaatgac 2220

caaatacatc tacctccacg gttttcttcc agccccctat ctgcgaaagc acaagatatt 2280

agcaagcgtt tcgcccaaat tcacatacag ctaacaatcc ctgatctcaa tgctggtgaa 2340

ttttctcagt taacaatcac gcgccaaatt caacaagttg ccgcaatttt ccctgataat 2400

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tctgaaccaa taacgctgat aggttctagt ttaggcggtt taactgctgc ttatctagga 2460

cagcgatatt tacaagtaca acgcttagtt ttattagcgc cagtttggtt ttttatccca 2520

ttggttgccc aaaatgggtg aagaagctgt cacaagttgg caacaaacga tataggttct 2580

ctcttctgcc gtta 2594

<210> SEQ ID NO 171
<211> LENGTH: 2819
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- SEQ ID NO: 171, example 171: a designer hox-promoter-controlled Methyltetrahydrofolate:corrinoid/iron-sulfur protein methyltransferase DNA construct (2819 bp)

<400> SEQUENCE: 171

agaaaatctg gcaccacacc gcagaaatat aggggctagg agttgagggt actctggttc 60

gtcaagcatt tgggatgatt tcccctcaca agttcctcaa attattctcc tataaacaat 120

agatataagg tcaaaacttg agttatgagt gctgagtaaa aaattactct ccacgcctca 180

gaggtagata tgtcaggcct taatcttccc ggcccgggcg gcagatatat actccaggca 240

gtattcatcc tggccgtaca gggcggtggc ggcccgcaac aggcccatta atggcatatc 300

caggggatca aggataaagg aatccatacc tttagtgagg cacataacca taaaggcccg 360

gttcagcagt cgcctttccg gcaggccata ggaaacgttg gaaaggccgc agatggtgtg 420

aaccccgggg tatttttgcc gcagggcggc aaccgattcc agagcctcca cgccgtactg 480

gctgttaact cccaggggtt taatcagggg atcaaggtag atatcgtctt ccggtatgcc 540

ggcctctacc agcccgggta ccagcttacc agcaacgcga aggcggtcct ctaccgaatc 600

cggcatgccg ccgtcatcca tgcaaagggc gataacctta gccttatatt tctgcactaa 660

aggcaaaact tcctcccagc gctgcttctc ggcggtgatg gagtttacca ttgcctggcc 720

cttatgggct gccaggccgg cagccagggc ctcggcgctg gggctatcaa tacacagggg 780

aacatcaacg acttcctgga cgatattcac gagccaggtc attaccttat tttcttcgcc 840

gatgcttgtc ccgcagttaa catcgataat atcggctccg gcctcggcct gcttcctggc 900

cagttcctgg atataatcct tatcccggtt agcaatagcc tgggcaatgg ctttgcggct 960

ggagttaatt aactctccga caacgagcat ttgcaggtaa ctgccatgga tgtataccga 1020

ttacttccaa aaacaaactg tggtaaatgt gacgagtcat catgcatggc cttcgccaca 1080

aaactcatag aaaaggaact cacactggat gactgcccgc agctcagtgg ggatgaaaga 1140

cagaagctcg aggacctcct tgcgccggct gtgagggaaa tcaccttcgg cccagaaaag 1200

aaccaggtgg tggttggggg tgatgaggtc ctctacaggt ttgaactcac atactataac 1260

cccacagccc tcgtggttga tcttccagat gacctaccat cagaggagat caggaagagg 1320

gccagtgata tcatgaatct taaattcgag cgtaccggtg aggaactgac cctggatgcc 1380

atagcgctca ggaacaaatc aggaagccct gaaaaatttg cagaggcagc agggaccctg 1440

gctgaactta acttccctgt tgttctatgc acattcgatc cagaggcaat gagggctgcc 1500

ctcgaggtcc tgggggatca gaggcccctc atgtatgcgg ctacaaagga caacctccag 1560

gagatggctg atctttccat ttcatacggc tgccccctgg tgctcttctc accgggggac 1620

cttgaggaga tgaagaacct cacaagaaga ctgcgggcaa tgggccttac tgaaattatc 1680

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ctggaccccg gaacattcac aggtgaggga ataggcgaca ccatagacaa ctttgtcatg 1740

ataaggcgcc ttgcagttga ggaaagggat gaggacttcc gcttccccat catgggcata 1800

ccagcactct caaggctttc aggaggggat ccagttgagg ataacataaa ggaggccact 1860

gttgcagcca cactcatgaa ccgctacgcc gacattctta tactcggagg aacagatatc 1920

tgggaactta tgcccatact caccctcaga cagggcctct acactgatcc aaggaagcca 1980

cagactgttg atccgggaat atatgagttt ggagacgttg atgagaactc ccctgtgata 2040

ctcacaacca acttctcact cacatactac acagtggagg gtgacctcaa ggcaggtgat 2100

gttacggcat atctccttgt gcttgacaca gagggaaggg ctgtggacgt ttcactggct 2160

ggaggacagc tcacgggaac cgcagtggct gaccttataa aggatagtgg tatagaggat 2220

agggtaaagg atagggttct catcattcct ggacttgcgg cacctgctag tggtgaaata 2280

gaagatgata ctggatggaa ggtgcttgtg gggccaaggg attcctcagg gatacctgac 2340

taccttgaaa aactggcatc ggagtagtga agtaagtagg aagcagggag caggggaaag 2400

aaaattgaca actgtacaag attaatcgcg tctctgagca atgaccaaat acatctacct 2460

ccacggtttt cttccagccc cctatctgcg aaagcacaag atattagcaa gcgtttcgcc 2520

caaattcaca tacagctaac aatccctgat ctcaatgctg gtgaattttc tcagttaaca 2580

atcacgcgcc aaattcaaca agttgccgca attttccctg ataattctga accaataacg 2640

ctgataggtt ctagtttagg cggtttaact gctgcttatc taggacagcg atatttacaa 2700

gtacaacgct tagttttatt agcgccagtt tggttttttа tcccattggt tgcccaaaat 2760

gggtgaagaa gctgtcacaa gttggcaaca aacgatatag gttctctctt ctgccgtta 2819

<210> SEQ ID NO 172
<211> LENGTH: 2771
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- SEQ ID NO: 172, example 172: a designer hox-promoter-controlled Corrinoid iron-sulfur protein DNA construct (2771 bp)

<400> SEQUENCE: 172

agaaaatctg gcaccacacc gcagaaatat aggggctagg agttgagggt actctggttc 60

gtcaagcatt tgggatgatt tcccctcaca agttcctcaa attattctcc tataaacaat 120

agatataagg tcaaaacttg agttatgagt gctgagtaaa aaattactct ccacgcctca 180

gaggtagata tgatggccgt ccagatttta cgtgatcgta gccgagctgc cgtccagaaa 240

gttgtcctgg gcgccaccaa agaccagggg ggtacccgca gccataccat cgtcgtcggt 300

ggcgatgctg ccctgccttt ccaccatttc gaaggagaga ttgtcaacag gccggtaatc 360

ggtatggaag tgcaggatat cgtacccgac tggcccgacg ttctcaaaga tcccttcacc 420

gatgttatta atgaaccagg gcgctgggcc caaaagtgcg tagccgagta tggtgctgac 480

cttatctacc tgaaacttga cggggccgac cccgaaggcg ccaaccattc tgtggaccag 540

tgcgtagcta ctgttaaaga ggtcctgcag gccgtggggg taccctggt agtggtaggt 600

tgcggcgatg tggaaaagga ccatgaggtc ctggaagcag tagccgaggc tgctgccggc 660

gagaatctcc tcctgggtaa cgctgaacag gaaaactata aatccctaac ggcagcctgc 720

atggtccaca agcataatat catcgcccgt tcgcccctgg atattaacat ttgtaaacaa 780

ctcaacatcc tgatcaatga aatgaacctg cccctggatc atatcgtcat cgacccgtcc 840

-continued

atcggcggcc tgggttatgg tattgaatac tccttctcga ttatggaacg catccgtctg 900

ggggccctgc agggagataa gatgctctcc atgccggtca tctgcaccgt aggctatgag 960

gcctggcgcg ccaaggaagc ctcggcaccg gtgagcgaat acccgggctg gggtaaggaa 1020

accgagcgtg gcatcctctg ggaagccgtt accgccactg ccctgctcca ggccggcgcc 1080

cacatcctcc tcatgcgcca tccggaagcc gtagccaggg tgaaggagaa tatcgaccag 1140

ttaatggtga gcaacgccta ttaaatggat aaattaacgg aacttctgaa attacttcag 1200

aacacggaat ccatcgaaat aaatgagttc aggattgatg ttgacgaact tgaactctac 1260

ctgatgcctg tggttcagca ggccatccag aaaacagttg aggttaggga ggcagttgag 1320

gcactccctg aggaggaatt tgaaccaccg gtaaagacat accctggtga ggttgcccag 1380

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gtgaggcttc tgcgggagat aggggaaacc ttcacaaggg aatacatgac gaccgaaaca 2280

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cgatatttac aagtacaacg cttagtttta ttagcgccag tttggttttt tatcccattg 2700

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ttctgccgtt a 2771

<210> SEQ ID NO 173
<211> LENGTH: 7061
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- SEQ ID NO: 173, example 173: a designer hox-promoter-controlled CO dehydrogenase /acetyl-CoA synthase DNA construct (7061 bp)

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<400> SEQUENCE: 173

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gtcaagcatt tgggatgatt tcccctcaca agttcctcaa attattctcc tataaacaat 120

agatataagg tcaaaacttg agttatgagt gctgagtaaa aaattactct ccacgcctca 180

gaggtagata tgtcacataa tgggatccat ggtcaaggcc gggtgtccct tttcctccaa 240

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accgacggga tggtcgggac cataggtccg gatggcctgg tttaaaagga tttccgcgta 2280

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aaagccaaga accttaaagg ggatttctgg gaccttaaaa atatccagat atccatagga 2460

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acaaggaccg ttatgggaag gaggccgcgg accctgggcg acctcatgga ggttatggac 2880

tacgccgagg aacagatgtc acacctcctc tcggcatgcc acacgggaca ggagggcgac 2940

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caagttgccg caattttccc tgataattct gaaccaataa cgctgatagg ttctagttta 6900

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<210> SEQ ID NO 174
<211> LENGTH: 1847
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- SEQ ID NO: 174, example 174 of a designer hox-promoter-controlled Thiolase (07) DNA construct (1847 bp)

<400> SEQUENCE: 174

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agatataagg tcaaaacttg agttatgagt gctgagtaaa aaattactct ccacgcctca 180

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gctttcaatg attatcatat gatccagaca gcagacaaca tctgcacaga gtggggtctt 720

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atggctacat tcgtagctgg agcacttgct ggtgttcgtc ctgaagttat gggtatcggt 1080

cctgtagcag ctactcagaa ggctatgaag aaggctggta tcgagaacgt atctgagttc 1140

gatatcatcg aggctaacga agcattcgca gctcagtctg tagcagttgg taaggatctt 1200

ggaatcgacg tccacaagca gctcaatcct aacggtggtg ctatcgctct tggacaccca 1260

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tccagccccc tatctgcgaa agcacaagat attagcaagc gtttcgccca aattcacata 1560

cagctaacaa tccctgatct caatgctggt gaatttttctc agttaacaat cacgcgccaa 1620

attcaacaag ttgccgcaat tttccctgat aattctgaac caataacgct gataggttct 1680

agtttaggcg gtttaactgc tgcttatcta ggacagcgat atttacaagt acaacgctta 1740

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tgtcacaagt tggcaacaaa cgatataggt tctctcttct gccgtta 1847

<210> SEQ ID NO 175
<211> LENGTH: 1514
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- SEQ ID NO: 175, example 175: a designer hox-promoter-controlled 3-Hydroxybutyryl-CoA dehydrogenase DNA construct (1514 bp)

<400> SEQUENCE: 175

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gctcaagtat ttgcacaaaa tggctttgaa gtaattttac gcgatattga tatgaagttc 300

gtagaaaaag gatttggcac aattgaaaaa atttacaaag aaatgttgac aaagggaaaa 360

ttacagcaga tgagaaaacg aattttaagc agaatcagag gtacaacaaa tttggaagac 420

gcaaaagaag cagattttgt agttgaagcg gctatagaaa atatggatct caagaaacaa 480

atattcaaag agctagatga aatatgcaaa atggaaacaa tccttgcgtc aaatacatca 540

tcactatcca taacagaaat agcaagtgcg acaaaaagac ctgagaaagt cataggaatg 600

catttcttca acccagttcc agtaatgaaa cttgttgaag tcataaaagg attaaagaca 660

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gcaattggaa tacttgcagt ggtgttggca actgacaaga gcatagatga agctatgaaa 840

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cagcgatatt tacaagtaca acgcttagtt ttattagcgc cagtttggtt ttttatccca 1440

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<210> SEQ ID NO 176
<211> LENGTH: 1430
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- SEQ ID NO: 176, example 176: a designer hox-promoter-controlled Crotonase DNA construct (1430 bp)

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<400> SEQUENCE: 176

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agatataagg tcaaaacttg agttatgagt gctgagtaaa aaattactct ccacgcctca 180

gaggtagata tgatggaatt aaaaaatgtt attcttgaaa aagaagggca tttagctatt 240

gttacaatca atagaccaaa ggcattaaat gcattgaatt cagaaacact aaaagattta 300

aatgttgttt tagatgattt agaagcagac aacaatgtgt atgcagttat agttactggt 360

gctggtgaga aatcttttgt tgctggagca gatatttcag aaatgaaaga tcttaatgaa 420

gaacaaggta aagaatttgg tattttagga aataatgtct tcagaagatt agaaaaattg 480

gataagccag ttatcgcagc tatatcagga tttgctcttg gtggtggatg tgaacttgct 540

atgtcatgtg acataagaat agcttcagtt aaagctaaat ttggtcaacc agaagcagga 600

cttggaataa ctccaggatt tggtggaact caaagattag caagaatagt tggaccagga 660

aaagctaaag aattaattta tacttgtgac cttataaatg cagaagaagc ttatagaata 720

ggcttagtta ataaagtagt tgaattagaa aaattgatgg aagaagcaaa agcaatggct 780

aacaagattg cagctaatgc tccaaaagca gttgcatatt gtaaagatgc tatagacaga 840

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tcttccagcc ccctatctgc gaaagcacaa gatattagca agcgtttcgc ccaaattcac 1140

atacagctaa caatccctga tctcaatgct ggtgaatttt ctcagttaac aatcacgcgc 1200

caaattcaac aagttgccgc aattttccct gataattctg aaccaataac gctgataggt 1260

tctagtttag gcggtttaac tgctgcttat ctaggacagc gatatttaca agtacaacgc 1320

ttagttttat tagcgccagt ttggtttttt atcccattgg ttgcccaaaa tgggtgaaga 1380

agctgtcaca agttggcaac aaacgatata ggttctctct tctgccgtta 1430

<210> SEQ ID NO 177
<211> LENGTH: 1784
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- SEQ ID NO: 177, example 177: designer hox-promoter-controlled Butyryl-CoA dehydrogenase DNA construct (1784 bp)

<400> SEQUENCE: 177

agaaaatctg gcaccacacc gcagaaatat aggggctagg agttgagggt actctggttc 60

gtcaagcatt tgggatgatt tcccctcaca agttcctcaa attattctcc tataaacaat 120

agatataagg tcaaaacttg agttatgagt gctgagtaaa aaattactct ccacgcctca 180

gaggtagata tgatgaattt ccaattaact agagaacaac aattagtaca acaaatggtt 240

agagaattcg cagtaaatga agttaagcca atagctgctg aaatcgacga aacagaaaga 300

ttccctatgg aaaacgttga aaaaatggct aagcttaaaa tgatgggtat cccattttct 360

aaagaatttg gtggagcagg cggagatgtt ctttcatata taatagctgt ggaagaatta 420

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tcaaaagttt gtggtactac aggagttatt ctttcagcgc atacatcatt atgtgcatca 480

gtaattaatg aaaatggaac taacgaacaa agagcaaaat atttacctga tctttgcagc 540

ggtaaaaaga tcggtgcttt cggattaact gaaccaggtg ctggtacaga tgctgcagga 600

caacaaacaa ctgctgtatt agaaggggat cattatgtat taaatggttc aaaaatcttc 660

ataacaaatg gtggagttgc tgaaactttc ataatatttg ctatgacaga taagagtcaa 720

ggaacaaaag gaatttctgc attcatagta gaaaagtcat tcccaggatt ctcaatagga 780

aaattagaaa ataagatggg gatcagagca tcttcaacta ctgagttagt tatggaaaac 840

tgcatagtac caaaagaaaa cctacttagc aaagaaggta agggatttgg tatagcaatg 900

aaaactcttg atggaggaag aattggtata gctgctcaag ctttaggtat tgcagaagga 960

gcttttgaag aagctgttaa ctatatgaaa gaaagaaaac aatttggtaa accattatca 1020

gcattccaag gattacaatg gtatatagct gaaatggatg ttaaaatcca agctgctaaa 1080

tacttagtat acctagctgc aacaaagaag caagctggtg agccttactc agtagatgct 1140

gcaagagcta aattatttgc tgcagatgtt gcaatggaag ttacaactaa agcagttcaa 1200

atctttggtg gatatggtta cactaaagaa tacccagtag aaagaatgat gagagatgct 1260

aaaatatgcg aaatctacga aggaacttca gaagttcaaa agatggttat cgcaggaagc 1320

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ctaacaatcc ctgatctcaa tgctggtgaa ttttctcagt taacaatcac gcgccaaatt 1560

caacaagttg ccgcaatttt ccctgataat tctgaaccaa taacgctgat aggttctagt 1620

ttaggcggtt taactgctgc ttatctagga cagcgatatt tacaagtaca acgcttagtt 1680

ttattagcgc cagtttggtt ttttatccca ttggttgccc aaaatgggtg aagaagctgt 1740

cacaagttgg caacaaacga tataggttct ctcttctgcc gtta 1784

<210> SEQ ID NO 178
<211> LENGTH: 2051
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- SEQ ID NO: 178, example 178, a designer hox-promoter-controlled Butyraldehyde dehydrogenase DNA construct (2051 bp)

<400> SEQUENCE: 178

agaaaatctg gcaccacacc gcagaaatat aggggctagg agttgagggt actctggttc 60

gtcaagcatt tgggatgatt tcccctcaca agttcctcaa attattctcc tataaacaat 120

agatataagg tcaaaacttg agttatgagt gctgagtaaa aaattactct ccacgcctca 180

gaggtagata tgatgattaa agacacgcta gtttctataa caaaagattt aaaattaaaa 240

acaaatgttg aaaatgccaa tctaaagaac tacaaggatg attcttcatg tttcggagtt 300

ttcgaaaatg ttgaaaatgc tataagcaat gccgtacacg cacaaaagat attatccctt 360

cattatacaa aagaacaaag agaaaaaatc ataactgaga taagaaaggc cgcattagaa 420

aataaagaga ttctagctac aatgattctt gaagaaacac atatgggaag atatgaagat 480

aaaatattaa agcatgaatt agtagctaaa tacactcctg ggacagaaga tttaactact 540

actgcttggt caggagataa cgggcttaca gttgtagaaa tgtctccata tggcgttata 600

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ggtgcaataa ctccttctac gaatccaact gaaactgtaa tatgtaatag tataggcatg 660

atagctgctg gaaatactgt ggtatttaac ggacatccag gcgctaaaaa atgtgttgct 720

tttgctgtcg aaatgataaa taaagctatt atttcatgtg gtggtcctga gaatttagta 780

acaactataa aaaatccaac tatggactct ctagatgcaa ttattaagca cccttcaata 840

aaactacttt gcggaactgg agggccagga atggtaaaaa ccctcttaaa ttctggtaag 900

aaagctatag gtgctggtgc tggaaatcca ccagttattg tagatgatac tgctgatata 960

gaaaaggctg gtaagagtat cattgaaggc tgttcttttg ataataattt accttgtatt 1020

gcagaaaaag aagtatttgt ttttgagaac gttgcagatg atttaatatc taacatgcta 1080

aaaaataatg ctgtaattat aaatgaagat caagtatcaa agttaataga tttagtatta 1140

caaaaaaata atgaaactca agaatactct ataaataaga aatgggtcgg aaaagatgca 1200

aaattattct tagatgaaat agatgttgag tctccttcaa gtgttaaatg cataatctgc 1260

gaagtaagtg caaggcatcc atttgttatg acagaactca tgatgccaat attaccaatt 1320

gtaagagtta aagatataga tgaagctatt gaatatgcaa aaatagcaga acaaaataga 1380

aaacatagtg cctatattta ttcaaaaaat atagacaacc taaataggtt tgaaagagaa 1440

atcgatacta ctatctttgt aaagaatgct aaatcttttg ccggtgttgg ttatgaagca 1500

gaaggcttta caactttcac tattgctgga tccactggtg aaggaataac ttctgcaaga 1560

aattttacaa gacaaagaag atgtgtactc gccggttaat gaagtaagta ggaagcaggg 1620

agcaggggaa agaaaattga caactgtaca agattaatcg cgtctctgag caatgaccaa 1680

atacatctac ctccacggtt ttcttccagc cccctatctg cgaaagcaca agatattagc 1740

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tctcagttaa caatcacgcg ccaaattcaa caagttgccg caattttccc tgataattct 1860

gaaccaataa cgctgatagg ttctagttta ggcggtttaa ctgctgctta tctaggacag 1920

cgatatttac aagtacaacg cttagtttta ttagcgccag tttggttttt tatcccattg 1980

gttgcccaaa atgggtgaag aagctgtcac aagttggcaa caaacgatat aggttctctc 2040

ttctgccgtt a 2051

<210> SEQ ID NO 179
<211> LENGTH: 1808
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- SEQ ID NO: 179, example 179: a designer hox-promoter-controlled NADH-dependent Butanol dehydrogenase DNA construct (1808 bp)

<400> SEQUENCE: 179

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gtcaagcatt tgggatgatt tcccctcaca agttcctcaa attattctcc tataaacaat 120

agatataagg tcaaaacttg agttatgagt gctgagtaaa aaattactct ccacgcctca 180

gaggtagata tgttacaggg aagcgcgcaa aatggcgagc acatcatcgc ggttcaatgt 240

tttgaaacgg ccgaactcgc caaacgccat cgctttatcg gccatcagct ccaagttttc 300

ctcgccgatg ccatagtccg caagccgcga cggcgccccg aggctcgacc agaactcgcg 360

cagccgctcg atgccttcaa gcgccacatc ccgctccgat ttgcccgccg gatcgacatc 420

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aaagacgcgc accgcgagct gggcgaaacg gctgacattt tcatcgagca catgcttcat 480

ccagttcggg aacaaaatcg ccaatccccc ggcgtgcggg atgtcataca cggcggaaac 540

ggcatgctca atattgtgcg tcgcccagtc gccgcggacg cccatttgca agaagccgtt 600

taaggcgatc gtgcccgagt acatgatcgt ctcgcgcagc tcgtagtttt ccaaatcgtt 660

gatcagtttg ggcgccgttt cgatcacggt tttcaacacc gcttcacaca tccggtcttg 720

caatggcgtg ttcggcgtat ggtggaaata ttgctcaaac acatgcgaca tcatatcgac 780

aatgccgtaa accgtatggt ctttcggaac ggtcatcgta tacgtcggat ccaaaatcga 840

aaattgcggg aacgtaaacg ggctgcccca gccgtatttt tctttcgtct cccagtttgt 900

gatcaccgaa ccagaattca tctccgaccc ggtcgccgcc agcgtcaaga cgacgccaaa 960

cggcagggcg ccggtgacgg gcgctttttt cgtgataaac tcccacggat cgccatcgaa 1020

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aggggaaaga aaattgacaa ctgtacaaga ttaatcgcgt ctctgagcaa tgaccaaata 1440

catctacctc cacggttttc ttccagcccc ctatctgcga aagcacaaga tattagcaag 1500

cgtttcgccc aaattcacat acagctaaca atccctgatc tcaatgctgg tgaattttct 1560

cagttaacaa tcacgcgcca aattcaacaa gttgccgcaa ttttccctga taattctgaa 1620

ccaataacgc tgataggttc tagtttaggc ggtttaactg ctgcttatct aggacagcga 1680

tatttacaag tacaacgctt agttttatta gcgccagttt ggtttttat cccattggtt 1740

gcccaaaatg ggtgaagaag ctgtcacaag ttggcaacaa acgatatagg ttctctcttc 1800

tgccgtta 1808

<210> SEQ ID NO 180
<211> LENGTH: 10538
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- SEQ ID NO: 180, example 180: a designer hox-promoter-controlled Energy converting heydrogenase (Ech) DNA construct (10538 bp)

<400> SEQUENCE: 180

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agatataagg tcaaaacttg agttatgagt gctgagtaaa aaattactct ccacgcctca 180

gaggtagata tgttattcta acattttctt aatatatggc tcaagaggga taatatctcc 240

agttgaacga ggtgttaaag ctgaaactgt taaaacacgt tcttcttgat ccatactaac 300

agtgatagta ccaggtgtta atgtgatagt atttgatagt attgcaagag atactggtct 360

ttcaagatca ggtttaatct ttacaactat aggatcaaca tcgcccttga gacagcaaat 420

acttgtgtca agtattgctt taattatttc gactactaat actacgaaaa attctattcc 480

gtagattatt ctagttaaaa acatttataa atcgccccca cctaatacgt aggatacagc 540

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tattgttcct acaggactta atataagtat tgcaaatgct atgtctctac agaaatctat 600

tccagtaagt gaagatacca ttgttaaaac aattgcaagt gcaattgtga aacctgctac 660

cccagctaaa gctgaaccaa ttgttcttct tgctgcaatt tttacatttg ctagcatgta 720

aacaattaga cataacatga ggaacaattc agatattgtt aaaaaatcca tttattgctc 780

cccctgttct ccacggaagt gtccacttgc tattgcatga gttgcaaatg gtgctaatat 840

aaagtatgtc attcctaaag ctggttctcc aagaagtatt aatattaaca cgccaagcat 900

atctacaata cctaacattt ctaatcttcc aaatacgaca tatttaacat cgtcatcggt 960

attacataat agtccttttg ctgtaattaa aacgaatata ccgcagatta taaatattaa 1020

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ttaggaatca ccttcctctt ttgatacagg ttgttctctt gttttaagaa ttgtaagagc 1140

tactaatgtt ggtacaatag ctgctcccac tacagcttgt gttaatgcta catcgggtgc 1200

taataaaact tgataaattg ctgctaaaat aaaaccagta atactagtta atacagccat 1260

tttaattaaa tctttttgaa ttaaacaaac aaatgcacct aatattgcaa ataaatataa 1320

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aagtactaat gcaaatggta atggatatga tgcttgacct aagaagttat ttacttccat 1560

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tactgataac atttacatta ttaaagcgga aaaagccatg actccaagtc tatttactac 1800

taaatcagga cataaaccta taattaaaca aataattaag aagaatacca ttattgccat 1860

agttgtttta ggaacttttg cagaagatac ttctaaatca tctggttttg gtctaaggaa 1920

cattgcatat gtgatttttа agaatgctaa gaaagttaca atacttaata taatcataat 1980

tattgcaagt tctggtattc ctgcacttaa tgcagcttga cataacatgt atttactttg 2040

gaatacattg aatggaggta ctccagccat tataaatcct gcaagtacaa ttaataatgc 2100

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gtataatact aaaccaaatc ctacaaacaa gaatgaagtt actactaatt catttactgc 2220

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tggtaaatat ccaaatattc taattaatac taaacctatg gatatacaac ctattacaga 2460

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tccatgaata tttttgtata ctccaccagt taaagcacat gctcctactg caacaactaa 6780

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acatccacca gtataaacta acataaggtg tattgccttt ttacgggctt gtgattttaa 7020

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tgatacaata gcaagttgtg catcctgaat tgggtgtcca atacaagatt cttgcattgc 7140

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ccagtttggt tttttatccc attggttgcc caaaatgggt gaagaagctg tcacaagttg 6660

gcaacaaacg atataggttc tctcttctgc cgtta 6695

<210> SEQ ID NO 183
<211> LENGTH: 3407
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- SEQ ID NO: 183, example 183: a designer hox-promoter-controlled Coenzyme F420-reducing hydrogenase (Frh) DNA construct (3407 bp)

<400> SEQUENCE: 183

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agatataagg tcaaaacttg agttatgagt gctgagtaaa aaattactct ccacgcctca 180

gaggtagata tgatgttaaa caatgcgatc gcaacgccgg ccctccagcc attccaggaa 240

ctcgagcaga gcgtctggaa gaaggagatg tgcgccggat gccggggctg tatcaccgta 300

tgcccggcca acacgttagc ctatgacctg aagctggcca ggccgtacca gatcactccc 360

tgtgtcgatt gtaaggcctg cctggacgcc tgtcccagga ctccagctaa catggataag 420

ctgtccctgg acattcttgg gccgcatctt gacgtttata atgtgaaggc tactgcgggc 480

aataagcgct accagaacgg cggcgccgtt actgcgttgc tgaagaccgc gctggacgaa 540

ggccttgtgg accgtgtgat cgtcatgggc gcggaccgct gggcacagaa ggcatacgcc 600

cgggtcgtct ccgactcatc gagcctggac agggctgcgg gcagtattta catgaacaac 660

gatgccctgg agacaatgaa ggacatcatg aaggacgact cgatcaggaa cgtggcgatc 720

gtgggaacgc cctgcgcgat acagtcgata ggcctgctcc ggaagtcctc gaacgagtac 780

tccgtaaagc tgacccagaa gatcaggttc gccatcggct tattctgctt tgagtcattc 840

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aagatgaacg ccggcgaggg caggctgacc gtcacgctga ggagtggcga ggtaaagacg 960

ctgcccctgt cgagcctggc cgagttcgtc aagcccggat gccgcaagtg caacgacttc 1020

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gttattacca ggacgcccga gggtgccggg ctactcgaga tcgcccgcga ggtgggcgct 1140

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gacgtgtcca ttcccatcaa ggagacccac aagtacgagc aggacggctg ccacgtttgc 1800

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gttttattag cgccagtttg gttttttatc ccattggttg cccaaaatgg gtgaagaagc 3360

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<210> SEQ ID NO 184
<211> LENGTH: 5417
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- SEQ ID NO: 184, example 184: a designer hox-promoter-controlled Methyl-H4MPT: coenzyme M methyltransferase (MtrA-H) DNA construct (5417 bp)

<400> SEQUENCE: 184

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agatataagg tcaaaacttg agttatgagt gctgagtaaa aaattactct ccacgcctca 180

gaggtagata tgatggcaga taaaaaagaa gttattcaaa attggccctt agaaactgga 240

gattatgcag tgggaaatgt tgaaagtcca gtagcagtag tctctctagg ttctaatatg 300

aatgatgaat tggtagctgc aggggctgca atttcaggac cattacacac agaaaacttg 360

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tgtggatctg aggttcaagg acatattact ggtaaaacag ttgaagcttt atatgaaaat 480

ggtattgatg aagagaaaaa atcaattatt ggttctcctg gagctattcc attcgttgaa 540

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aataatgagg atgttagtga aatatcatct aaaatagatg aatgtattag taatgatcct 660

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gaagttgatg aagtcacatt ttctgatgat tcagcagttg atttagcatc aatagttcta 780

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gaaaaaatat cttcaggata ttatgctgga aaaatagaag gtatagttat tggatttatt 900

ttaacattgg tttttcttat aattattatt caaggtttgt gattggtaga tacaacagca 960

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gtggcaatta ataatctaga atcatcatta gatcctagaa caacatctaa tctatcacaa 1140

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cctgtggttg gtggtatttt ttcaattatt gcaacaatat taggtgttat ttgtggaaca 1380

aatacactta gacacatagg aaaatatagt ttaggtactg gagttccatc aatagtttat 1440

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gaatttttctc agttaacaat cacgcgccaa attcaacaag ttgccgcaat tttccctgat 5220

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<210> SEQ ID NO 185
<211> LENGTH: 5042
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- SEQ ID NO: 185, example 185: a designer hox-promoter-controlled Methyl-coenzyme M reductase (Mcr) DNA construct (5042 bp)

<400> SEQUENCE: 185

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gatcaattag atcaaagatt tgtaatcgac atcaacaaag agttccctga agaacaagct 780

gaaatgctca aaaaatacat aggtcagaag acctaccaag taagtagagt acctacatta 840

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gcaagtgaag taaccttata cggattagaa caatacgaaa tccctgcagc attagaagac 1380

cactttggtg gatcacaaag agcagcagtt cttgcagcag gtgcaggttg ttcagtagca 1440

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ccacacgcag caagaggaga cgcatttgca cttaacccat taataaaagt agcatttgct 1740

gataaaaact tatccttcga ttgggctcac ccaagagaat gtattgcaaa aggtgctgtt 1800

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gaaaaatctg aaacacaggg tactattgtt gaactcataa ctgatgttat tcgtggagaa 3720

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ccacctcttg atgaaatgga ctttgaagaa gatactatga aagacttcgt agaaccaatc 4020

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gcacctgctc aaccatacga cagagcaaga tcatacatga gaagattcag aggagtagat 4140

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accgtacacg gtcactcatt aagacttgat gaagacggat taatgtttga tgcattacaa 4320

ttatacgtat tcgataaaga aactggtcac gttgtatacg taaaagatca agtaggagta 4380

gaacttgatg aacctattga tgtaggagaa ccattaccag aagacgaact taagaaaata 4440

acaaccatct acagatctga caacgtcagc ttaagagatg atgaagaagt tattaaagta 4500

gttgaagcta ttcacttcgc aagaactgat ggtggatatg gtttagaagt attcaacaac 4560

gatttaaaaa gtaaattagg tggtaactaa tgaagtaagt aggaagcagg gagcagggga 4620

aagaaaattg acaactgtac aagattaatc gcgtctctga gcaatgacca aatacatcta 4680

cctccacggt tttcttccag ccccctatct gcgaaagcac aagatattag caagcgtttc 4740

gcccaaattc acatacagct aacaatccct gatctcaatg ctggtgaatt ttctcagtta 4800

acaatcacgc gccaaattca acaagttgcc gcaattttcc ctgataattc tgaaccaata 4860

acgctgatag gttctagttt aggcggttta actgctgctt atctaggaca gcgatattta 4920

caagtacaac gcttagtttt attagcgcca gtttggtttt ttatcccatt ggttgcccaa 4980

aatgggtgaa gaagctgtca caagttggca acaaacgata taggttctct cttctgccgt 5040

ta 5042

<210> SEQ ID NO 186
<211> LENGTH: 5450
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- SEQ ID NO: 186, example 186: a designer hox-promoter-controlled Formate dehydrogenase DNA construct (5450 bp)

<400> SEQUENCE: 186

agaaaatctg gcaccacacc gcagaaatat aggggctagg agttgagggt actctggttc 60

gtcaagcatt tgggatgatt tcccctcaca agttcctcaa attattctcc tataaacaat 120

agatataagg tcaaaacttg agttatgagt gctgagtaaa aaattactct ccacgcctca 180

gaggtagata tgatggttaa cctgaccatt gacggacaaa gggttacggc tccagagggc 240

atgaccatcc tggaggtggc ccgggaaaat ggtatccata tccccaccct gtgccaccat 300

ccaaagttgc ggcccctggg gtattgccgt ctgtgcctgg tcgacatcga gggcgccgca 360

aaacccatga cggcctgcaa tacgccggtc gccgagggta tggtgatccg gaccagcacg 420

cctgttatag aggagatgcg caagggtatt attgaaatgc ttttaagcct ccacccggag 480

gactgcctga cctgcgaaaa agcaggtaac tgccagctcc aggattgcgc ctacacttac 540

ggtgtaaagc atggcgaact gccagtaaaa cgcgaggaat tgcccgtttt gaaggaaaat 600

cccttcattg tgcgggatta taataaatgt atcgtttgcg gccgttgcgt ccgcgcctgc 660

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caggaggtgc aggtccagag ggtcgtggac ctggtgggta aaggcagcgc cgcccgggtg 720

ggggcgacga aggccggagc ggaagtaagc ctggaagaag ggggctgcgt cttttgcggt 780

aactgtgtcc aggtctgccc ggtgggagct ctgacggaga aggccggcct gggccagggc 840

cgcgagtggg agttcaaaaa agtccgcagt atttgttctt actgcggcgt gggttgtaat 900

ctcacccttt atgtaaaaga tggtaaggtg gtaaaagtta ggggttacga aaaccctgag 960

gtaaacaacg gctggctgtg cgtaaaaggc cgctttggtt ttgactatat tcacaatcct 1020

gacaggataa ccaggccgtt gatccgggag ggagataggg aaaaaggcta tttccgggag 1080

gcttcctggg aagaagcttt agcccttgta tcccagaaat taactcagat taaaggcagc 1140

tacggctctg aagctctggg ctttctttgt tcagctaaat gtaccaatga agagaattat 1200

ctcttacaaa agctggcccg gggggtactg ggcaccaata atgttgatca ctgtgctcgc 1260

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attgttgctg atccccggcg tattgaactg gtgaacttca gttacttgtg gttaagacaa 1500

aaacccggaa cagatcttgc tctgctgaat ggactgcttc atgtaatcat caaggaagag 1560

ctttatgaca aagaatttat tgcccagagg acggaaggtt ttgaggctct aaaacttgcc 1620

gtagaggagt atacaccagc aaaggtgtca gaagttacag gtgttccggc aggcgatatt 1680

atcgaggcag caaggactta tgcccggggt ccgagctcta ctattttgta cgcaatggga 1740

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tgtggtcagg tcggtaaaga aggtaacggc gtaaatcccc tgcgggggca gagcaatgtc 1860

cagggtgcct gcgatatggg tggattaccc aatgtattac cgggatacca accagtaaca 1920

gatccggggg ttcgccataa atttagcgaa acctgggggg taccggactt acccggagaa 1980

cctggcctga cattaatgga gatgatggcg gcagcccaag aaggcaaatt gaaagggatg 2040

tatattttag gagaaaaccc tgtcttgact gatccagatg tctcccatgt aaaagaggcg 2100

ttaaagaacc tggagtttct ggtggtacag gatatttttt tgacggagac agccaggatg 2160

gcggatgttg ttttacctgg agcttccttt gcggaaaagg aaggtacctt taccagtacg 2220

gagcgccggg tgcagctttt gcataaagcc attgaacctc ccggtgaagc acggccggat 2280

tggcttattt taaacgattt gttgctgtta atgggatatc cgcggaaata ttcgtcgcct 2340

ggggagataa tgcaggagat agcagggtta actcccagct atgcgggtat aacttatgag 2400

cgcctggaag ataaagggtt acagtggccg gtgctttccc tcgaacatcc gggtacaccc 2460

gttctccatc gggaaaaatt tagcagaggt tatgggcagt tccaggtagt gcattaccgg 2520

ccgccggccg aagaacctga tgaagagtac ccgttcttat ttaccactgg caggaatttg 2580

tatcactatc atactgttat ttcccgtaag tccagggggc tggaagagat gtgtcctgct 2640

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ccccggggcc aggtatttat gaatttccat ttccatgaag cagcagccaa cctgcttaca 2820

attgctgccc tggatccggt tgctaaaata ccgattataa aacctgtgct gtagttggga 2880

gaggtggtat ttagcacctg gggaggaaaa gttgtcgatc accggggcgg tccgtcgggg 2940

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ggaggaccgt cctgggccgg ggaatttggc ggtcggcagt taaaggcctt tattggctgg 3000

gatggtctcg tagtcaccga cccggccgta gacctgctgg ctgctttaca ggcttactac 3060

caggccgtcc agggggaatc ctgcggccgc tgcgtaccct gccgggtagg gaccagggtt 3120

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ctggccatca tccgccagcg gaccgccctg gccggtgtcc tgggacgggt ctgcgtccac 3600

ccgtgtgaag aaaactgccg ccgcggcaat gttgacgaac ccctggccat ccggggcctg 3660

aagcgcttcg tagccgatta tgaggtgaaa cgcggccgcc ggccggtcgc cgtctgcggg 3720

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gagccggacg attctggccg gcgccggccc gtacccgtgc cgggaacgga gtttttcctg 4500

ccctgcgata ttgtggtgcc ggctatcggc caggcggccg acctgtcttt cctggacggc 4560

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gccgagcggg taaaggactt ccgggaagtt gaaggcggct tcgatttcta cgcaggcagg 4920

gccgaagccg aacgctgcct gcgctgttac cgggtcggga tgatggtcct ggccggagag 4980

ggggagagta atggttaatg aagtaagtag gaagcaggga gcaggggaaa gaaaattgac 5040

aactgtacaa gattaatcgc gtctctgagc aatgaccaaa tacatctacc tccacggttt 5100

tcttccagcc ccctatctgc gaaagcacaa gatattagca agcgtttcgc ccaaattcac 5160

atacagctaa caatccctga tctcaatgct ggtgaatttt ctcagttaac aatcacgcgc 5220

caaattcaac aagttgccgc aattttccct gataattctg aaccaataac gctgataggt 5280

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tctagtttag gcggtttaac tgctgcttat ctaggacagc gatatttaca agtacaacgc 5340

ttagttttat tagcgccagt ttggtttttt atcccattgg ttgcccaaaa tgggtgaaga 5400

agctgtcaca agttggcaac aaacgatata ggttctctct tctgccgtta 5450

<210> SEQ ID NO 187
<211> LENGTH: 2324
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- SEQ ID NO: 187, example 187: a designer hox-promoter-controlled 10-Formyl-H4 folate synthetase DNA construct (2324 bp)

<400> SEQUENCE: 187

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gtcaagcatt tgggatgatt tcccctcaca agttcctcaa attattctcc tataaacaat 120

agatataagg tcaaaacttg agttatgagt gctgagtaaa aaattactct ccacgcctca 180

gaggtagata tgttgtccaa ggtacccagt gatattgaga ttgcccaggc agccaaaatg 240

aaaccggtca tggaactggc ccggggactg ggcatccaag aggacgaggt cgagctttat 300

ggtaagtaca aggccaagat ctccctcgat gtctatcgtc gcctcaaaga caagcctgac 360

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cgggagccct ccctgggacc cagctttggt atcaaaggcg gtgccgccgg cggtggttat 540

gcccaggtag tacccatgga agatatcaac ctgcacttca ccggcgatat ccacgccgtc 600

acctatgccc acaacctgct ggcggccatg gtggataacc acctgcagca gggtaacgtc 660

ctgaatattg atccccgtac catcacctgg cgccgggtca tcgaccttaa tgaccgggct 720

ctgaggaaca tagtcatcgg cctgggtggc aaagccaacg gcgtaccgcg ggagacaggg 780

tttgacatct ccgttgcctc ggaggttatg gcctgcctgt gcctggccag cgacctcatg 840

gatctcaagg aacgtttcag ccgcattgtt gtcggctaca cctatgacgg caaaccggtc 900

accgccggcg atctggaggc ccagggttcc atggctcttc tcatgaagga cgccattaaa 960

cccaacctgg tccaaaccct ggagaatacg ccggccttta tccacggtgg tcccttcgcc 1020

aatatcgccc acggttgcaa cagcattatc gcaaccaaga cggccctgaa actggcggat 1080

tatgtcgtga cggaagccgg tttcggtgcc gacctgggtg ccgagaagtt ctatgacgtt 1140

aaatgccgtt atgccggctt taaacccgat gccacagtca tcgtggctac cgtccgcgcc 1200

ctcaagatgc acggcggcgt acccaaatca gacctggcca ctgaaaacct ggaagccctg 1260

cgggaaggct ttgccaacct ggagaaacac atcgaaaata tcggcaagtt cggcgtaccg 1320

gcagtcgtgg ccatcaatgc cttccccacc gataccgagg ccgagctaaa tctcctctac 1380

gagttgtgcg ccaaagctgg ggccgaagtt gccctctcgg aagtctgggc taagggcggc 1440

gaaggcggtc tggaacttgc ccggaaggtg ttgcagaccc tggagagcag gccatccaac 1500

ttccatgtcc tctacaacct ggacctgagt attaaagaca aaattgccaa aatcgccacc 1560

gagatctacg gggccgacgg cgtcaactat acggccgaag ccgacaaagc tatccagcgt 1620

tatgaatccc tgggctacgg caacctgccg gtggtcatgg ccaagaccca atactccttt 1680

tccgatgaca tgaccaagct cgggcggccg cggaacttta ccatcaccgt gcgcgaggtg 1740

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cgcctctcgg ccggagcagg ctttatcgtc cccatcaccg gcgccataat gaccatgccc 1800

gggctgccca aacgcccggc ggcctgcaac atcgacatcg atgccgacgg cgtcattacc 1860

ggtctttttct agtgaagtaa gtaggaagca gggagcaggg gaaagaaaat tgacaactgt 1920

acaagattaa tcgcgtctct gagcaatgac caaatacatc tacctccacg gttttcttcc 1980

agccccctat ctgcgaaagc acaagatatt agcaagcgtt tcgcccaaat tcacatacag 2040

ctaacaatcc ctgatctcaa tgctggtgaa ttttctcagt taacaatcac gcgccaaatt 2100

caacaagttg ccgcaatttt ccctgataat tctgaaccaa taacgctgat aggttctagt 2160

ttaggcggtt taactgctgc ttatctagga cagcgatatt tacaagtaca acgcttagtt 2220

ttattagcgc cagtttggtt ttttatccca ttggttgccc aaaatgggtg aagaagctgt 2280

cacaagttgg caacaaacga tataggttct ctcttctgcc gtta 2324

<210> SEQ ID NO 188
<211> LENGTH: 1487
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- SEQ ID NO: 188, example 188: a designer hox-promoter-controlled 10-Methenyl-H4 folate cyclohydrolase DNA construct (1487 bp)

<400> SEQUENCE: 188

agaaaatctg gcaccacacc gcagaaatat aggggctagg agttgagggt actctggttc 60

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agatataagg tcaaaacttg agttatgagt gctgagtaaa aaattactct ccacgcctca 180

gaggtagata tgctagcgcc gggccgcctc gactgtattc ttcaagagca tggcaatggt 240

catgggacct accccgccgg gtacgggagt gatccaaccg gccttctggg ccgcactctc 300

gaagtggacg tcgcccacca gctttttctc gccgacccgg ttgataccta cgtcgataac 360

taccgcgccc tctttaatca tatccccggt aatcaactcc ggcttcccta cggccgcaat 420

gagaatgtcg gcctgccggc attcggctgc caggtccctg gtgcgggagt gacagatggt 480

caccgtggcg tggcgggcca ggagcatcat tgctactggc ttgccgacga tattgctccg 540

gccgacgacc actgcctttt tacccttggg atcaataccg gctttttcca gcaaaaccat 600

acagccgtgg ggtgtgcatg gatagaagca tttatcgccg ataaccaggt tgccgacgtt 660

ggccgggctg aacccgtcaa catccttttc cagggcgatg gcatcgatga ctttcttctc 720

atcaatatga tcaggcaacg gcaactggac caggatgccg tgaatcttgg gatctttatt 780

gagctggtcg atcagcttta agagttcggc ctggctggtc gccgccggca ggcggtgaac 840

ctcggagtag ataccgacct cctcacaggc gcggtgcttg ttacggacgt acacctggga 900

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ccgggatacc tcctccttta cttcagccct tacttcggca gcaatctttt tcccgtcgag 1020

gatctgggct ggcattgaag taagtaggaa gcagggagca ggggaaagaa aattgacaac 1080

tgtacaagat taatcgcgtc tctgagcaat gaccaaatac atctacctcc acggttttct 1140

tccagccccc tatctgcgaa agcacaagat attagcaagc gtttcgccca aattcacata 1200

cagctaacaa tccctgatct caatgctggt gaattttctc agttaacaat cacgcgccaa 1260

attcaacaag ttgccgcaat tttccctgat aattctgaac caataacgct gataggttct 1320

agtttaggcg gtttaactgc tgcttatcta ggacagcgat atttacaagt acaacgctta 1380

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gttttattag cgccagtttg gtttttttatc ccattggttg cccaaaatgg gtgaagaagc 1440

tgtcacaagt tggcaacaaa cgatataggt tctctcttct gccgtta 1487

<210> SEQ ID NO 189
<211> LENGTH: 1487
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- SEQ ID NO: 189, example 189: a designer hox-promoter-controlled 10-Methylene-H4 folate dehydrogenase DNA construct (1487 bp)

<400> SEQUENCE: 189

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gtcaagcatt tgggatgatt tcccctcaca agttcctcaa attattctcc tataaacaat 120

agatataagg tcaaaacttg agttatgagt gctgagtaaa aaattactct ccacgcctca 180

gaggtagata tgctagcgcc gggccgcctc gactgtattc ttcaagagca tggcaatggt 240

catgggacct accccgccgg gtacgggagt gatccaaccg gccttctggg ccgcactctc 300

gaagtggacg tcgcccacca gctttttctc gccgacccgg ttgataccta cgtcgataac 360

taccgcgccc tctttaatca tatccccggt aatcaactcc ggcttcccta cggccgcaat 420

gagaatgtcg gcctgccggc attcggctgc caggtccctg gtgcgggagt gacagatggt 480

caccgtggcg tggcgggcca ggagcatcat tgctactggc ttgccgacga tattgctccg 540

gccgacgacc actgcctttt taccccttggg atcaataccg gctttttcca gcaaaaccat 600

acagccgtgg ggtgtgcatg gatagaagca tttatcgccg ataaccaggt tgccgacgtt 660

ggccgggctg aacccgtcaa catccttttc cagggcgatg gcatcgatga ctttcttctc 720

atcaatatga tcaggcaacg gcaactggac caggatgccg tgaatcttgg gatctttatt 780

gagctggtcg atcagcttta agagttcggc ctggctggtc gccgccggca ggcggtgaac 840

ctcggagtag ataccgacct cctcacaggc gcggtgcttg ttacggacgt acacctggga 900

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gatctgggct ggcattgaag taagtaggaa gcagggagca ggggaaagaa aattgacaac 1080

tgtacaagat taatcgcgtc tctgagcaat gaccaaatac atctacctcc acggttttct 1140

tccagccccc tatctgcgaa agcacaagat attagcaagc gtttcgccca aattcacata 1200

cagctaacaa tccctgatct caatgctggt gaatttttctc agttaacaat cacgcgccaa 1260

attcaacaag ttgccgcaat tttccctgat aattctgaac caataacgct gataggttct 1320

agtttaggcg gtttaactgc tgcttatcta ggacagcgat atttacaagt acaacgctta 1380

gttttattag cgccagtttg gtttttttatc ccattggttg cccaaaatgg gtgaagaagc 1440

tgtcacaagt tggcaacaaa cgatataggt tctctcttct gccgtta 1487

<210> SEQ ID NO 190
<211> LENGTH: 1565
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- SEQ ID NO: 190, example 190: a designer hox-promoter-controlled 10-Methylene-H4 folate reductase DNA construct (1565 bp)

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<400> SEQUENCE: 190

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agatataagg tcaaaacttg agttatgagt gctgagtaaa aaattactct ccacgcctca 180

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gaactcaaag gggtcggcaa aggggttggc ggcggcgccg atgaagaagc ggggttcctg 660

gcccttaatc tcttcaccgc aggcgaattt tttctcatcc cggaggtcct tcacgatccg 720

gatcagctgg agggaatcca cgtcatggac gtttttcgcc gtcggatggt taccaaaaga 780

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gttgtccgtc aggttcatgg catcaacgta gtccttgagg agagcggcgt gcttcttgat 1020

ctctgtagga tcggcgtgct tcggcggtcc aatctcaccg ctgaccagaa attgcccctg 1080

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ctacctccac ggttttcttc cagcccccta tctgcgaaag cacaagatat tagcaagcgt 1260

ttcgcccaaa ttcacataca gctaacaatc cctgatctca atgctggtga attttctcag 1320

ttaacaatca cgcgccaaat tcaacaagtt gccgcaattt tccctgataa ttctgaacca 1380

ataacgctga taggttctag tttaggcggt ttaactgctg cttatctagg acagcgatat 1440

ttacaagtac aacgcttagt tttattagcg ccagtttggt tttttatccc attggttgcc 1500

caaaatgggt gaagaagctg tcacaagttg gcaacaaacg atataggttc tctcttctgc 1560

cgtta 1565

<210> SEQ ID NO 191
<211> LENGTH: 1442
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- SEQ ID NO: 191, example 191: a designer hox-promoter-controlled Methyl-H4 folate: corrinoid iron-sulfur protein Methyltransferase DNA construct (1442 bp)

<400> SEQUENCE: 191

agaaaatctg gcaccacacc gcagaaatat aggggctagg agttgagggt actctggttc 60

gtcaagcatt tgggatgatt tcccctcaca agttcctcaa attattctcc tataaacaat 120

agatataagg tcaaaacttg agttatgagt gctgagtaaa aaattactct ccacgcctca 180

gaggtagata tgttaatccg ctaacaaatc tttacgatat gcctttaaaa agttcttgcc 240

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gaaacggtcg ttacccagca gtaaatcggt ggtggtgact gcagtcatga tttttccatc 300

caagggatcg agaatggccg cgtccatgcc gctcgccata catattgtca ggaagtaacg 360

gttgatgagc ttcctcttcg gcatgttaaa cgagatgttg cttaaaccgg atactgtctt 420

cactttaaat aacctcttga tttccctcag gcactggaaa aacatcaccg cgttggtgtg 480

gtttacggcc agggggagaa ccagcggatc gatatacagg ttgctcaaat cataattctt 540

cctgctcagg gtctctatca gtccctcagt tatcttgatc ctttcttcag ccgttttcgg 600

gataccattg tcgtcaaccg tcaggccgat taccgggcac tggtattcga gtacaagtgg 660

caatacttct tccagccgct ttttttccat ggatatggag ttgattatca ccttgctctt 720

atcgcccttg acggtctcca gacccttttt tattgcctcc cctgctgtgc tatcaatgca 780

taaaggtaca tcagttactt cttgcactgt atgcacaagc cactccatat cggccacttc 840

gtcacagtgg gcggtattta gatccaggta atctgctccc gcttccgcct gcctgcgggc 900

caggtcctgc acggccgcgg cgtttttgtc attaatgatt tgacggacac tggggatcgc 960

gctatttagt ttttcaccga tgattaacat tgaagtaagt aggaagcagg gagcagggga 1020

aagaaaattg acaactgtac aagattaatc gcgtctctga gcaatgacca aatacatcta 1080

cctccacggt tttcttccag ccccctatct gcgaaagcac aagatattag caagcgtttc 1140

gcccaaattc acatacagct aacaatccct gatctcaatg ctggtgaatt ttctcagtta 1200

acaatcacgc gccaaattca acaagttgcc gcaattttcc ctgataattc tgaaccaata 1260

acgctgatag gttctagttt aggcggttta actgctgctt atctaggaca gcgatattta 1320

caagtacaac gcttagtttt attagcgcca gtttggtttt ttatcccatt ggttgcccaa 1380

aatgggtgaa gaagctgtca caagttggca acaaacgata taggttctct cttctgccgt 1440

ta 1442

<210> SEQ ID NO 192
<211> LENGTH: 2942
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- SEQ ID NO: 192, example 192: a designer hox-promoter-controlled Corrinoid iron-sulfur protein DNA construct (2942 bp)

<400> SEQUENCE: 192

agaaaatctg gcaccacacc gcagaaatat aggggctagg agttgagggt actctggttc 60

gtcaagcatt tgggatgatt tcccctcaca agttcctcaa attattctcc tataaacaat 120

agatataagg tcaaaacttg agttatgagt gctgagtaaa aaattactct ccacgcctca 180

gaggtagata tgatggcttt aacaggatta aatatattta aattaacacc aaaaaagaat 240

tgtaaggatt gtggtttccc tacttgtcta gctttttcaa tgaaagtagc agcaggagct 300

gtggaaatag gaaaatgtcc tcatatgagt gacgaggcaa tggaaaaatt agctgaagct 360

actgcaccaa ttatgaagac aataactatt ggtaagggag ataatgaata taaattaggt 420

ggagaaactg ttttattccg tcatgaaaaa acttttgtaa atagaaatag atttgcagtt 480

gcattttccg atagtatgga tgatgcagaa gtagatgcta agatccaaca tataaaagat 540

gtagattatg ttagaatcgg tgaacaaatg aaaaccgaat ttgctgcaat aaaatatgca 600

ggaaataaag acaaatatct tgctttaata aacaaaataa aagcaagtgg agtaaaagta 660

gcttatgccc tagtttgtga agatgtagca gtaatgaaag aagctcttcc actagttaaa 720

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gatgaaaatc cattagttta tggagctaat aaagataatt ttaaagaaat ggttgaactt 780

gtaaaaggag ataaattagc tttaggtgta aaggcagacg gattggaagc tctttatggt 840

ttagtagaag aaatacaaaa attaggatat aagaacttag tacttgatcc aggtggaaaa 900

tccattaaag aagcttttga aaatacagtt caaattagaa gaataaatat tgaaggtcag 960

gatagaactt ttggatatcc ttctataata ttcctagatg aacttactaa agctgataaa 1020

tttatggaag tagctttatc tacattattt actttgaaat atggttcatt acttgtttta 1080

agtgatatgg attattcaag agcacttcct ctttatagta taagacagaa tgtatttaca 1140

gatccacaaa aaccaatgac agttgatttg ggtatacatg gaattaacaa cccagatgaa 1200

aactcaccag tattatgtac tgttgacttt gctcttactt acttcctagt ttcaggagaa 1260

gttgagagat ctaaagttcc agtatggatg gttataccag atgcaggcgg atattctgtt 1320

cttacatctt gggctgcagg taaatttact ggtgctgcaa tagctgatga aataaagaaa 1380

tgtggaatag cagagaagac taagaacaga actcttttaa tcccaggaaa ggttgcagtt 1440

ttgaaaggtg aattagagga acttcttcca gactggaata tagtaattag tagtacagaa 1500

gctatgttta ttcctaagtt attaaaagag ttaactgcta agtaaatgtt caaaaaacca 1560

acacaaaaat tttcaggcaa aattggtgaa gttgaaattg gaacaggaga aaaagcatta 1620

aaattaggag gagaatcagt attaccattt tatacttttg atggagatac aggaaatacc 1680

ccaaaagtag gtatggaaat tttagatgta tatccagaag actggataga tcctttaaag 1740

gacatataca aggatgttgc aaaagaccct gttaaatggg cacaatttgt agaagaaaaa 1800

tatagtccag attttatatg cctaagactt ataagtgctg atccaaacgg tacagatgct 1860

gcaccagaag attgtgctaa aacagctaaa gcagtagttg aagctataaa aactccatta 1920

gtagttgcag gtacaggaaa tcatgaaaaa gatgcaaaat tatttgaaaa agttgctcag 1980

gaaactgaag gacacaatat acttttaatg tcagcagtag aagataacta taagtcagta 2040

ggagctgcag gtgtaatggc ttataatgac aaagttgtag ctgaatcttc agttgatata 2100

aaccttgcaa aacaaataaa tattttaatg aatcaacttg gaatagacaa tacaaagttt 2160

gttgacaacg taggatgtgc agcaggtgga tatggttatg aatatgttat atcaacttta 2220

gacagagtaa agcttgcagc acttggtcaa gatgataaaa ctcttcaagt tcctataata 2280

agccctgttt ctttcgaagc ttgcaaagta aaagaagcaa tggattcaga agaagattca 2340

ccacaatggg gaagtcagga agacagaaca gtttccatgg aagttgcaac agcatccgga 2400

gtattagcat caggaacaga tgctgtaata ttacgtcatc caaaatctgt agaagtaatt 2460

agaaacttta ttaaggaatt attaggttaa tgaagtaagt aggaagcagg gagcagggga 2520

aagaaaattg acaactgtac aagattaatc gcgtctctga gcaatgacca aatacatcta 2580

cctccacggt tttcttccag ccccctatct gcgaaagcac aagatattag caagcgtttc 2640

gcccaaattc acatacagct aacaatccct gatctcaatg ctggtgaatt ttctcagtta 2700

acaatcacgc gccaaattca acaagttgcc gcaattttcc ctgataattc tgaaccaata 2760

acgctgatag gttctagttt aggcggttta actgctgctt atctaggaca gcgatattta 2820

caagtacaac gcttagtttt attagcgcca gtttggtttt ttatcccatt ggttgcccaa 2880

aatgggtgaa gaagctgtca caagttggca acaaacgata taggttctct cttctgccgt 2940

ta 2942

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<210> SEQ ID NO 193
<211> LENGTH: 4859
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- SEQ ID NO: 193, example 193: a designer hox-promoter-controlled CO dehydrogenase/acetyl-CoA synthase DNA construct (4859 bp)

<400> SEQUENCE: 193

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agatataagg tcaaaacttg agttatgagt gctgagtaaa aaattactct ccacgcctca 180

gaggtagata tgatgactga ttttgataaa atcttcgagg gtgctattcc agaaggtaaa 240

gagccggtag ccctgttccg ggaggtttac cacggcgcca ttacagctac cagttacgcg 300

gaaatccttt taaaccaggc catccggacc tatggtcccg accatcccgt cggttatcct 360

gatacagcct attacctgcc ggttattcgc tgtttcagcg gggaagaggt caaaaaactg 420

ggggatttac cacctatttt aaaccgcaag cgagcgcagg taagccctgt cctgaatttc 480

gagaatgccc gcctggccgg ggaagccacc tggtatgcgg ccgagatcat tgaagccctg 540

cgttaccttа aatataagcc tgatgaaccc ctcctgcccc caccctggac gggtttcatc 600

ggcgacccgg ttgtccgccg tttcggtatc aagatggtcg actggaccat tccgggtgaa 660

gctattatcc tgggtcgagc caaagactcg aaggccctgg ccaaaatcgt caaggaactc 720

atgggtatgg gctttatgct cttcatctgt gatgaagcgg tagaacagct gctggaagaa 780

aacgtcaaac tggggattga ctatatcgcc tatcccctgg ggaacttcac ccagattgtt 840

catgccgcca actatgccct gcgggctggt atgatgttcg gtggcgttac cccgggtgcc 900

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gactatgata aaatagtcca gatagccatg gagacccgtg ggatcaagct caccaagatc 1140

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gatatgtacg tagaaatggg cggcaaccgg acgccggcct ttgagctggt acgcaccgtt 1260

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ccggaaggga gcaaactgcc cctgggcatt ctggtggaca tctatggccg taaaatgcag 1380

gccgattttg aaggagtcct cgaacggcgc atccacgact tcatcaacta cggtgaaggt 1440

ctctggcaca ccggccagcg taacatcaac tggttgcggg tcagcaaaga tgccgtagcc 1500

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attgatccca ttaagggtat ctggaagagt gtaaatgact atctctatac agcttccaac 1920

cgtaacctgg aacaggtctg cctgtacacc cttatggaga atcccatgac ctcctgcggt 1980

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tgctttgagg ccattatggc catcctgccg gagtgcaacg gcatcatgat taccaccagg 2040

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cctgttaacc tggtcttcag cgccatcagg gtagccctgg ctgactatac gggtgaacat 3120

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aacatggggg tcctggatcc ggatcaagtc aacttcgtcc tccatggcca taatcccttg 3240

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gccaaaggca tcaacctggt gggtatctgc tgcaccggta acgaagtcct gatgcgccag 3360

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gacgccatgt gcgtcgacgt ccagtgtatt atgccttcca tcagcgccgt agccgagtgt 3480

tatcataccc ggatcatcac tactgccgat aacgccaaga ttcccggtgc ctaccatatc 3540

gactatcaaa cggctacggc tatcgaaagc gcgaaaaccg ccatccgcat ggccatcgag 3600

gcattcaagg aaagaaaaga aagtaaccgt ccggtttaca tcccccagat taagaaccgg 3660

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aatcccatcc gggtactcaa ccaggccatc ctggacggtg aactggctgg cgtagcctta 3780

atctgcgggt gtaacaacct caaagggttc caggataact cccacctgac ggtaatgaaa 3840

gaactgctga aaaataatgt ctttgtggtg gctacgggtt gctccgccca ggccgccgga 3900

aagcttggcc tcctggatcc ggccaatgtg gaaacctact gcggcgatgg tctcaagggc 3960

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ccacggtttt cttccagccc cctatctgcg aaagcacaag atattagcaa gcgtttcgcc 4560

caaattcaca tacagctaac aatccctgat ctcaatgctg gtgaattttc tcagttaaca 4620

atcacgcgcc aaattcaaca agttgccgca attttccctg ataattctga accaataacg 4680

ctgataggtt ctagtttagg cggtttaact gctgcttatc taggacagcg atatttacaa 4740

gtacaacgct tagttttatt agcgccagtt tggtttttta tcccattggt tgcccaaaat 4800

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<210> SEQ ID NO 194
<211> LENGTH: 6428
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- SEQ ID NO: 194, example 194: a designer hox-promoter-controlled F420 systhesis enzymes DNA construct (6428 bp)

<400> SEQUENCE: 194

agaaaatctg gcaccacacc gcagaaatat aggggctagg agttgagggt actctggttc 60

gtcaagcatt tgggatgatt tcccctcaca agttcctcaa attattctcc tataaacaat 120

agatataagg tcaaaacttg agttatgagt gctgagtaaa aaattactct ccacgcctca 180

gaggtagata tgatgaaagt attgattgat ggagaggatt ttgacagcgg cgaccattat 240

gaagtaaaaa acccatatga tggtgagctt gtagatactg ttccaatttg ttttaggcaa 300

gatgtagata gggccataga tgcagcaaat agggctaaaa aggaattgca ggatatgtct 360

gcaaaggaag tgtccaataa tctttattct gcttatgaag agctcgaatc aagaagcgaa 420

gaattggcaa agcttatagt cttggaggct ggaaagccaa ttaagcaggc tattggagag 480

cttaacaggt cttgtgagac attgaagttt gcagcagagg aagccaaaag aatctatgga 540

gaatctgtcc ctatagatgc tacaggttct gtagatgagc gttttttggc atttacaaag 600

aaagtacctt taggtgtcgt tggagcaata actccattca attatccggt taatcttgca 660

ttgcataaga tagctccagc cattgcagca aagaatgctg ttgtggtaaa gccttccact 720

gaagctccat tagctgcact taaattggtt gaaattattg ataatcattt cccaaatggg 780

gtgataaact ctgtaactgg ctatggaagt gaagttggag atgcattggt tgtttcagag 840

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gatgcagata ttgaaaaggc agttagtgct gcggtgtccg gcgcatttct attctccgga 1020

caggtttgca taggtgttaa aagaataata ttggataata agattgcaga tgagttcatt 1080

gacttatttg ttaaagaggc aagtaaattg aagatgggca atcctatgga tgagtctaca 1140

gatatcggtc cgcttataaa tgaaaatgct tcaatcaatg ttgaaactgc agtaaacaat 1200

gctataaaag atggggcaga acttattttg ggtggaaacc gtaaggactg cttctatgag 1260

ccaacaatat tggatggtgt caatatgtct atggaccttg ttgcaaatga aacattcgga 1320

ccagttgcac ctatcataag ggtagataga atagatgagg caataaaagt ggcaaatgac 1380

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accagatacg gtcttcaagc aggtgttttc actgaaaatg ttcatagtgc attaagatgt 1440

gcaaatgaga tagatgcagg ttcagtctta atcaataagg aatccacttt cagaacagat 1500

gccatgccat ttgggggatt caaatcaagt ggaatgggta aggaaggaat taaatatgca 1560

gttgaggata tgtgcaagtt taaattgatt gcttttaatt gtaggtgaat gaagacctgc 1620

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cccctcatag ggaaaaccga tatcactgaa ctcctccaca gggcatccca ctttgatgtt 1980

gtgatagccc ctgccaaggg tggcgggacc aacaccctga tattcaggcc agggtccatg 2040

aggctgaggt ttggtgactg cagcttcttt gagcatgtga gtgaagctga gagtaggggt 2100

ctcagcgtct cagtgtatga ctcattctac ctttcactgg acgttaacac agcagaggac 2160

ctcggggaga taatactcca tggagaaggg acccatgcaa gggagtacct cagaaagctc 2220

agtttcatcg tgaggccctc aaggggttct gacaggcttg aggtttcaag atcattctag 2280

atgaagataa ctattctttc aggcggaact ggaaccccaa aattaataca gggttttaaa 2340

gaaattcttc caaacgaaga tatttcggtt attgtaaaca ctggtgaaga tacttatatt 2400

ggcgacattt acctgtcccc tgatattgat actgttttgt acacgttttc taatctgata 2460

aatgacgaaa cctggtatgg gctaaaaggg gatacattct tctgccatga acagcttaaa 2520

aattttggat ttgacgaagt tttgaggatt ggagataaag atcgggcatt aaaaatgcat 2580

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tcattatcaa taaactcaaa aatttatcca atgtccgatg aaaaaattga atccaaagtt 2700

ttaatcgaag aaaacaatga aaaaatcctt ttaaagtttc acgatttttg ggtgtcaaga 2760

cgcggaaatg caaaagtttt agatatattc tacgaaaact caaattatgc aaaagcagca 2820

gacggagttt taaaagcaat tgaggaaagc gattttgtga ttattggtcc atcaaacccg 2880

ataacctcaa ttggacctat tttaagcatt tctgaaataa aagatgcatt aaaagaaaag 2940

ctggtttttg cagtttcgcc aatagttggt gaaaatcctg taagtggacc tgctggaacg 3000

ctgatgcatg caaaaggcta ccctgtgaat gcagttggag tttatgaata ttataaagat 3060

attgtagatg ttttagtttt agacaatagt gatattaaca aaaagaaaga aatgaattgt 3120

gaagttttat atgctaatac gataatgaag actattgatg ataaaataac tctcgcaaga 3180

aatattctcg actattataa atccagataa atgtcagttc aggtaacggg aatttccgga 3240

atcccgctca ttcagaaagg cgatgatctc ccggcaataa tctgcagaaa taccacgttc 3300

gaagacgagg atatcctttg tatagcatca acgatcgttt cgaaagcaaa agggtatacc 3360

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agtaatatag aaggcgaaaa tatcatcatc cttccaaaag acccctcggc cgagtgcaga 3600

gaaatacgtg actcaataaa aaagatcacg ggaaagaatg tcggcgtcat cgtgaccgac 3660

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gaagaagcgg tcgtcgatga gatcgccgcc ttctccaact tcattatggg ggagagcaac 3840

aacgggatcc cggccgtgaa attttccggc tgcggtacct ggaaaggcca cgactcgctc 3900

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cgtttcgccc aaattcacat acagctaaca atccctgatc tcaatgctgg tgaatttttct 6180

cagttaacaa tcacgcgcca aattcaacaa gttgccgcaa ttttccctga taattctgaa 6240

ccaataacgc tgataggttc tagtttaggc ggtttaactg ctgcttatct aggacagcga 6300

tatttacaag tacaacgctt agttttatta gcgccagttt ggtttttttat cccattggtt 6360

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tgccgtta 6428

<210> SEQ ID NO 195
<211> LENGTH: 1778
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- SEQ ID NO: 195, example 195: a designer hox-promoter-controlled Pyridoxal phosphate-dependent L-tyrosine decarboxylase(mfnA for methanofuran synthesis) DNA construct (1778 bp)

<400> SEQUENCE: 195

agaaaatctg gcaccacacc gcagaaatat aggggctagg agttgagggt actctggttc 60

gtcaagcatt tgggatgatt tcccctcaca agttcctcaa attattctcc tataaacaat 120

agatataagg tcaaaacttg agttatgagt gctgagtaaa aaattactct ccacgcctca 180

gaggtagata tgttgaggga gcatggggtc gacgaagata cgataatacg ggagctaaag 240

ggcgcctgtg cgaggaacgt cccgtacgag cgcgtgctca gctccatgtg cacgaccccg 300

catcccatcg ccattaaagc ccataaagag ttcatcgtct ctaacctggg cgaccccagg 360

ctttttccgg gtacggcctc gctcgagcat gcctgtatcg gcatgctggg cgagcttttg 420

catttgccat ccgccgtggg ctatatcact accgggggca ccgagagcaa tattcaggcc 480

cttcgtacgg cccgtcagtt aaaacacgtc gacccgggca aggccaacat cgtgctgccc 540

gagtccgcac attattcgtt tgataaggcg gcccagatgc tgggcgtatc cctccggcgc 600

acaccgcttg acgacgaaat gaaagccgac atggacgcca tggccggcct cgtcgataaa 660

aacaccatcg ccctcgtggc cgtcgccggc accacggagt tcgggcaggt cgaccccata 720

ccggccatca gtaagctggc gctcgatgag aacatctttt tacacgtcga cgccgccttc 780

ggcggcttcg tcataccgtt catgaaagac ccgtcgaagt acaggttcga cttcgagctc 840

cccggcgtca tgtccatcgc catcgacccc cacaagatgg gcatgagcac gataccctcc 900

ggagggctgc tttaccggga cgagcgccac atgaagtcgc ttgagatcag cgcccagtac 960

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atggataaca ccatgttcct ccgggacagc ctggtcgaca tggacattga gctggccctc 1140

gagcccatta tgaacatagt gacggcgaag ctgcccgatg cgcagtcgac ccgcaagaag 1200

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gtcatgcccc acgtcaccag ggacgtcatc gaggcgttca tggccgacct caaaaaaata 1320

tcgtagtgaa gtaagtagga agcagggagc aggggaaaga aaattgacaa ctgtacaaga 1380

ttaatcgcgt ctctgagcaa tgaccaaata catctacctc cacggttttc ttccagcccc 1440

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ctatctgcga aagcacaaga tattagcaag cgtttcgccc aaattcacat acagctaaca 1500

atccctgatc tcaatgctgg tgaatttttct cagttaacaa tcacgcgcca aattcaacaa 1560

gttgccgcaa ttttccctga taattctgaa ccaataacgc tgataggttc tagtttaggc 1620

ggtttaactg ctgcttatct aggacagcga tatttacaag tacaacgctt agttttatta 1680

gcgccagttt ggtttttttat cccattggtt gcccaaaatg ggtgaagaag ctgtcacaag 1740

ttggcaacaa acgatatagg ttctctcttc tgccgtta 1778

<210> SEQ ID NO 196
<211> LENGTH: 3215
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- SEQ ID NO: 196, example 196: a designer hox-promoter-controlled Methanopterin synthesis enzymes DNA construct (3215 bp)

<400> SEQUENCE: 196

agaaaatctg gcaccacacc gcagaaatat aggggctagg agttgagggt actctggttc 60

gtcaagcatt tgggatgatt tcccctcaca agttcctcaa attattctcc tataaacaat 120

agatataagg tcaaaacttg agttatgagt gctgagtaaa aaattactct ccacgcctca 180

gaggtagata tgatgacagt ttcagaattt ccagatactc aggataaaca accatccatt 240

ccaatatcac taacaagagt tggagtaaca ggtgtaaaga aattaataaa aataaaaaga 300

gaagataaac gtcctattat tctaatacca acatttgatg cttttgtaga tttacctagt 360

actcagaaag gagtacacat gtctagaaat ccagaagcta tatctgaaat tgttgatgag 420

gctgcaaatc aatcggaaat tcatcttgaa aatatatgtg caaatcttgt aaaaagatta 480

cttgaaaaac atgaatatgc attacatgca gaaacagagg caaggggaga atatattata 540

aataaattat ctccagtatc taaaagaaaa acacaggaaa caacacatat catagcaaga 600

gcaattgcta tgaaagatga tgagggtaat atttctgtta gaaaaatgat tggtgcagaa 660

gttattggaa tgactgtatg tccatgtgca caagaatctg ttgaaaagga ttctaaagat 720

aaattactgg aatttttaga tgaagaaact acacaaaaag tgttggatgt agtaacattt 780

gcttctcata atcaaagggg tgttgggaca atacttcttg aagtaccaga aaaacaagat 840

gttaatgtgg atgatttaat aaaaataata caggatgcta tgagttctcc tgtttgtgaa 900

atattaaaac gtccagatga aaatagaatt gtaacaaatg cacatcaaaa tccagtattt 960

gttgaggatt gtgtaagaaa catggtaata ggattacttg aaaaatatcc taatttacct 1020

gatgattctg tagttacaat taaacaagta aatcaagaaa gtattcatca acataatgct 1080

tatgctgaaa aagttgcatc ttttggtaaa ttacgagaag aaaataagga gtagatgaat 1140

gatctgatcg ctcttgcaga ggatattaag aacgaaaaat taaaaaaaaa ggttgtcgaa 1200

tttataaacg atccgattcc aaaacatcct gaaattgaaa gtactggcat aacacttgaa 1260

acctcccccg caagcgttaa aagacatcac aaatactccg gaggattaat cgaacatacg 1320

atcgcagtta caaaaatggc tgtaaaaatg gctgaagcct tggaagaaac atatggaatt 1380

gaattaaata gagatttgct aatttccgga ggaatactcc acgatcttat gaaaccacaa 1440

aattatcagt taaaagacgg aaaattcgac catctttcaa attttcacct cgaccatttg 1500

acacttggaa ttgcagaact gtacagaagg gactttccac ttgaagttat aaaagttgta 1560

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gctagccatc acggagatca tggtcctgta agtccagatt caatagaagc gtggctaatt 1620

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agagctagag aatttggaat tgatgattca caaatatata aaatcgtcaa tccattaaaa 1740

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ttggaaataa aggatgaata attgttaagg atacgaacac cttcccgcct ccacatgacg 1860

ctcatcgaca tgaacggaga gatcggcagg atcgacggcg ggatcggaat aacgctcgac 1920

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gacctgcgcg agcgcatgcg caaggcatgc gaggcattcg gcccgggata tggcgtggag 2040

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tagtgaagta agtaggaagc agggagcagg ggaaagaaaa ttgacaactg tacaagatta 2820

atcgcgtctc tgagcaatga ccaaatacat ctacctccac ggttttcttc cagcccccta 2880

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gccgcaattt tccctgataa ttctgaacca ataacgctga taggttctag tttaggcggt 3060

ttaactgctg cttatctagg acagcgatat ttacaagtac aacgcttagt tttattagcg 3120

ccagtttggt tttttatccc attggttgcc caaaatgggt gaagaagctg tcacaagttg 3180

gcaacaaacg atataggttc tctcttctgc cgtta 3215

<210> SEQ ID NO 197
<211> LENGTH: 4226
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- SEQ ID NO: 197, example 197: a designer hox-promoter-controlled Coenzyme M synthesis enzymes DNA construct (4226 bp)

<400> SEQUENCE: 197

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gtcaagcatt tgggatgatt tcccctcaca agttcctcaa attattctcc tataaacaat 120

agatataagg tcaaaacttg agttatgagt gctgagtaaa aaattactct ccacgcctca 180

gaggtagata tgttaaagat tcacctttcc gagagtatct cccctcaagc ctcttcttat 240

ggtttcaagg gctgttatct cttcgggggg tatgtttcca aggttaacgt ctggtcctat 300

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tatacctata ttatggccgc tctcccgggc ctccatgagc accatgcagg ctccagcttt 480

gaggtcggcc ctgacaagtt caaccctatc ctccgggctg agaagtctgt cccttaccgg 540

gtccttttta ccaacctctg atatgatctg gaacccctcg ttgaccgctt tctctataag 600

ttcacatttt tcatcggttt caatctcaac ggttccattt gatatttcca gtgtttcaaa 660

accaaggctt cttgcctcgt caaagtactc ctgaatttta tcgttgagat aggcgatctc 720

aaatagggtg cccccaggat aggcctccac atcgaatgaa cggtacatct caatttttc 780

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gcaggggagc gtggtggtga gaccctgcca ggattcctgg ccaactcccc actggaggtg 1200

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aaatccaggt cagccaggag gctcagggaa cttggttttg ccggtgatat tgaatactgc 1560

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aaggccaggg ataccggcgt cgggcttgtt ggtgtccatg actcaaacca ctttggtgtt 1980

gccggatact actcggacat ggcggtcatg aacgacatga taggggttgt gatagcaaat 2040

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gccataggga tcccatcaaa caggcactat gtctcggttg acatggcaac ctcagcatcc 2160

gccaggggca aactcctgga ggccgccagg aagggtgaga gtatacccga aaacatagca 2220

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gaaaagcccg agaacctcac catcatttgc ttcgataaca gcgcccacgg ctccactggc 3540

aaccagaaga cctattcgga gagcatggac ctcgagcttc tggcgaaggc gttcggcatc 3600

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cctttgacac cggtagagat caaggagcgg tttatggggg cggtcacgcg ctgatgaagt 3780

aagtaggaag cagggagcag gggaaagaaa attgacaact gtacaagatt aatcgcgtct 3840

ctgagcaatg accaaataca tctacctcca cggttttctt ccagcccccc atctgcgaaa 3900

gcacaagata ttagcaagcg tttcgcccaa attcacatac agctaacaat ccctgatctc 3960

aatgctggtg aattttctca gttaacaatc acgcgccaaa ttcaacaagt tgccgcaatt 4020

ttccctgata attctgaacc aataacgctg ataggttcta gtttaggcgg tttaactgct 4080

gcttatctag gacagcgata tttacaagta caacgcttag ttttattagc gccagtttgg 4140

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gatataggtt ctctcttctg ccgtta 4226

<210> SEQ ID NO 198
<211> LENGTH: 5198
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Construct- SEQ ID NO: 198, example 198: a designer hox-promoter-controlled Coenzyme B synthesis enzymes DNA construct (5198 bp)

<400> SEQUENCE: 198

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gtcaagcatt tgggatgatt tcccctcaca agttcctcaa attattctcc tataaacaat 120

agatataagg tcaaaacttg agttatgagt gctgagtaaa aaattactct ccacgcctca 180

gaggtagata tgttgcccga tcgggtacgg atcttcgaca cgacgctaag agacggtgag 240

cagacaccgg gcgtcagcct cacggtggag gaaaaggtcg agatcgcgag gaagttggac 300

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gaggacgcca cacggacgga ccgggactac ctactcgagg tctataaagc taccgtggaa 660

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1. A method for autotrophic production of butanol and related higher alcohols comprising:

introducing a transgenic autotrophic organism into a reactor system, the transgenic autotrophic organism comprising transgenes coding for a set of enzymes configured to confer a hydrogenotrophic pathway for production of a higher alcohol comprising at least four carbon atoms;

using reducing power such as NADPH, reduced ferredoxin, and energy ATP associated with the transgenic autotrophic organism acquired from hydrogenotrophic process in the biological reactor to synthesize the higher alcohol from carbon dioxide and water; and

using a product separation process to harvest the synthesized alcohol from the photobioreactor.

2. The method of claim **1**, wherein:

said designer transgenic autotrophic organism comprises at least one of designer Calvin-cycle-channeled pathways and designer hydrogenotrophic pathways for producing at least one of the higher alcohols selected from the group consisting of: 1-butanol, 2-methyl-1-butanol, isobutanol, 3-methyl-1-butanol, 1-hexanol, 1-octanol, 1-pentanol, 1-heptanol, 3-methyl-1-pentanol, 4-methyl-1-hexanol, 5-methyl-1-heptanol, 4-methyl-1-pentanol, 5-methyl-1-hexanol, 6-methyl-1-heptanol and combinations thereof.

3. The method of claim **1**, wherein the transgenic autotrophic organism comprises at least one of a transgenic designer plant or transgenic designer plant cell, or bacterial cell selected from the group consisting of blue-green algae (oxyphotobacteria including cyanobacteria and oxychlorobacteria), hydrogenotrophic bacteria, methanogens, aquatic plants, plant cells, green algae, red algae, brown algae, diatoms, marine algae, freshwater algae, salt-tolerant algal strains, cold-tolerant algal strains, heat-tolerant algal strains, antenna-pigment-deficient mutants, butanol-tolerant algal strains, higher-alcohols-tolerant algal strains, butanol-tolerant oxyphotobacteria, butanol-tolerant hydrogenotrophic bacteria and methanogens, higher-alcohols-tolerant oxyphotobacteria and hydrogenotrophic bacteria or methanogens.

4. The method of claim **1**, wherein said transgenic autotrophic organism comprises a set of designer genes that express a designer anaerobic hydrogenotrophic butanol-production-pathway system comprising: energy converting hydrogenase (Ech), [NiFe]-hydrogenase (Mvh), Coenzyme F_{420}-reducing hydrogenase (Frh), native (or heterologous) soluble hydrogenase (SH), heterodissulfide reductase (Hdr), formylmethanofuran dehydroganse, formyl transferase, 10-methenyl-tetrahydromethanopterin cyclohydrolase, 10-methylene-H_4 methanopterin dehydrogenase, 10-methylene-H_4-methanopterin reductase, methyl-H_4-methanopterin: corrinoid iron-sulfur protein methyltransferase, corrinoid iron-sulfur protein, CO dehydrogenase/acetyl-CoA synthase, thiolase, 3-hydroxybutyryl-CoA dehydrogenase, crotonase, butyryl-CoA dehydrogenase, butyaldehyde dehydrogenase, and butanol dehydrogenase.

5. The method of claim **1**, wherein the transgenic autotrophic organism comprises bacteria selected from the group consisting of *Thermosynechococcus elongatus* BP-1, *Nostoc* sp. PCC 7120, *Synechococcus elongatus* PCC 6301, *Syncechococcus* sp. strain PCC 7942, *Syncechococcus* sp. strain PCC 7002, *Syncechocystis* sp. strain PCC 6803, *Prochlorococcus marinus* MED4, *Prochlorococcus marinus* MIT 9313, *Prochlorococcus marinus* NATL1A, *Prochlorococcus* SS120, *Spirulina platensis* (*Arthrospira platensis*), *Spirulina pacifica, Lyngbya majuscule, Anabaena* sp., *Synechocystis* sp., *Synechococcus elongates, Synechococcus* (MC-A), *Trichodesmium* sp., *Richelia intracellularis, Synechococcus* WH7803, *Synechococcus* WH8102, *Nostoc punctiforme, Syncechococcus* sp. strain PCC 7943, *Synechocyitis* PCC 6714 phycocyanin-deficient mutant PD-1, *Cyanothece* strain 51142, *Cyanothece* sp. CCY0110, *Oscillatoria limosa, Lyngbya majuscula, Symploca muscorum, Gloeobacter violaceus, Prochloron didemni, Prochlorothrix hollandica, Synechococcus* (MC-A), *Trichodesmium* sp., *Richelia intracellularis, Prochlorococcus marinus, Prochlorococcus* SS120, *Synechococcus* WH8102, *Lyngbya majuscula, Symploca muscorum, Synechococcus bigranulatus, cryophilic Oscillatoria* sp., *Phormidium* sp., *Nostoc* sp.-1, *Calothrix parietina*, thermophilic *Synechococcus bigranulatus, Synechococcus lividus*, thermophilic *Mastigocladus laminosus, Chlorogloeopsis fritschii* PCC 6912, *Synechococcus vulcanus, Synechococcus* sp. strain MA4, *Synechococcus* sp. strain MA19, *Methanocella paludicola* SANAE, *Acinetobacter baumannii* ABNIH3, *Acinetobacter baumannii* ABNIH4, *Acinetobacter* sp. DR1, *Agrobacterium* sp. H13-3; *Agrobacterium vitis* S4, *Alcaligenes* sp., *Allochromatium vinosum* DSM 180, *Amycolatopsis mediterranei S*699, *Anoxybacillus flavithermus* WK1, *Aquifex aeolicus* VF5, *Archaeoglobus fulgidus* DSM 4304, *Archaeoglobus veneficus* SNP6, *Azospirillum* sp. B510, *Burkholderia cenocepacia* HI2424, *Caldicellulosiruptor bescii* DSM 6725, *Carboxydothermus hydrogenoformans, Centipeda periodontii* DSM 2778, *Clostridium autoethanogenum, Clostridium ragsdalei, Clostridium sticklandii* DSM 519, *Clostridium sticklandii, Corynebacterium glutamicum, Cupriavidus metallidurans CH*34, *Cupriavidus necator* N-1, *Desulfobacca acetoxidans* DSM 11109, *Exiguobacterium* sp. AT1b, *Ferrimonas balearica* DSM 9799, *Ferroglobus placidus* DSM 10642, *Geobacillus kaustophilus* HTA426, *Helicobacter bilis* ATCC 43879, *Herbaspirillum seropedicae* SmR1, *Hydrogenobacter thermophilus* TK-6, *Hydrogenovibrio marinus, Klebsiella variicola* At-22, *Methanobacterium* sp. SWAN-1, *Methanobrevibacter ruminantium* M1, *Methanocaldococcus*

fervens AG86, *Methanocaldococcus infernus* ME, *Methanocaldococcus jannaschii*, *Methanocaldococcus* sp. FS406-22, *Methanocaldococcus vulcanius* M7, *Methanococcus aeolicus* Nankai-3, *Methanococcus maripaludis* C6, *Methanococcus maripaludis* S2, *Methanococcus voltae* A3, *Methanocorpusculum labreanum* Z, *Methanoculleus marisnigri* JR1, *Methanohalophilus mahii* DSM 5219, *Methanolinea tarda* NOBI-1, *Methanoplanus petrolearius* DSM 11571, *Methanoplanus petrolearius*, *Methanopyrus kandleri* AV19, *Methanoregula boonei* 6A8, *Methanosaeta harundinacea* 6Ac, *Methanosalsum zhilinae* DSM 4017, *Methanosarcina acetivorans* C2A, *Methanosarcina barkeri* str. *Fusaro*, *Methanosarcina mazei* Go1, *Methanosphaera stadtmanae*, *Methanospirillum hungatei* JF-1, *Methanothermobacter marburgensis* str. *Marburg*, *Methanothermobacter marburgensis*, *Methanothermobacter thermautotrophicus*, *Methanothermococcus okinawensis* IH1, *Methanothermus fervidus* DSM 2088, *Methylobacillus flagellates*, *Methylobacterium organophilum*, *Methylococcus capsulatus*, *Methylomicrobium kenyense*, *Methylomonas methanica* MC09, *Methylomonas* sp. LW13, *Methylosinus* sp. LW2, *Methylosinus trichosporium* OB3b, *Methylotenera mobilis* JLW8, *Methylotenera versatilis* 301, *Methylovorus glucosetrophus* SIP3-4, *Moorella thermoacetica* ATCC 39073, *Moorella thermoacetica*, *Oligotropha carboxidovorans* OM5, *Paenibacillus terse* HPL-003, *Pelotomaculum thermopropionicum* SI, *Planctomyces brasiliensis* DSM 5305, *Pyrococcus furiosus* DSM 3638, *Pyrococcus horikoshii* OT3, *Pyrococcus yayanosii* CH1, *Ralstonia eutropha* H16, *Rubrivivax* sp., *Selenomonas noxia* ATCC 43541, *Shewanella baltica* BA175, *Stenotrophomonas* sp. SKA14, *Synechococcus* sp. JA-2-3B' a(2-13), *Synechococcus* sp. JA-3-3Ab, *Thermococcus gammatolerans* EJ3, *Thermococcus kodakarensis* KOD1, *Thermococcus onnurineus* NA1, *Thermococcus* sp. 4557, *Thermodesulfatator indicus* DSM 15286, *Thermofilum pendens* Hrk 5, *Thermotoga lettingae* TMO, *Thermotoga petrophila* RKU-1, *Thiocapsa roseopersicina*, *Thiomonas intermedia* K12, *Xanthobacter autotrophicus*, *Yersinia pestis Antigua*, and *Thermosynechococcus elongatus*.

6. The method of claim **1**, wherein the transgenic autotrophic organism comprises a biosafety-guarded feature selected from the group consisting of a designer proton-channel gene inducible under pre-determined inducing conditions, a designer cell-division-cycle iRNA gene inducible under pre-determined inducing conditions, a high-CO_2-requiring mutant as a host organism for transformation with designer biofuel-production-pathway genes in creating designer cell-division-controllable autotrophic organisms, and combinations thereof; and wherein said transgenic autotrophic organism comprises a set of designer genes exemplified with exemplary designer DNA constructs of SEQ ID NOS. 1-198 shown in the sequence listings for expressing at least one of the enzymes selected from the group consisting of oxygen-tolerant soluble hydrogenase (SH), oxygen-tolerant membrane bound hydrogenase (MBH), energy converting hydrogenase (Ech), methyl-H4MPT: coenzyme-M methyltransferase (Mtr), methyl-coenzyme M reductase (Mcr), heterodissulfide reductase (Hdr), [NiFe]-hydrogenase (Mvh), Coenzyme F_{420}-reducing hydrogenase (Frh), A_1A_o-ATP synthase, formate dehydroganse, 10-formyl-H_4 folate synthetase, methenyltetrahydrofolate cyclohydrolase, 10-methylene-H_4 folate dehydrogenase, 10-methylene-H_4 folate reductase, methyl-H_4 folate: corrinoid iron-sulfur protein methyltransferase, corrinoid iron-sulfur protein, CO dehydrogenase/acetyl-CoA synthase, formylmethanofuran dehydroganse, formyl transferase, 10-methenyl-tetrahydromethanopterin cyclohydrolase, 10-methylene-H_4 methanopterin dehydrogenase, 10-methylene-H_4-methanopterin reductase, methyl-H_4-methanopterin: corrinoid iron-sulfur protein methyltransferase, corrinoid iron-sulfur protein, CO dehydrogenase/acetyl-CoA synthase, thiolase, 3-hydroxybutyryl-CoA dehydrogenase, crotonase, butyryl-CoA dehydrogenase, butyaldehyde dehydrogenase, butanol dehydrogenase, 2-keto acid decarboxylase, alcohol dehydrogenase, 2-methylbutyraldehyde reductase, 3-methylbutanal reductase, hexanol dehydrogenase, octanol dehydrogenase, and short-chain alcohol dehydrogenase.

7. The method of claim **1**, wherein the set of enzymes comprises at least one of the enzymes selected from the group consisting of NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase, NAD-dependent glyceraldehyde-3-phosphate dehydrogenase, phosphoglycerate mutase, enolase, pyruvate kinase, citramalate synthase, 2-methylmalate dehydratase, 3-isopropylmalate dehydratase, 3-isopropylmalate dehydrogenase, 2-isopropylmalate synthase, isopropylmalate isomerase, 2-keto acid decarboxylase, alcohol dehydrogenase, NADPH-dependent alcohol dehydrogenase, and butanol dehydrogenase.

8. The method of claim **1**, wherein the set of enzymes comprises at least one of the enzymes conferring a designer anaerobic hydrogenotrophic system and butanol-production pathway selected from the group consisting of energy converting hydrogenase (Ech), [NiFe]-hydrogenase Mvh, Coenzyme F_{420}-reducing hydrogenase (Frh), soluble hydrogenase (SH), reduced ferredoxin (Fd_{red}^{2-}), and heterodissulfide reductase (Hdr), NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase, NAD-dependent glyceraldehyde-3-phosphate dehydrogenase, phosphoglycerate mutase, enolase, phosphoenolpyruvate carboxylase, aspartate aminotransferase, aspartokinase, aspartate-semialdehyde dehydrogenase, homoserine dehydrogenase, homoserine kinase, threonine synthase, threonine ammonia-lyase, 2-isopropylmalate synthase, isopropylmalate isomerase, 3-isopropylmalate dehydrogenase, 2-keto acid decarboxylase, and NAD-dependent alcohol dehydrogenase, NADPH-dependent alcohol dehydrogenase, butanol dehydrogenase and combinations thereof.

9. The method of claim **1**, wherein the set of enzymes comprises at least one of the enzymes conferring a designer hydrogenotrophic methanogenic 2-methylbutanol-production pathway selected from the group consisting of methyl-H4MPT: coenzyme-M methyltransferase Mtr, A_1A_o-ATP synthase, methyl-coenzyme M reductase Mcr, energy converting hydrogenase (Ech), [NiFe]-hydrogenase (Mvh), Coenzyme F_{420}-reducing hydrogenase (Frh), soluble hydrogenase (SH), heterodissulfide reductase (Hdr), NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase, NAD-dependent glyceraldehyde-3-phosphate dehydrogenase, phosphoglycerate mutase, enolase, pyruvate kinase, citramalate synthase, 2-methylmalate dehydratase, 3-isopropylmalate dehydratase, 3-isopropylmalate dehydrogenase, acetolactate synthase, ketol-acid reductoisomerase, dihydroxy-acid dehydratase, 2-keto acid decarboxylase, NAD-dependent alcohol dehydrogenase, NADPH-dependent alcohol dehydrogenase, and 2-methylbutyraldehyde reductase.

10. The method of claim **1**, wherein the set of enzymes comprises at least one of the enzymes selected from the group consisting of membrane bound hydrogenase (MBH), soluble

hydrogenase (SH), NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase, NAD-dependent glyceraldehyde-3-phosphate dehydrogenase, phosphoglycerate mutase, enolase, phosphoenolpyruvate carboxylase, aspartate aminotransferase, aspartokinase, aspartate-semialdehyde dehydrogenase, homoserine dehydrogenase, homoserine kinase, threonine synthase, threonine ammonia-lyase, acetolactate synthase, ketol-acid reductoisomerase, dihydroxy-acid dehydratase, 2-keto acid decarboxylase, and NAD dependent alcohol dehydrogenase, NADPH dependent alcohol dehydrogenase, and 2-methylbutyraldehyde reductase.

11. The method of claim **1**, wherein the set of enzymes comprises at least one of the enzymes selected from the group consisting of methyl-H4MPT: coenzyme-M methyltransferase Mtr, A_1A_o-ATP synthase, energy converting hydrogenase (Ech), [NiFe]-hydrogenase Mvh, Coenzyme F_{420}-reducing hydrogenase (Frh), native (or heterologous) soluble hydrogenase (SH), reduced ferredoxin (Fd_{red}^{2-}), methyl-coenzyme M reductase Mcr, heterodissulfide reductase (Hdr), NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase, NAD-dependent glyceraldehyde-3-phosphate dehydrogenase, phosphoglycerate mutase, enolase, pyruvate kinase, acetolactate synthase, ketol-acid reductoisomerase, dihydroxy-acid dehydratase, 2-keto acid decarboxylase, and NAD-dependent alcohol dehydrogenase, and NADPH-dependent alcohol dehydrogenase.

12. The method of claim **1**, wherein the set of enzymes comprises at least one of the enzymes selected from the group consisting of membrane bound hydrogenase (MBH), soluble hydrogenase (SH), NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase, NAD-dependent glyceraldehyde-3-phosphate dehydrogenase, phosphoglycerate mutase, enolase, pyruvate kinase, acetolactate synthase, ketol-acid reductoisomerase, dihydroxy-acid dehydratase, 2-isopropylmalate synthase, 3-isopropylmalate dehydratase, 3-isopropylmalate dehydrogenase, 2-keto acid decarboxylase, and NAD-dependent alcohol dehydrogenase, NADPH-dependent alcohol dehydrogenase, and 3-methylbutanal reductase.

13. The method of claim **1**, wherein the set of enzymes comprises at least one of the enzymes conferring a designer anaerobic reductive-acetyl-CoA butanol-production pathway selected from the group consisting of: formate dehydroganse, 10-formyl-H_4 folate synthetase, methenyltetrahydrofolate cyclohydrolase, 10-methylene-H_4 folate dehydrogenase, 10-methylene-H_4 folate reductase, methyl-H_4 folate: corrinoid iron-sulfur protein methyltransferase, corrinoid iron-sulfur protein, CO dehydrogenase/acetyl-CoA synthase, thiolase, 3-hydroxybutyryl-CoA dehydrogenase, crotonase, butyryl-CoA dehydrogenase, butyaldehyde dehydrogenase, butanol dehydrogenase, and alcohol dehydrogenase.

14. The method of claim **1**, wherein the set of enzymes comprises at least one of the enzymes selected from the group consisting of membrane bound hydrogenase (MBH), soluble hydrogenase (SH), NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase, NAD-dependent glyceraldehyde-3-phosphate dehydrogenase, phosphoglycerate mutase, enolase, pyruvate kinase, citramalate synthase, 2-methylmalate dehydratase, 3-isopropylmalate dehydratase, 3-isopropylmalate dehydrogenase, 2-isopropylmalate synthase, isopropylmalate isomerase, 3-isopropylmalate dehydrogenase, designer isopropylmalate synthase, designer isopropylmalate isomerase, designer 3-isopropylmalate dehydrogenase, designer 2-keto acid decarboxylase, short-chain alcohol dehydrogenase, hexanol dehydrogenase, designer isopropylmalate synthase, designer isopropylmalate isomerase, designer 3-isopropylmalate dehydrogenase, designer 2-keto acid decarboxylase, and designer short-chain alcohol dehydrogenase.

15. The method of claim **1**, wherein the set of enzymes comprises at least one of the enzymes selected from the group consisting of membrane bound hydrogenase (MBH), soluble hydrogenase (SH), NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase, NAD-dependent glyceraldehyde-3-phosphate dehydrogenase, phosphoglycerate mutase, enolase, phosphoenolpyruvate carboxylase, aspartate aminotransferase, aspartokinase, aspartate-semialdehyde dehydrogenase, homoserine dehydrogenase, homoserine kinase, threonine synthase, threonine ammonia-lyase, 2-isopropylmalate synthase, isopropylmalate isomerase, 3-isopropylmalate dehydrogenase, designer isopropylmalate synthase, designer isopropylmalate isomerase, designer 3-isopropylmalate dehydrogenase, designer 2-keto acid decarboxylase, short-chain alcohol dehydrogenase, hexanol dehydrogenase, designer isopropylmalate synthase, designer isopropylmalate isomerase, designer 3-isopropylmalate dehydrogenase, designer 2-keto acid decarboxylase, and designer short-chain alcohol dehydrogenase.

16. The method of claim **1**, wherein the set of enzymes comprises at least one of the enzymes conferring a designer hydrogenotrophic Calvin-cycle-channeled pathway selected from the group consisting of membrane bound hydrogenase (MBH), soluble hydrogenase (SH), NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase, NAD-dependent glyceraldehyde-3-phosphate dehydrogenase, phosphoglycerate mutase, enolase, pyruvate kinase, citramalate synthase, 2-methylmalate dehydratase, 3-isopropylmalate dehydratase, 3-isopropylmalate dehydrogenase, acetolactate synthase, ketol-acid reductoisomerase, dihydroxy-acid dehydratase, designer isopropylmalate synthase, designer isopropylmalate isomerase, designer 3-isopropylmalate dehydrogenase, designer 2-keto acid decarboxylase, short-chain alcohol dehydrogenase, designer isopropylmalate synthase, designer isopropylmalate isomerase, designer 3-isopropylmalate dehydrogenase, designer 2-keto acid decarboxylase, and designer short-chain alcohol dehydrogenase.

17. The method of claim **1**, wherein the set of enzymes comprises at least one of the enzymes conferring a designer hydrogenotrophic Calvin-cycle-channeled pathway selected from the group consisting of membrane bound hydrogenase (MBH), soluble hydrogenase (SH), NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase, NAD-dependent glyceraldehyde-3-phosphate dehydrogenase, phosphoglycerate mutase, enolase, phosphoenolpyruvate carboxylase, aspartate aminotransferase, aspartokinase, aspartate-semialdehyde dehydrogenase, homoserine dehydrogenase, homoserine kinase, threonine synthase, threonine ammonia-lyase, acetolactate synthase, ketol-acid reductoisomerase, dihydroxy-acid dehydratase, designer isopropylmalate synthase, designer isopropylmalate isomerase, designer 3-isopropylmalate dehydrogenase, designer 2-keto acid decarboxylase, short-chain alcohol dehydrogenase, designer isopropylmalate synthase, designer isopropylmalate isomerase, designer 3-isopropylmalate dehydrogenase, designer 2-keto acid decarboxylase, and designer short-chain alcohol dehydrogenase.

18. The method of claim **1**, wherein the set of enzymes comprises at least one of the enzymes conferring a designer

hydrogenotrophic Calvin-cycle-channeled pathway selected from the group consisting of membrane bound hydrogenase (MBH), soluble hydrogenase (SH), NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase, NAD-dependent glyceraldehyde-3-phosphate dehydrogenase, phosphoglycerate mutase, enolase, pyruvate kinase, acetolactate synthase, ketol-acid reductoisomerase, dihydroxy-acid dehydratase, isopropylmalate synthase, dehydratase, 3-isopropylmalate dehydrogenase, designer isopropylmalate synthase, designer isopropylmalate isomerase, designer 3-isopropylmalate dehydrogenase, designer 2-keto acid decarboxylase, short-chain alcohol dehydrogenase, designer isopropylmalate synthase, designer isopropylmalate isomerase, designer 3-isopropylmalate dehydrogenase, designer 2-keto acid decarboxylase, and designer short-chain alcohol dehydrogenase.

19. The method of claim **1**, wherein the set of enzymes comprises at least one of the enzymes conferring a designer methanogenic hydrogenotrophic butanol-production-pathway selected from the group consisting of: methyl-H4MPT: coenzyme-M methyltransferase Mtr, A_1A_o-ATP synthase, methyl-coenzyme M reductase Mcr, energy converting hydrogenase (Ech), [NiFe]-hydrogenase (Mvh), Coenzyme F_{420}-reducing hydrogenase (Frh), soluble hydrogenase (SH), heterodissulfide reductase (Hdr), formate dehydroganse, 10-formyl-H_4 folate synthetase, methenyltetrahydrofolate cyclohydrolase, 10-methylene-H_4 folate dehydrogenase, 10-methylene-H_4 folate reductase, methyl-H_4 folate: corrinoid iron-sulfur protein methyltransferase, corrinoid iron-sulfur protein, CO dehydrogenase/acetyl-CoA synthase, thiolase, 3-hydroxybutyryl-CoA dehydrogenase, crotonase, butyryl-CoA dehydrogenase, butyaldehyde dehydrogenase, butanol dehydrogenase, and alcohol dehydrogenase.

20. The method of claim **1**, wherein the designer transgenic organism a designer autotrophic organism comprises a set of designer genes that express a designer methanogenic hydrogenotrophic butanol-production-pathway system comprising: methyl-H4MPT: coenzyme-M methyltransferase Mtr, A_1A_o-ATP synthase, methyl-coenzyme M reductase Mcr, energy converting hydrogenase (Ech), [NiFe]-hydrogenase (Mvh), Coenzyme F_{420}-reducing hydrogenase (Frh), soluble hydrogenase (SH), heterodissulfide reductase (Hdr), formate dehydroganse, 10-formyl-H_4 folate synthetase, methenyltetrahydrofolate cyclohydrolase, 10-methylene-H_4 folate dehydrogenase, 10-methylene-H_4 folate reductase, methyl-H_4 folate: corrinoid iron-sulfur protein methyltransferase, corrinoid iron-sulfur protein, CO dehydrogenase/acetyl-CoA synthase, thiolase, 3-hydroxybutyryl-CoA dehydrogenase, crotonase, butyryl-CoA dehydrogenase, butyaldehyde dehydrogenase, and butanol dehydrogenase; and wherein said autotrophic organism comprise a set of designer genes that express a designer methanogenic hydrogenotrophic butanol-production-pathway system comprising: methyl-H4MPT: coenzyme-M methyltransferase Mtr, native (or heterologous) A_1A_o-ATP synthase, methyl-coenzyme M reductase Mcr, energy converting hydrogenase (Ech), [NiFe]-hydrogenase (Mvh), Coenzyme F_{420}-reducing hydrogenase (Frh), native (or heterologous) soluble hydrogenase (SH), heterodissulfide reductase (Hdr), formylmethanofuran dehydroganse, formyl transferase, 10-methenyl-tetrahydromethanopterin cyclohydrolase, 10-methylene-H_4 methanopterin dehydrogenase, 10-methylene-H_4-methanopterin reductase, methyl-H_4-methanopterin: corrinoid iron-sulfur protein methyltransferase, corrinoid iron-sulfur protein, CO dehydrogenase/acetyl-CoA synthase, thiolase, 3-hydroxybutyryl-CoA dehydrogenase, crotonase, butyryl-CoA dehydrogenase, butyaldehyde dehydrogenase, and butanol dehydrogenase.

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